

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
 BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
 de-Desmaures, Québec, Canada, G3A 2N2
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 10 Canada, G1S 4J3
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 Lévis, Québec, Canada, G0S 2W0
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 15 PICARD, François J. ¹, 1245 de la Sapinière, Cap-
 Rouge, Québec, Canada, G1Y 1A1
 ROY, Paul H. ², 28 Charles Garnier, Loretteville,
 Québec, Canada, G2A 2X8

20 ¹:Canadian citizenship
²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR
 25 USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND
 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO
 RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL,
 FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL
 SPECIMENS FOR DIAGNOSIS

30 (iii) NUMBER OF SEQUENCES: 2297

(iv) CORRESPONDENCE ADDRESS:

35 (A) ADDRESSEE:
 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

40 (v) COMPUTER READABLE:

45 (A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING:
 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

55 (A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:
- (B) REGISTRATION NUMBER:

5

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE:
- (B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

	CAAAC	TCGTG	AGCAC	ATCCT	TCTTT	CTCGT	CAGGT	AGGTG	TACCT	TACAT	50
	CATCG	TATTC	TTAAAC	AAAT	GCGAC	CTTGT	TGATG	ACGAA	GAATT	ACTTG	100
20	AATTAG	TAGA	AATGGA	AGTA	CGTGA	AACTTC	TTTCT	ACTTA	TGACT	TCCCA	150
	GGTGAT	GACA	CTCCAG	TAAAT	CCGTG	GGTTCA	GCTCT	TGCAG	CGCTT	AACGG	200
	TGAAG	CTGGT	CCTTAC	CGGTG	AAGAAT	CAGT	TCTTG	CTCTT	GTAGC	AGCAC	250
	TTGACT	CTTA	CATCCC	AGAG	CCAGAG	CGGTG	CAATC	GACAA	AGCAT	TCTTG	300
	ATGCCA	ATCG	AAGACG	TATT	CTCAAT	TTTCT	GGTCG	TGGTA	CAGTA	GTAAAC	350
25	AGGCCG	TGTT	GAAGCT	TGGTA	TCATCA	AAAGT	TGGTGA	AAGAA	GTAAG	ATCG	400
	TTGGT	ATTAA	AGATAC	AGTT	AAAACA	AACTG	TAACT	GCGCG	AGAAAT	GTTC	450
	CGTAA	ACTTC	TTGACG	AAGG	CCGTG	CAGGT	GAGAA	CTGTG	GTATC	TTACT	500
	TCGTG	GTA	CTA	AG	AAGTAC	AACG	TGGTCA	AGTA	CTTGCT	AAAC	550
	CAGGT	TAAAT	CAAGCC	GCAC	ACTAA	ATTCTG	ACGCAG	AAGT	ATACG	TACTT	600
30	TCTAA	AGAAG	AAGGTG	GGTCG	TCACAC	TCCA	TTCTTA	AAATG	GTTACC	GTC	650
	ACAGT	TCTAC	TTCCGT	TACAA	CTGAC	GTAAC	TGGTG	CRATC	CAGTT	GAAAG	700
	AAGGC	GTTGA	AATGGT	AATG	CCAGGT	GCAC	ACGTT	GAAAT	GTCAG	TAGAA	750

35 2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

	CGGTG	CGATC	CTCGT	GGTCG	CCGCG	ACCGA	CGGCC	CCCATG	GCCCAG	ACCC	50
	GCGAG	CACGT	CCTGCT	CGCC	CGTCAG	GTCG	GCGTT	CCCCAC	CATCCT	CATC	100
	GCCCT	CAACA	AGTCC	GACAT	GGTTG	ACGAC	GAGGA	AATGA	TGGAAC	TGGT	150
55	CGAGG	AGGAG	TGCCG	CGACC	TGCTG	GAGTC	CCAGG	ACTTC	GATCG	CGATG	200
	CCCCG	ATCGT	CCAGG	TTTCC	GCTCT	GAAAG	CCCTC	GAGGG	CGACG	CGGAG	250
	TGGGT	TGCCA	AGATC	GAGGA	GCTCAT	GAGAG	GCTGT	GGAAT	CCTAC	ATCCC	300
	CACCC	CCGAG	CGCGAT	ATGG	ACAAG	CCCTT	CCTCAT	GCCG	ATCGA	GGACG	350
	TCTTC	ACGAT	CACAGG	TCGT	GGCAC	GGTGC	TCACG	GGGCG	TGTTG	AGCGT	400
60	GGCAAG	CTGC	CGATCA	AACTC	CGAGGT	CGAG	ATCCT	CGGTA	TCCGT	GATCC	450

CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG 500
 AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC 550
 GATGAGGTTG AGCGCGGCCA GGTGTGGCC ATTCCCGGCT CCATCACGCC 600
 TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG 650
 5 GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT 700
 ACCACGGACG TGACCGGCGT CATCACCTC CCCGAGGGCA CCGACATGGT 750
 CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG 800
 CCATGGAGCC CGGCTGGGCT TCGCCA 826

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2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

TGGTGCATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTCCTGC ATTCGTAGTA 100
 30 TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG 200
 ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA 250
 GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT 300
 TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG 350
 35 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
 CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA 450
 ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTT CGTAAAAACT 500
 TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGT 550
 CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT 600
 40 CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG 650
 AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC 700
 TTCCGTACTA CTGACATTAC TGGTGTATC ACTTTACCAG AAGACGTAGC 750
 TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCACC 800
 CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC 835

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2) INFORMATION FOR SEQ ID NO: 4

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Achromobacter xylosoxidans* subsp.
 60 *denitrificans*

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

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5  CCTGGTGGTG TCGGCCGCTG ACGGCCCGAT GCCGCAAACG CGCGAACACA      50
   TCCTGCTGAG CCGCCAGGTT GGC GTGCCGT ACATCATCGT CTTCTGAAC      100
   AAGGCCGACA TGGTTGACGA CGCCGAGCTG CTTGAGCTGG TGGAAATGGA      150
   AGTTCGCGAR CTGCTGAGCA AGTACGACTT CCCGGGCGAC GACACCCCGA      200
   TCGTGAAGGG TTCGGCCAAG CTGGCGCTGG AAGGCGACAA GGGCGAACTG      250
10  GCGAACAGG CCATCATGGC GCTGGCCGCT GCGCTGGACT CGTACATCCC      300
   GACGCCTGAG CGTGCCGTTG ACGGCGCGTT CCTGATGCCG GTTGAAGACG      350
   TGTTCTCGAT CTCGGGTCGC GGCACCGTGG TGACCGGCCG TATCGAACGC      400
   GGCATCATCA AGGTCGGCGA GGAAATCGAA ATCGTCGGTC TGGTGCCGAC      450
   GGTGAAGACG ACCTGCACGG GCGTGGAAAT GTTCCGCAAG CTGCTGGACC      500
15  AAGGTCAAGC CGGCGACAAC GTGGGCATCC TRCTGCGCGG CACCAAGCGT      550
   GAAGACGTCC AGCGCGGCCA GGTTCCTGGCC AAGCCGGGCT CGATCACCCC      600
   GCACACGGAC TTCACGTCCG AGGTGTACAT CCTGTCCAAG GAAGAAGGCG      650
   GCCGTACAC TCCGTTCTTC CAAGGCTATC GTCCCCAGTT CTACTTCCGC      700
   ACGACGGACG TGACGGGCAC GATCGAGCTG CCGGCCGACA AGGAAATGGT      750
20  CCTGCCGGGC GACAACGTGG CCATGACGGT CAAGCTGCTG GCTCCGATCG      800
   CCATGGAAGA AGGCCTGCGT TCGCCAC      827

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25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Anaerorhabdus furcosus
(B) STRAIN: ATCC 25662

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

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40  TGGATCAATC CTAGTAGTTG CTGCAACTGA TGGACCAATG CCTCAAACCTC      50
   GTGAACATAT CTTACTTGCT CGTCAAGTAG GTGTTCCAAG AATGGTTGTA      100
   TTCTTGAACA AATGCGACAT GGTGGAAGAT GAAGAATTAA TCGACCTTGT      150
   TGAAATGGAA GTTCGTGAAC TTCTAAGTGC TTACGGTTTC GAAGGTGATG      200
45  ATACACCAGT TATCCGTGGT TCTGCATTAA AATCTCTTGA AGGAAATGCT      250
   GATTGGGAAG CAAAAGTTGC TGAATTAATG GATGCAGTTG ACTCTTGGAT      300
   TCCAACCTCA ACTCATGAAA CAGACAAACC ATTCTTAATG GCTGTTGAAG      350
   ATGTATTAC AATTACAGGT CGTGGTACAG TTGCTACTGG ACGTGTGAA      400
   CGTGGACACT TAAACCTTAA CGAAGAAGTT GAAATCGTTG GTATTTCATGA      450
50  TACTAAGAAA TCAGTTGTTA CTGGTATCGA AATGTTCCGT AAATTATTAG      500
   ACTATGCTGA AGCAGGAGAC AACATTGGTG CATTATTACG TGGTGTTTCT      550
   CGTGATGAAA TCGAACGTGG ACAATGTCTA GCTAAACCTG GATCAGTTAC      600
   TCCACATACA GCTTTCAAAG CTCAAGTATA CGTATTAACCT AAAGAAGAAG      650
   GTGGACGTCA TACACCATTC GTAACCTAAT ACCGTCCTCA ATTCTATTTT      700
55  CGTACAACTG ACGTAACAGG AGTTGTAAAT CTTCTGAAG GTACTGAAAT      750
   GGTATATGCT GGAGACAACA TCGAAATGAT CGTTGAATTA ATCGCTCCAA      800
   TCGCTGTTGA ACAAGGAAC AAG      823

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2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

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CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACCTC      50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA      100
TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
20 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG      200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT      250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT      300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG      350
ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG      400
25 CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA      450
AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC      500
TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT      550
GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT      600
AAAAGCTCAC GCTAAATTCA AAGCTGAAAG TTTCGTATTA TCTAAAGAAG      650
30 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC      700
TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA      750
AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC      800
CAATCGCTAT CGAAGAGGGA ACTAA      825

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2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

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CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC      50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCTTCA CATCGTTGTA      100
55 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT      150
AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG      200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT      250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT      300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG      350
60 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG      400

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CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA      450
AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC      500
TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT      550
GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT      600
5 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG      650
AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC      700
TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA      750
AATGGTAATG CCTGGTGACA ACATTGAAAT GACTATCGAA CTTATCGCTC      800
CAATCGCTAT CGAAGAGGGA ACTAAATTC      829
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2) INFORMATION FOR SEQ ID NO: 8

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15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 818 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Bacteroides distasonis
25    (B) STRAIN: ATCC 8503

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

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CGGTGCTATC ATCGTAGTTG CTGCTACTGA TGGTCCTATG CCTCAAACCTC      50
30 GCGAGCACAT CCTTTTGGCT CGTCAGGTAA ACGTTCCGAG ATTGGTTGTA      100
TTCATGAACA AGTGTGACAT GGTTGACGAC GAGGAAATGT TGGAATTGGT      150
TGAGATGGAG ATGAGAGAGT TGCTTTTCATT CTATCAATTC GACGGTGACA      200
ACACTCCGAT CATCCGTGGT TCTGCTCTTG GTGCATTGAA CGGTGATGCT      250
CAATGGGAAG ATAAAGTAAT GGAGTTGATG GAAGCTTGTG ATAATTGGAT      300
35 TCCTCTGCCT CCGCGCGAAA TCGACAAGCC GTTCTTGATG CCGGTTGAGG      350
ACGTATTCTC AATCACGGGT CGTGGTACTG TTGCTACAGG TCGTATCGAG      400
ACAGGTATTG TTAAGGTTGG TGAGGAAGTT CAGATCATCG GTCTTGGCGC      450
TGCTGGTAAG AAATCTGTTG TTACAGGTGT TGAGATGTTC CGTAAGTTAT      500
TGGATCAAGG TGAGGCTGGT GATAACGTTG GTTGTGTGCT TCGCGGTATC      550
40 GATAAGAATG AGATCAAGCG TGGTATGGTA ATCTGCCACC CGGGTCAGGT      600
TAAAGAGCAT TCTAAGTTCA AGGCTGAGGT TTATATCTTG AAGAAAGAGG      650
AAGGTGGTCG TCACACTCCG TTCCACAACA AATATCGTCC TCAGTTCTAT      700
ATCCGTACAT TGGATGTAAC TGGTGAGATC ACTTTGCCGG AAGGAACTGA      750
AATGGTAATG CCGGGTGATA ACGTAACGAT CGAGGTTGAG TTGATCTATC      800
45 CGGTAGCATG TAGCGTAG      818

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2) INFORMATION FOR SEQ ID NO: 9

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50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 639 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
55    (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
60    (A) ORGANISM: Enterococcus casseliflavus

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(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

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5  GGTCTTATGC CTCAAACACG TGAACACATC TTGTTATCAC GTAACGTTGG      50
   TGTACCATAC ATCGTTGTTT TCTTAAACAA AATGGATATG GTTGATGACG      100
   AAGAATTACT AGAATTAGTT GAAATGGAAG TTCGTGACTT ATTGTCAGAA      150
   TATGACTTCC CAGGCGACGA TGTTCCTGTA ATCGCTGGTT CTGCTTTGAA      200
   AGCTCTTGAA GGCGATGCTT CATACGAAGA AAAAATCATG GAATTAATGG      250
10 CTGCAGTTGA CGAATACGTT CCAACTCCAG AACGTGACAC TGACAAACCA      300
   TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT      350
   TGCTACAGGC CGTGTTGAAC GTGGACAAGT TCGCGTTGGT GACGAAGTTG      400
   AAATCGTTGG TATTGCTGAA GAAACTGCTA AAACAACGTG AACTGGTGTG      450
   GAAATGTTCC GTAAATTGTT AGACTATGCT GAAGCAGGGG ATAACATTGG      500
15 TGCATTGCTA CGTGGTGTTG CTCGTGAAGA CATCCAACGT GGACAAGTAT      550
   TGGCTAAAGC TGGTACAATC ACACCTCATA CAAAATTTAA AGCTGAAGTT      600
   TACGTTTTAA CAAAAGAAGA AGGTGGACGT CACACACCA      639

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2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 692 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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     (A) ORGANISM: Staphylococcus saprophyticus
     (B) STRAIN: CSG 197

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35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

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   GAACACATTC TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT      50
   CTTAAACAAA GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG      100
   AAATGGAAGT TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT      150
40  GTACCTGTAA TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA      200
   CTATGAGCAA AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC      250
   CAACACCAGA ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC      300
   GTATTCTCAA TCACTGGTCC TGGTACTGTT GCTACAGGCC GTGTTGAACG      350
   TGGTCAAATC AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG      400
45  AATCAAGCAA AACAACGTG ACTGGTGTAG AAATGTTCCG TAAATTATTA      450
   GACTACGCTG AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTC      500
   ACGTGATGAC GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA      550
   CACCACATAC AAAATTCAAA GCGGATGTTT ACGTTTTATC TAAAGATGAA      600
   GGTGGTCGTC ATACACCATT CTTCATAAC TACCGCCAC AATTCTATTT      650
50  CCGTACTACT GACGTAACGT GTGTTGTAA CTTACCAGAA GG      692

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2) INFORMATION FOR SEQ ID NO: 11

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(i) SEQUENCE CHARACTERISTICS:

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60  (A) LENGTH: 821 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

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10  CGGTGCTATC ATCGTTTGTG CTGCAACTGA TGGTCCGATG CCTCAAACCTC      50
    GCGAACACAT TCTGTTAGCT CGTCAGGTAA ACGTACCTCG TCTGGTTGTA      100
    TTCTTGAACA AATGCCGATAT GGTAGACGAC GAAGAAATGT TGGAACCTCGT      150
    TGAAATGGAA ATGAGAGAAC TCCTTTCATT CTATGATTTC GATGGTGACA      200
    ATACTCCTAT CATCCGTGGT TCTGCTCTTG GCGCATTGAA CGGTGTTGAA      250
15  AAATGGGAAG ACAAAGTTAT GGAAGTATG GATGCAGTTG ATAAGTGGAT      300
    TCCACTGCCT CCGCGCGATG TTGATAAACC ATTCTTGATG CCGGTTGAAG      350
    ACGTGTTCTC TATCACAGGT CGTGGTACTG TAGCAACAGG TCGTATCGAA      400
    ACAGGTGTCA TCCACGTTGG TGATGAAGTC GAAATTCCTG GTTTAGGTGA      450
    AGATAAGAAA TCAGTTGTAA CTGGTGTGTA AATGTTCCGT AAAGTGTGG      500
20  ATCAAGGTGA AGCTGGTGAC AACGTAGGTC TTTTGCTTCG TGGTATTGAC      550
    AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAACCAG GTCAGATTAA      600
    ACCGCACTCT AAATTCAAAG CTGAGGTTTA TATCTTGAAG AAAGAAGAAG      650
    GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTACTTG      700
    CGTACTATGG ACTGTACAGG TGAAATCACT TTGCCGGAAG GAACAGAAAT      750
25  GGTAATGCCG GGTGATAACG TAACATTAC AGTTGAGTTG ATTTACCCAG      800
    TAGCATTGAA CCCGGGCTTC G                                821
  
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30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

```

45  TGGTGCGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC      50
    GTGAGCATAT TCTTCTTGCC CGTCAGGTTG GTGTTCCAGC GATTGTTGTT      100
    TTTCTTAATA AGGTTGATCA GGTGATGAT GCTGAGCTTT TGGAGCTTGT      150
    TGAGCTTGAA GTTCGGGAGT TATTGTGCGA ATATGATTTT CCAGGAGACG      200
50  ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAGAT      250
    AAAAGCATTG GTGAAGATGC GGTTCTGCTT TTGATGAGTG AAGTTGATAA      300
    TTATATACCG ACGCCTGAAC GTCCTGTTGA TCAGCCGTTT TTGATGCCAA      350
    TTGAAGATGT TTTTTCGATT TCGGGTCGTG GAACTGTTGT GACGGGTCGT      400
    GTTGAGCGTG GTGTTATTAA GGTGTTGAA GAAGTTGAGA TTATCGGCAT      450
55  TCGTCCAAC TCTAAGACAA CAGTTACAGG GGTGAAATG TTCCGCAAGC      500
    TTTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT      550
    ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTTGGCGA AGCCTGCTTC      600
    GGTTACACCT CATACGAGAT TTAAAGCAGA GGCTTACATT TTGACGAAAG      650
    ATGAAGGTGG TCGTCATACT CCATTTTTCG CGAATTATCG TCCTCAGTTT      700
60  TATTTCCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC      750
  
```

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
 TTCCAATTGC CATGGAAGAA AACTTCGTT TTGCTATC 838

5

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
 GCTCTGAACA AGTGCGATAT GGTGACGAC GACGAGCTCA TCGAGCTCGT 150
 25 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
 GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
 GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
 TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
 30 CGTGTGCGAG GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 35 AGGACGAAGG CGGCCGTAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*
 (B) STRAIN: ATCC 27534

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
 60 GCCCTGAACA AGTGCGATAT GGTGACGAC GAAGAGCTCA TCGAGCTCGT 150

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TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAACGGCTTC GATCGCGATT      200
GCCCCGGTCAT CCACACCTCC GCCTACGGCG CGCTGCACGA TGACGCTCCG      250
GACCACGACA AGTGGGTTGA GTCCGTCAAG GAACTCATGA AGGCCGTCGA      300
CGAGTACATC CCGACCCCGA CCCACGATCT GGACAAGCCG TTCCTGATGC      350
5  CGATCGAAGA TGTGTTTACC ATCTCCGGCC GTGGCACCGT GGTTACCGGC      400
CGTGTGCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTTG AGATCGTCCG      450
CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA      500
AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC      550
GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG      600
10 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA      650
AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG      700
TTCTACTTCC GTACCACCGA CGTACCCGGC GTCATCACCC TGCCGGAAGG      750
CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA      800
TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG      839

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15

2) INFORMATION FOR SEQ ID NO: 15

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 838 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Brucella abortus
30  (B) STRAIN: S2308

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

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TGGCGCGATC CTGGTGGTTT CGGCTGCTGA CGGCCCGATG CCGCAGACCC      50
35  GCGAGCACAT CCTGCTTGCC CGTCAGGTTG GCGTTCCGGC GATCGTCGTG      100
TTCCTCAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT      150
TGAAGTGGAA GTGCGCGAAC TTCTGTGCGA GTACGAATTC CCCGGCGACG      200
AAATCCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCC      250
AAGGAAGTGG GCGAAGATGC CATCCGCAAC CTGATGGACG CCGTTGACAG      300
40  CTACATTCCG ACCCCGGAAC GCCCGATCGA CCAGCCGTTT CTGATGCCGA      350
TCGAAGACGT GTTCTCGATC TCCGGCCGTG GTACGGTTGT GACGGGTCCG      400
GTTGAGCGCG GTATCGTTAA GGTGCGTGAA GAAGTTGAAA TCGTCCGGCAT      450
CAAGGCGACG ACGAAGACCA CGGTTACCGG CGTTGAAATG TTCCGCAAGC      500
TGCTCGACCA GGGCCAGGCT GGCGACAACA TTGGCGCGCT GATCCGCGGC      550
45  GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTT      600
TGTGAAGCCG CACACCAAGT TTAAGGCAGA AGCCTATATT CTGACCAAGG      650
ACGAAGGTGG CCGTCATACG CCGTCTTTCA CCAACTACCG TCCGCAGTTC      700
TACTTCCGTA CGACGGACGT GACGGGTGTT GTGACGCTTC CGGCTGGCAC      750
GGAAATGGTC ATGCCTGGCG ATAACGTCGC CATGGACGTT ACCCTGATCG      800
50  TGCCGATCGC CATGGAAGAG AAGCTTCGCT TCGCTATC      838

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2) INFORMATION FOR SEQ ID NO: 16

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55  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 771 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
60  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*
 (B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

```

10 GGCAGCAGAC GGCCCGATGC CGCAAACGCG TGAGCACATC CTGCTGGCGC      50
   GTCAGGTTGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA GTGCGACATG      100
   GTGGACGACG CCGAACTGCT CGAGCTGGTC GAGATGGAAG TTCGCGAACT      150
   CCTGTGGAAG TACGACTTCC CGGGCGACGA CACGCCGATC GTGAAGGGTT      200
   CGGCGAAGCT GGCGCTGGAA GGCGACACGG GCGAGCTGGG CGAAGTGGCG      250
15 ATCATGAGCC TGGCCGACGC GCTGGACACG TACATCCCGA CGCCGGAGCG      300
   TGCAGTTGAC GGCGCGTTCC TGATGCCGGT GGAAGACGTG TTCTCGATCT      350
   CGGGCCGCGG TACGGTGGTG ACGGGTCGTG TCGAGCGCGG CATCGTGAAG      400
   GTCGGCGAAG AAATCGAAAT CGTCGGTATC AAGCCGACGG TGAAGACGAC      450
   CTGCACGGGC GTTGAAATGT TCCGCAAGCT GCTGGACCAA GGTCAAGCAG      500
20 GCGACAACGT TGGTATCCTG CTGCGCGGCA CGAAGCGTGA AGACGTGGAG      550
   CGTGCCAGG TTCTGGCGAA GCCGGGTTTC ATCACGCCGC ACACGCACTT      600
   CACGGCTGAA GTGTACGTGC TGAGCAAGGA CGAAGGCGGC CGTCACACGC      650
   CGTTCTTCAA CAACTACCGT CCGCAGTTCT ACTTCCGTAC GACGGACGTG      700
   ACGGGCTCGA TCGAGCTGCC GAAGGACAAG GAAATGGTGA TGCCGGGCGA      750
25 CAACGTGTCT ATCACGGTGA A                                     771

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2) INFORMATION FOR SEQ ID NO: 17

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

```

45 GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG      50
   TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCGTAC ATCATCGTGT      100
   TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
   GAAATGGAAG TTCGTGAAC TCTGTCCAG TACGACTTCC CGGGCGACGA      200
   TACTCCAATC GTTCGTGGTT CTGCTCTGAA AGCGCTGCAA GGCGAAGCAG      250
50 AGTGGAAGC TAAATCGTT GAGCTGGCTG GCTACCTGGA TTCTTACATC      300
   CCTGAGCCAG AGCGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA      350
   CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTACCGGT CGTGTAGAGC      400
   GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT      450
   ACTGCGAAAT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
55 CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
   GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCAGG CTCTATCAAG      600
   CCACACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG      650
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
   GTACAACTGA CGTGACCGGC ACCATCGAAC TGCCAGAAGG CGTTGAGATG      750
60 GTAATGCCTG GCGACAACAT CAAAATGTTT GTTACCCTGA TCCACCCAAT      800

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CGCGATGGAT GACGGTCTGC GTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 AATGGAAGTT CGTGAAC TTCGTCAGTA CGACTTCCCG GGCGATGACA 200
 25 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGATAC CCTGTCCAAA GACGAAGGCG 650
 GCCGTCTATC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTA CTCTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCG 824

40

2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTC 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 60 AATGGAAGTT CGTGAAC TTCGTCAGTA CGACTTCCCA GGCGATGATA 200

CCCC AATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TGTAAGAGCGC 400
 5 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 TGCGAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG 650
 10 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT 700
 ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCGCAA 827

15

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAACT 50
 AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT 100
 35 TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG 150
 ACCTTGTTGA GATGGAACTT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA 200
 GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC 250
 AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA 300
 TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA 350
 40 GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA 400
 GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG 450
 AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTTCA GAAAGAACTT 500
 CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTAATCCTCA GAGGTATTGG 550
 AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTTCAGCT AACAGCGTGA 600
 45 AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA 650
 GGCGGACGTC ATAAGCCTTT CTTAGCGGA TACAGACCTC AGTTCTTCTT 700
 CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAAGTGAAG 750
 TGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA 800
 GTTGCTCTTG AAGAAGGAAT GAGATTGCA A 831

50

2) INFORMATION FOR SEQ ID NO: 21

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

	TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCGATG CCTCAGACCA	50
	AAGAACATAT TCTTTTGGCG AGACAGGTTG GTGTTCCCTTA CATCGTTGTT	100
10	TTCCTTAACA AAATCGATAT GATTTCTCAA GAAGATGCTG AGCTCGTAGA	150
	CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GGTTATAAAG	200
	GTTGCCCAAT TATCCGTGGT TCTGCTTTGA AAGCCTTAGA AGGTGATGCA	250
	AGCTACGTTG AAAAAATTCTG CGAGTTAATG CAAGCAGTGG ATGATAACAT	300
	CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG	350
15	ACGTATTCTC TATTTCTGGT CGTGGTACTG TGGTCACAGG ACGTATCGAG	400
	CGTGGAATCG TTAAAGTGGG TGATAAAGTA CAGATTGTTG GTTTAAGAGA	450
	TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTCAGA AAAGAACTTC	500
	CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT	550
	AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA	600
20	ATCTCACACA CAATTTAAAG GTGCTGTCTA CATTCTACAA AAAGAAGAGG	650
	GTGGACGTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC	700
	CGTACAACAG ATGTTACAGG TGTGTAACT CTCCCAGAAG GTACAGAGAT	750
	GGTTATGCCA GGCGATAACG TTGAATTCGA AGTTCAATTA ATTAGCCAG	800
	TAGCTCTAGA AGAAGGTATG AGATT	826
25		

2) INFORMATION FOR SEQ ID NO: 22

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

40

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

	GGGGCTATTC TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACATA	50
45	AGAGCATATT CTTTTGGCAA GACAAAGTTG GGTTCCTTAC ATCGTTGTTT	100
	TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC	150
	TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG	200
	GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGGGATGCTG	250
	CATACATAGA GAAAGTTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC	300
50	CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA	350
	CGTGTCTCT ATCTCCGAC GAGGAACTGT AGTAACTGGA CGTATTGAGC	400
	GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT	450
	ACTAAAGAAA CGATTGTTAC TGGGCTTGAA ATGTTTCAGAA AAGAACTCCC	500
	AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA	550
55	AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA	600
	CCTCATACAC GGTTTAAAGT TGCTGTTTAC GTTCTGCAAA AAGAAGAAGG	650
	TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC	700
	GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG	750
	GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAGTTGA TTAGCCCTGT	800
60	GGCTTTAGAA GAAGGTATGA GA	822

- 2) INFORMATION FOR SEQ ID NO: 23
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Chryseobacterium meningosepticum*
- (B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

20	CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACCTA	50
	GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG	100
	TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT	150
	TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA	200
	ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT	250
25	AAGTGGGTAG CTA CTGTAGTA AGCTCTAATG GATGCTGTTG ATACTTGGAT	300
	CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCCTTATG CCAATCGAAG	350
	ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG	400
	GCTGGTGTA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA	450
	CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC	500
30	TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT	550
	GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCACT	600
	TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG	650
	AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT	700
	GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA	750
35	AATGGTAATG CCTGGTGATA ACTTAACAT CACTGTAGAA TTGTTACAAC	800
	CAATCGCTCT TAACGAGGGT CTTAGATTCTG CGATC	835

- 2) INFORMATION FOR SEQ ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Citrobacter amalonaticus*
- (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCTTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAACTGGT	150
	AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG	200
60	ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250

GAGTGGGAAG CGAAAATCAT CGAACTGGCC GGCTTCCTGG ATTCTTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 5 GACTGCCAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG 500
 ACGAAGGCCG TGC GG GTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCWCCATCAA 600
 GCCGCACACC ATGTTTCAAT CYGAAAGTGA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 10 CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTTGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGG 816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CGCGATCCTG GTTGTGCTG CAACTGACGG CCCGATGCCG CAGACTCGTG 50
 AGCACATCCT GCTGGGTCGY CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
 CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA 150
 35 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGATTTCCTG GGCGACGACA 200
 CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAWGCAGAG 250
 TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATCCC 300
 GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCT ATCGAAGACG 350
 TATTCTCCAT CTCTGGTCTG GGTACCGTTG TTACCGGTCT TGTAGAGCGC 400
 40 GGTATCATCA AAGTTGGTGA AGAAGTTGAA ATCGTTGGTA TCAARGACAC 450
 TGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAGCGT 550
 GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGATCAT TCTGTCCAAA GACGAAGGCG 650
 45 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCGCAGTT CTACTTCCGT 700
 ACTACTGACG TGACTGGTAC CATCGAAGT CCGGAAGGCG TTGAGATGGT 750
 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCGC 825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

```

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10 TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
TGAGATGGAA GTGCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG      200
ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCT      250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
CCCGGAACCA GAGCGTGCAG TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
15 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATYGTG GTATCAAAGA      450
GACTGCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG      500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GYTCCATCAA      600
20 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATYCTGTCY AAAGATGAAG      650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GCGGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA      800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
25

```

2) INFORMATION FOR SEQ ID NO: 27

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

```

CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCG CAGACTCGTG      50
45 AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTT      100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA      150
GATGGAAGTT CGTGAAGTGC TGTCTCAGTA CGATTTCCTG GCGACGACA      200
CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG      250
TGGGAAGCGA AAATCATCGA ACTGGCAGGC TTCCTGGATT CTTACATCCC      300
50 GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG      350
TATTCTCCAT CTCTGGTCTG GGTACCGTTG TTACCGGTCTG TGTAAGAGCGC      400
GGTATCATCA AAGTGGGTGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC      450
TGCCAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG      500
AAGGCCGTGC TGGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT      550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCW CCATCAAGCC      600
RCACACTATG TTCGAATCTG AAGTGATAC TCTGTCCAAA GACGAAGGCG      650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGAGTT CTACTTCCGT      700
ACGACTGACG TGAAGGACAC CATCGAAGTG CCGGAAGGTG TTGAGATGGT      750
TATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG      800
60 CGATGGACGA CGGTCTGCGT TTCGCAA      827

```

2) INFORMATION FOR SEQ ID NO: 28

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA	50
	TCCTGCTGGG TCGTCAGGTA GGC GTTCCGT ACATCATCGT GTTCCTGAAC	100
	AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA	150
	AGTTCGTGAA CTTCTGTCTC AGTACGATTG CCCGGGCGAC GAACTCCGA	200
	TCGTTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGAAGC AGAGTGGGAA	250
25	GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCAGAACC	300
	AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCTATCGAA GACGTATTCT	350
	CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC	400
	ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTGCTAA	450
	GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC	500
30	GTGCTGGTGA GAACGTTGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA	550
	ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCTCTATCA AGCCGCACAC	600
	CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGACGAA GGCGGCCGTC	650
	ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT	700
	GACGTGACTG GTACCATCGA ACTGCCGGA GCGGTAGAGA TGGTAATGCC	750
35	GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC CTGGTTGTTG CCGCGACTGA CGGCCCGATG CCGCAGACCC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGCCACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG	200
	ACACGCCGAT CGTTCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCGACGCA	250
60	GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT	300

```

TCCGGAACCA GAGCGTCCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTGCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG 500
5  ACGAAGGCCG TGCGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCGAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA TATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
10 GGTAATGCCG GGCACACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTC 826

```

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

```

30  GCGATCCTGG TTGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA 50
GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC 100
TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GATTTCCTCG GCGACGACAC 200
35  TCCGATCGTT CGTGGTCTG CTCTGAAAGC GCTGGAAGGC GAAGCAGAGT 250
GGGAAGCGAA AATCATCGAA CTGGCTGGCT TTCTGGATTC TTACATCCCG 300
GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTRCCTA TCGAAGACGT 350
ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG 400
GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGACACC 450
40  GCTAAGTCTA CCTGTACCGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA 500
AGGCCGTGCT GGTGAGAACG TTGGTGTTCT GCTGCGTGGT ATCAAACGTG 550
AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCTC TATCAAGCCG 600
CACACCAAGT TCGAATCTGA AGTGACATC CTGTCCAAAG ACGAAGGCCG 650
CCGTCATACT CCGTTCCTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA 700
45  CTACTGACGT GACTGGTACC ATCGAAGTGC CGGAAGGCGT AGAGATGGTA 750
ATGCCGGGCG ACAACATYAA AATGGTTGTT ACYCTGATCC ACCCGATCGC 800
GATGGACGAC GGTCTGCGTT TCG 823

```

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

```

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
10 GAAATGGAAG TTCGTGAAC TCTGTCTCAG TACGATTTCG CGGGCGACGA      200
TACGCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGAAGCAG      250
AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC      300
CCGGAACCAG AACGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACTGGT CGTGTAGAAC      400
15 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
ACTGCCAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACCTTGGTGT TCTGCTGCGT GGTATCAAAC      550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG      600
CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG      650
20 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
GTACTACTGA CGTGACGGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT      800
CGCGATGGAT GACGGTCTGC GTTTCG                                826

```

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

```

CGGAGCTATA TTAGTTTGTT CAGCAGCTGA TGGTCCAATG CCTCAAACAA      50
GAGAGCACAT CTTATTATCA TCAAGAGTTG GAGTTGACCA CATCGTAGTA      100
45 TTCTTAAACA AAGCAGATAT GGTGACGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTAGAGAGT TATTAAGCGA GTACAAC TTCAGGAGACG      200
AYATTCCAGT AATCAARGGA TCAGCTTTAG TAGCATTAGA AAACCCCACT      250
GACGAAGCTG CAACAGCTTG TATCAGAGAG TTAATGGATG CTGTAGATAG      300
CTACATCCCA ACACCAGAAA GAGCAACAGA TAAGCCATTC TTAATGCCAG      350
50 TAGAGGACGT ATTCACAATC ACTGGTAGAG GAACAGTTGC AACAGGAAGA      400
GTTGAAAGAG GAGTTCTACA TGTAGGAGAC GAAGTAGAAG TAATCGGATT      450
AACTGAAGAA AGAAGAAAAA CTGTTGTAAC AGGAATCGAA ATGTTCAAGAA      500
AGTTATTAGA TGAAGCACAA GCTGGAGATA ACATCGGAGC ATTATTAAGA      550
GGTATCCAAA GAACTGAYAT CGAAAGAGGT CAAGTTT TAGCTCAAGTTGG      600
55 AACATCAAC CCACACAAAA AATTCGTAGG TCAAGTATAC GTACTTAAAA      650
AAGAAGAAGG TGAAGACAT ACTCCATTCT TCGATGGATA CAGACCACAA      700
TTCTACTTCA GAACAACAGA CGTTACAGGA TCAATCAAAT TACCAGAAGG      750
AATGGAAATG GTTATGCCTG GAGACCACAT CGACATGGAA GTTGAATTAA      800
TCACAGAAAT CGCTATGGAY GAAGGATTAA GATTCGCTAT C                                841

```

60

2) INFORMATION FOR SEQ ID NO: 33

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Comamonas acidovorans*
 15 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
20	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCAGGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GA CTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCCGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCAACCG	CGTGGAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACA ACTACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGGGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC 350
 GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
 ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
 CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
 5 GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
 GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
 CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTCGACAAC TACCGTCCGC 650
 AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
 GG 702
 10

2) INFORMATION FOR SEQ ID NO: 35

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Corynebacterium cervicis*
 25 (B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGC GTTCCGA 50
 30 CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
 CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
 CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
 GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC 250
 ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
 35 GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC 350
 GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
 ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA 450
 GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
 GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT 550
 40 TCGATCACCC CGCACACCAA CTTACCGGA CAGGTCTACA TCCTCAAGAA 600
 GGAAGAAGGC GGTCGTCAAC ACCCGTTCTT CTCGAACTAC CGTCCGCAGT 650
 TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

45

2) INFORMATION FOR SEQ ID NO: 36

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 804 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Corynebacterium flavescens*
 (B) STRAIN: ATCC 10340

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

	GGTTGTTGCT	GCAACCGATG	GTCCTATGCC	GCAGACCCGC	GAGCACGTTT	50
	TTCTGGCTCG	CCAGGTTGGC	GTTTCCTTACA	TCCTCGTTGC	TCTTAACAAG	100
	TGCGACATGG	TTGATGATGA	GGAAATCATC	GAGCTCGTTG	AGATGGAAAT	150
5	CCGCGAACTG	CTCGCTGAGC	AGGACTACGA	CGAGGATGCC	CCCATCATCC	200
	ACATCTCCGC	TCTCAAGGCT	CTTGAGGGTG	ACGAGAAGTG	GGTACAGGCC	250
	ATCGTCGACC	TCATGCAGGC	CTGCGATGAC	TCCATTCCGG	ATCCGGAGCG	300
	CGAGACCGAC	AAGCCCTTCC	TCATGCCTAT	CGAGGACATC	TTCACCATCA	350
	CCGGCCGCGG	TACCGTTGTT	ACCGGCCGTG	TTGAGCGTGG	CGTTTTGAAG	400
10	GTCAACGAGG	ATGTTGAGAT	CATCGGCATC	AAGGAGAAGT	CCATCTCCAC	450
	CACCGTTACC	GGTATCGAAA	TGTTCCGCAA	GATGATGGAC	TACACCGAGG	500
	CTGGCGACAA	CTGTGGTCTG	CTTCTGCGTG	GTACCAAGCG	TGAAGAGGTC	550
	GAGCGCGGCC	AGGTTGTTAT	CAAGCCGGGC	GCCTACACCC	CCCACACCAA	600
	GTTCGAGGGT	TCCGTCTACG	TCCTCAAGAA	GGAAGAGGGC	GGCCGCCACA	650
15	CCCCGTTTAT	GGACAACACTAC	CGTCCGCAGT	TCTACTTCCG	TACCACTGAC	700
	GTGACCGGCG	TTGTTTACCT	GCCTGAGGGC	ACCGAGATGG	TCATGCCTGG	750
	CGACAACGTT	GATATGACCG	TTGAGCTCAT	CCAGCCCGTC	GCTAGGATGA	800
	GGGC					804

20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| 25 | (A) | LENGTH: 692 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- | | | |
|--|-----|--------------------------------------------|
| | (A) | ORGANISM: <i>Corynebacterium kutscheri</i> |
| | (B) | STRAIN: ATCC 15677 |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

	TGCCTCAGAC	CCGTGAGCAC	GTTCTTCTTG	CTCGCCAGGT	TGGCGTTCCT	50
	TACATCCTCG	TTGCTCTTAA	CAAGTGCGAC	ATGGTTGACG	ATGAGGAAAT	100
40	CATCGAGCTC	GTTGAGATGG	AAGTTCGCGA	GCTTCTTGCT	GAGCAGGAGT	150
	ACGATGAAGA	GGCTCCAATC	ATCCACATCT	CTGCTTTGAA	GGCTCTTGAG	200
	GGCGACGAGA	AGTGGACTCA	GGCCATCATC	GACCTCATGC	AGGCTTGTGA	250
	TGACTCCATC	CCAGATCCAG	AGCGTGAGAC	CGACAAGCCA	TTCCTCATGC	300
	CTATCGAGGA	TATCTTCACC	ATCACCGGTC	GTGGCACCGT	TGTTACCGGT	350
45	CGTGTTGAGC	GCGGTTCCCT	GAAGGTGAAT	GAGGACGTCG	AGATCATCGG	400
	CATCAAGGAG	AAGTCCACCA	CTACTACCGT	TACCGGTATC	GAAATGTTCC	450
	GTAAGCTTCT	TGATTACACC	GAAGCTGGCG	ATAACTGTGG	TCTGCTTCTT	500
	CGTGGTATCA	AGCGCGAAGA	CGTTGAGCGT	GGTCAGGTTG	TTGTTAAGCC	550
	AGGCGCTTAC	ACACCTCACA	CCGAGTTCGA	GGGCTCTGTT	TACGTTCTTT	600
50	CCAAGGACGA	GGGCGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	TGACGTTACC	GGTGTTGTGA	AG	692

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 797 bases |
| | (B) | TYPE: Nucleic acid |
| 60 | (C) | STRANDEDNESS: Double |

24

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG 50
 TTCTTCTGGC CCGCCAGGTT GCGGTTCCGT ACATCCTCGT TGCAGTGAAC 100
 AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA 150
 GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG 200
 15 TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG 250
 TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA 300
 GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA 350
 TTACCGGCCG CCGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG 400
 AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC 450
 20 CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG 500
 AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG 550
 GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GCGGCTTACA CCGCGCACAC 600
 CAAGTTCGAG GGTTCGGTCT ACGTCCTGAA GAAGGAAGAG GCGGCGCCG 650
 ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC 700
 25 GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC 750
 GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA 797

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GCGGTCCCCT 50
 ACATCCTCGT TCGCTGAAC AAGTGCACGA TGGTTGATGA TGAGGAGATC 100
 ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA 150
 CGACGAGGAC GCGCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG 200
 50 GCGACGAGAA GTGGGTTTCA TCCGTGCTCG ACCTCATGCA GCGGTGCGAC 250
 GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC 300
 GATCGAGGAC ATCTTCACCA TCTCCGGCCG CCGCACCCTG GTTACCGGTC 350
 GTGTGGAGCG CCGCGTGCTC AACCTCAACG ACGAGGTCTG GATCATCGGC 400
 ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA 450
 55 CAAGCTGCTC GATACCGCTG AGGACGGCGA CAACGCGGCT CTGCTGCTCC 500
 GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG 550
 GCGGCCTACA CCGCGCACAC CAAGTTCGAG GGTTCGGTCT ACGTCTGTCT 600
 CAAGGACGAG GCGGCGCCG CACCCCGTT CTTCGACAAC TACCGTCCGC 650
 AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG 700
 60 GG 702

2) INFORMATION FOR SEQ ID NO: 40

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20 GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGGCGCTGA ACAAGTGCGA 50
 CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG 100
 AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC 150
 TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT 200
 TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA 250
 25 CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC 300
 CGCGGTACCG TTGTTACCGG CCGTGTGAG CGTGGCCGTC TGAACGTCAA 350
 CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG 400
 TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC 450
 GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG 500
 30 TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTTCG 550
 AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG 600
 TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC 650
 CGGTGTTGTT CACCTGCCAG AGGG 674

35

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 (B) STRAIN: ATCC 19412

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT 50
 TACATCCTCG TTGCACTGAA CAAGTGCGAC ATGGTCGACG ACGAAGAAAT 100
 55 CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT 150
 ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC 200
 GGCGAGCAGA AGTGGGTGGA CTCCATCGTC GAACTGATGG AAGCTTGCGA 250
 CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC 300
 CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC 350
 60 CGTGTGCGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG 400

TATCAAGGAC AAGTCCCAGA AGACCACCGT CACCGGTATC GAGATGTTCC 450
 GCAAGATGCT GGACTACACC GAAGCTGGCG ACAACTGTGG TCTGCTGCTC 500
 CGCGGCATCG GCCGTGAGGA TGTCGAGCGT GGCCAGGTTA TCATCAAGCC 550
 AGGCGCTTAC ACCCCTCACT CTGAGTTCGA GGGCTCTGTC TACGTCTGT 600
 5 CCAAGGACGA GGGTGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA 650
 CAGTTCTACT TCCGCACCAC CGACGTGACC GCGTTGTGC ACCT 694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25 GCCGCAGACC CGCGAGCAGC TTCTGCTGGC TCGCCAGGTT GGCGTTCCKT 50
 ACATCCTSGT TGCACCTGAAC AAGTGCGACA TGGTTGACGA TGAGGARCTC 100
 CTSCAGCTCG TCGAGATGGA GGTCCGCGAG CTGCTGGCTG AGCAGGACTA 150
 CGACGAGGAA GCTCCGRTCG TTCACATCTC CGCWCTGAAC GCCCTGGACG 200
 30 GCGACSAGAA GTGGGCTVAC TCCATCCTCG AGCTGATGCA GGCTTGCGAC 250
 GAGTCCATCC CGGATCCGGA GCGCGAGACC GACAAGCCGT TCCTGATGCC 300
 GATTGAGGAC ATCTTCACCA TTACCGGTCG CGGYACCGTT GTTACCGGCC 350
 GTGTTGAGCG TGGCDTCCTG AACGTSAAAG ACGASGTTGA GATCATGGGY 400
 ATCCGGGAGA AGTCCCAGAA GACCACCGTY ACCKSCATCG AGATGTTCAA 450
 35 CAAGMTGMTG GACWCCGCAG AGGCTGGCGA CAACGCTGSW CTGCTGCTGC 500
 GTGGTMTSAA GCGTGAGGAC GTTGAGCGTG GCCAGATCAT CGYTAAGCCG 550
 GCGCCKTACA CCCCACACAC CGAGTTCGAG GGCTCCGTCT ACGTCCTGTC 600
 CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTGACAAAC TACCGTCCGC 650
 AGTTCTACTT CCGCACCACC GACGTSACCG GTGTTGT 687
 40

2) INFORMATION FOR SEQ ID NO: 43

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium urealyticum*
 55 (B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT 50
 60 TCTGCTGGCT CGCCAGGTTG GCGTCCGTA CATCCTCGTT GCACTGAACA 100

```

AGTGGCGACAT GGTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG      150
GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT      200
CCCAGTCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAG TGGGTCTGACT      250
CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG      300
5  CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT      350
TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTGAGCGT GGCGTCCTGA      400
ACCTGAACGA CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG      450
ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA      500
GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG      550
10 TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC      600
GAGTTCGAGG GCTCCGTCTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA      650
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGTACCACCG      700
ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTTCATGCCG      750
GGCGACAACG TTGAGATGAG CGTCAAGC      778
15

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2) INFORMATION FOR SEQ ID NO: 44

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 703 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Corynebacterium xerosis
30  (B) STRAIN: ATCC 373

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```

CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC      50
35 ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT      100
CGAGCTCGTG GAGATGGAGG TGCGTGAGCT TCTCGCCGAG CAGGACTACG      150
ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC      200
GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA      250
GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCCC      300
40 TCGAGGACAT CTTCACCATC ACCGCGCCGC GCACCGTCGC CACCGGTCCG      350
GTGGAGCGCG GCACCCTGAA GGTCAACGAC GAGGTGCGAG TCCTGGGCAT      400
CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA      450
AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC      500
GGCATCAAGC GCGAGGACAT CGAGCGCGGC CAGATCATCG CGAAGCCGGG      550
45 CGCCTACACC CCGCACACCG AGTTCGAGGG CTCCGTCTAC ATCCTGGCCA      600
AGGACGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAACTA CCGTCCGCAG      650
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGAGGG      700
CAC      703
50

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2) INFORMATION FOR SEQ ID NO: 45

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55  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 832 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
60  (ii) MOLECULE TYPE: Genomic DNA

```


(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coxiella burnetii*
 (B) STRAIN: Nine Mile phase II

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

```

GGAGCGATAT TGGTGGTGAG CGCAGCGGAC GGCCCGATGC CGCAAACGCG      50
GGAACACATT GTATTGGCGA AGCAAGTGGG TGTTCGGAAC ATAGTGGTTT      100
10  ACTTGAACAA AGCGGACATG GTGGATGACA AAGAGCTGTT GGAATTAGTG      150
   GAAATGGAAG TGAGGGATTT ATTGAACAGT TATGATTTCC CTGGGGATGA      200
   GACGCCGATA ATAGTGGGGT CAGCGTTAAA GCGGTTAGAA GGTGACAAGA      250
   GTGAGGTTGG GGAGCCATCG ATAATCAAAT TAGTGGAAAC GATGGACACG      300
   TACTTCCCGC AGCCGGAGCG AGCGATAGAC AAACCGTTTT TAATGCCGAT      350
15  CGAAGATGTG TTTTCGATAT CGGGCCGAGG GACGGTGGTG ACGGGACGCG      400
   TAGAGCGAGG GATCATCAAA GTGGGCGACG AGATAGAGAT TGTGGGGATC      450
   AAGGACACGA CGAAGACGAC GTGCACGGGC GTTGAGATGT TTCGCAAATT      500
   ATTGATGAA  GGTCAAGCGG GTGACAACGT AGGAATTTTA TTGAGAGGGA      550
   CGAAACGCGA AGAAGTGGAG CGTGGTCAAG TATTGGCGAA ACCGGGATCG      600
20  ATCACGCCAC ACAAGAAATT TGAGGCGGAG ATTTATGTGT TGTGGAAGGA      650
   AGAAGGGGGA CGCCACACAC CGTTTTTACA AGGCTATCGA CCGCAATTTT      700
   ATTTCCGCAC GACGGACGTG ACGGGCCAGT TATTGAGTTT ACCGGAGGGG      750
   ATAGAGATGG TGATGCCGGG AGATAACGTG AAAGTGACGG TTGAATTGAT      800
   TGCGCCGGTA GCGATGGATG AAGGGCTACG AT                      832
25

```

2) INFORMATION FOR SEQ ID NO: 46

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 40 (B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

```

GGCGCTATCC TGGTTGTTGC TGCAGCTGAC GGCCCGATGC CGCAGACCCG      50
45  TGAGCACATC CTGCTGGGTC GCCAGGTAGG CGTTCGTAC ATCATCGTGT      100
   TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
   GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA      200
   TACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG      250
   AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACGCTGGA CTCCTACATT      300
50  CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA      350
   CGTATTCTCA ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
   GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTAGG TATCAAGCCG      450
   ACCACCAAGA CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
   CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC      550
55  GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT      600
   CCGCACACCA AGTTCGAATC AGAAGTGTAC ATCCTGAGCA AGGATGAAGG      650
   CGGCCGTCTA ACTCCGTTCT TCAAAGGTTA CCGTCCGCAG TTCTACTTCC      700
   GTACCACTGA CGTGAAGTGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
   GTAATGCCCG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT      800
60  CGCCATGGAC GATGGT                      816

```

2) INFORMATION FOR SEQ ID NO: 47

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20 GGC GCG ATCC TGG TTG TTG C TGC GACT GAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGTTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 CACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG 250
 25 AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACCTCTGGA CTCCTACATC 300
 CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 CGTATTCTCT ATCTCTGGCC GTGGTACCGT TGTACCGGT CGTGTAGAGC 400
 GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTTGG TATCAAGCCG 450
 ACCACCAAGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 30 CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAGC 550
 GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT 600
 CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGAGCA AGGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGAAGTGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 35 GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCCATGGAC GATGGTCTGC G 821

40 2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55

CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCCATG CCTCAGACTC 50
 GCCAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCCTA CATCCTCGTA 100
 TTCATGAACA AATGCGACAT GGATAGATGAT GCCGAGCTGC TTGAGTTGGT 150
 TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG 200
 60 ACTGCCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC 250

GGTTACAAAG AAAAATCTT CGAACTAGCT GCTGCTTTGG ATAGCTACAT 300
 CCCCCTCTCT CAACGTGCTG TAGACAAACC CTTCTGTGTG CCGATCGAAG 350
 ACGTATTCTC TATCTCCGGC CGTGGTACCG TAGTAACCGG TCGTGTAGAG 400
 CGCGGCATCA TCAAAGTAGG TGAAGAGATC GAAATCGTTG GTCTGAAGCC 450
 5 CACTCAGAAA ACTACCTGTA CTGGCGTGGA AATGTTCCGC AAAGTCTGCTG 500
 ACGAAGGTCA GGCCGGTGAC AACGTAGGCG TACTGCTGCG CCGTACCAAA 550
 CGTGAAGAAG TTGAGCGTGG TCAAGTATTG GCTAAACCCG GCACCATCAC 600
 TCCGCACACC AAGTTCAAAG CCGAAGTATA CGTATTGAGC AAAGAAGAAG 650
 GTGGTTCGTC CACCCCGTTC TTTGCCAACT ACCGTCCACA GTTCTACTTC 700
 10 CGTACTACTG ACGTAACCGG TGCTGTAGAG CTGGAGCCTG GTGTAGAAAT 750
 GGTTATGCCT GGTGAGAACG TAACCATCAC CGTAGAACTG ATTGCTCCGA 800
 TTGCTATGGA AGAAGGTCTG CGCTTTGCGA 830

15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*
 (B) STRAIN: ATCC 13048

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTCCGTAC ATCATCGTGT 100
 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 35 GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC 300
 CCRGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCAGGT CGTGTAGAGC 400
 40 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
 ACCGCGAAAA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCTGGTGAGA ACGTAGGYGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CAGCATCAAG 600
 CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGTCCA AAGACGAAGG 650
 45 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGRTG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCGATGG 808

50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

31

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

```

CGGCGCGATC CTGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10 TTCCTGAACA AATGTGACAT GGTGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG      200
ATACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCW      250
GAGTGGGAAG CGAAAATCAT CGARCTGGCT GGCCACCTGG ATACCTATAT      300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
15 ACGTATTCTC CATCTCCGGT CGCGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TYAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
TACYCGGAAA TCAACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
20 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
GCGGTCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCSCA GTTCTACTTC      700
CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GCGGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA      800
25 TCGCGATGGA CGACGGTCTG CGTTCGCA      828
  
```

2) INFORMATION FOR SEQ ID NO: 51

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

```

TGGCGCGATC CTGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACGC      50
45 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG      100
TTCCTGAACA AATGCGACAT GGTGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG      200
ACACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
GAGTGGGAAG CTAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCTTACAT      300
50 CCCGGAACCA GAACGTGCTA TCGATAAGCC ATTCCTGCTG CCAATCGAAG      350
ACGTATTCTC TATCTCCGGC CGTGGTACTG TTGTAACCGG TCGTGTAGAG      400
CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCAG GCTCAATCAA      600
GCCGCACACC AAATTCGAAT CTGAAGTTTA TATTCTGTCC AAAGATGAAG      650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTGACCGG CACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GCGGACAACA TTCAGATGGT TGTACCCTG ATCCACCCAA      800
60 TCGCGATGGA TGACGGTCTG CGTTT      825
  
```

2) INFORMATION FOR SEQ ID NO: 52

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTT CATCATCGTG	100
	TTCTTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTT CCGGGCGACG	200
	ATACTCCAAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250
25	GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT	300
	CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TCAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG	500
30	ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA	550
	CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA	600
	GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG	650
	GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT	750
35	GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA	800
	TCGCGATGGA CGACGGTCTG CG	822

40 2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55

55	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG	100
	TTCTTGAACA AGTGCACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAAATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTT CCAGGCGACG	200
60	ACACTCCAAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAAGCT	250

```

GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG      350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
5  TACTGCKAAA TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG      500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
CGCGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA      600
GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG      650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
10 CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACGCTG ATCCACCCAA      800
TCGCGATGGA CGACGGTCTG CGTTTC      826

```

15

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 806 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Enterobacter cloacae
      (B) STRAIN: ATCC 13047

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

```

GATCCTGGTA GTAGCTGCGA CTGACGGCCC AATGCCTCAG ACTCGTGAGC      50
ACATCCTGCT GGGTCGTCAG GTAGGCGTTC CTTACATCAT CGTGTTCTTG      100
AACAAATGCG ACATGGTTGA TGACGAAGAG CTGCTGGAAC TGGTAGAGAT      150
35  GGAAGTTCGT GAACTGCTGT CTCAGTACGA TTTCCCAGGC GACGATACCC      200
CAATCGTTTCG TGGTTCGTCT CTGAAAGCGC TGAAGGCGA CGCAGAGTGG      250
GAAGMGA AAA TCATCGAACT GGCTGGCTAC CTGGATTCTT ACATCCCAGA      300
ACCAGAGCGT GCGATTGAYA AGCCATTCTT GCTGCCAATC GAAGACGTAT      350
TCTCCATCTC CGGTCGTGGT ACCGTTGTTA CCGGTCGTGT AGAGCGCGGT      400
40  ATCATCAAAG TGGGTGAAGA AGTTGAAATC GTTGGTATCA AAGAGACTGC      450
GAAGTCTACC TGTACTGGCG TTGAAATGTT CCGCAAACCTG CTGGACGAAG      500
-----
GCCGTGCTGG TGAGAACGTT GGTGTTCTGC TGCGTGGTAT CAAACGTGAA      550
GAAATCGAAC GTGGTCAGGT TCTGGCGAAG CCAGGCTCAA TCAAGCCACA      600
CACCAAGTTC GAATCTGAAG TGTACATCCT GTCCAAAGAC GAAGGCGGCC      650
45  GTCATACTCC GTTCTTCAAA GGCTACCGTC CACAGTTCTA CTTCCGTACA      700
ACTGACGTGA CCGGTACCAT CGAACTGCCA GAAGGCGTAG AGGTGGTAAT      750
GCCAGGCGAC AACATCAAGA TGTTGTGAC TCTGATCCAC CCAATCGCGA      800
TGGACG      806

```

50

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

```

55  (A) LENGTH: 826 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

```

CGGCGCGATC CTGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10 TTCCTGAACA AGTGCACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG      200
ACACCCCGAT CGTTCGCGGT TCTGCGCTGA AAGCGCTGGA AGGCGACGCA      250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCCACCTGG ATACCTAYAT      300
CCCGBAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
15 ACGTATTCTC CATTTCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TCAAGGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
CACC CGGAAA ACCACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGTT      500
ACGAAGGCCG TGCTGGTGAG AACGTCGGCG TTCTGCTGCG TGGTATCAAG      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCCATCAA      600
20 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG      650
GCGGCCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACAACCTG ACGTGAAGTG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GCGACAACA TCAAGATGGT TGTACCCTG ATCCACCCGA      800
TCGCGATGGA CGACGGTCTG CGTTTC      826
25

```

2) INFORMATION FOR SEQ ID NO: 56

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 40 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

```

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG      50
45 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTC CAGGCGACGA      200
CACCCCAATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAMGCAG      250
AGTGGGAAGM GAAAATCATC GARCTGGCTG GCTTCCTGGA TTCTTACATC      300
50 CCAGAACCAG AGCGTGCGAT TGACAAGCCA TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCCTG CGTGTWAGC      400
GCGGTATCAT CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
55 GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CGAAGCCAGG CTCAATCAAG      600
CCACACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG      650
CGGCCGTCTAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACAACCTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      750
GTAATGCCAG GCGACAACAT CAAGATGGTT GTGACGCTGA TCCACCCAAT      800
60 CGCGATGGAC GACGGTCTGC GTTTCGCAA      829

```

35

2) INFORMATION FOR SEQ ID NO: 57

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

```

20  GCGCGTATCC TGGTTGTTGC TCGACTGAC GGCCCGATGC CGCAGACCCG      50
    TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
    TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAC TGGTT      150
    GAGATGGAAG TGCGCGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA      200
    CACCCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCTG      250
25  AGTGGGAAGC GAAAATCATC GAGCTGGCAG GTCACCTGGA TTCCTACATC      300
    CCGGAACCGG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA      350
    CGTATTCTCC ATCTCYGGTC GTGGTACCGT TGT TACCGT CGTGTAGAGC      400
    GCGGTATCAT CAAGGTTGGT GAAGAAGTTG AAATCGTGGG CATCAAAGAC      450
    ACCGCGAAAT CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
30  CGAAGGCCGT GCGGGCGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC      550
    GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCCATCAAG      600
    CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG      650
    CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
    GTACRACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG      750
35  GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
    CGCGATGGAC GACGGTCTGC GTTTCGCAAT C                               831
  
```

40 2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55

```

    CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACAC      50
    GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT      100
    TTCTTAAACA AAATGGATAT GGTGATGAC GAAGAATTAC TAGAATTAGT      150
    TGAAATGGAA GTTCGTGACT TATTGTCAGA ATATGACTTC CCAGGCGACG      200
60  ATGTTCCCTGT AATCGCTGGT TCTGCTTTGA AAGCTCYTGA AGGCGATGCT      250
  
```


	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAAACTGCT	AAAACAACTG	TAAGTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

15

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
 (B) STRAIN: ATCC 43198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAGTGAA	TACGACTTCC	CAGGAGACGA	200
	TGTTCTCTGT	ATCGCTGGTT	CTGCATTAAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAACCTCAG	AACGTGACAA	CGATAAACCA	TTCATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTTGAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAGTG	TACGTTTTAA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTGTAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAACTATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

```

CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTCTTCA CATCGTCGTT      100
10 TTCTTGAACA AAATGGACAT GGTTGATGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG      200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT      250
TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
15 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
AGAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT      500
TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG      550
GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAC CAGGTTCAAT      600
20 CACTCCACAT ACAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC      800
CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC      835
25

```

2) INFORMATION FOR SEQ ID NO: 61

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 40 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

```

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC      50
45 GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTCTTCA CATCGTYGTA      100
TTCTTGAACA AAGTAGATAT GGTTCGATGAC GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTTCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
TCATACGAAG AAAAAATCCT TGAATTAATG GCTGCAGTTG ACGAATATAT      300
50 CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG      350
ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACAG TTAAGTGGT TGAAATGTTC CGTAAATTAT      500
TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGT      550
55 GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
CACKCCTCAT ACAAATTTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACCTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
60 CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835

```

2) INFORMATION FOR SEQ ID NO: 62

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
25	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
30	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

35

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
55	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
60	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400

```

CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA      450
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      500
AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT      550
ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC      600
5  AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC      650
   ACACTCCATT CTTCACTAAC TACCGTCTCT      680

```

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

```

25 AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACCTCGT GAACACATCC      50
   TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA      100
   GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT      150
   TCGTGACCTA TTAACAGAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG      200
30 TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA      250
   AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA      300
   ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA      350
   TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT      400
   CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AACTTCAAA      450
35 AACAACAGTT ACTGGTGTTG AAATGTTCCG TAAATTGTTA GACTACGCTG      500
   AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTGTC ACGTGAAGAC      550
   ATCCAACGTG GACAAGTTTT AGCTAAACCA GGTACAATCA CACCTCATAC      600
   AAAATTCTCT GCAGAAGTAT ACGTGTTGAC AAAAGAAGAA GGTGGACGTC      650
   ATACTCCATT CTTCACTAAC TACCGTCTCT AATTT      685
40

```

2) INFORMATION FOR SEQ ID NO: 65

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 55 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

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CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC      50
60 GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT      100

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	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACTG	TAACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAAGT	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAAGTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACCTCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAAGT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCCGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACTGTAA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

50

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

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CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
GTGAACATAT CCTAYTATCT CGTCAAGTTG GTGTTCCATA CATCGTTGTA      100
TTCTTGAACA AAGTAGATAT GGTGACGAC GAAGAATTAC TAGAATTAGT      150
10 TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTCTGT AGTTGCTGGT YCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
TCATACGAAG AAAAAATCCT TGAATTGATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTCGAAG      350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
15 CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACAG TTAGTGGTGT TGAAATGTTC CGTAAATTAT      500
TAGACTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGT      550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
CACACCTCAT ACAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAGAAG      650
20 AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
TTCCGTACRA CTGACGTAAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
CAATCGCTAT CGAAAACGGT ACTAAATTCT CAATC      835

```

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

```

CGGAGCAATC TTAGTTGTTT CTGCTGCTGA CGGCCCTATG CCTCAAACCTC      50
GTGAACACAT CCTATTATCT CGTCAAGTTG GTGTACCATA CATCGTTGTA      100
45 TTCTTGAACA AAGTAGATAT GGTGATGAC GAAGAATTAC TTGAATTAGT      150
TGAAATGGAA GTTCGTGACC TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTCTGT AATCGCTGGT TCAGCTTTAA GAGCTTTAGA AGGCGACGCT      250
KCATACGAAG AAAAAATTCT TGAATTGATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GAACGTGATA ACGACAAACC ATTCATGATG CCAGTTGAGG      350
50 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG ACGTGTTGAA      400
CGTGGACAAG YTCGTGTTGG TGACGTTATC GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACCTG TAACTGGTGT TGAAATGTTC CGTAAATTAT      500
TAGACTACGC TGAAGCAGGC GATAACATTG GTGCGTTACT ACGTGGTGT      550
TCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTAAAC CAGGTACAAT      600
55 CACACCTCAT ACAAATTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
TTCYGTACGA CTGACGTAAAC TRGTGTTGTY GAATTACCAG AAGGAACTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835
60

```

2) INFORMATION FOR SEQ ID NO: 69

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus pseudoavium*
 15 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
20	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATACGATTTC	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTG	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAACT	TTACGTTTTC	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTG	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

2) INFORMATION FOR SEQ ID NO: 70

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAACGTA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

```

      CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGYGGAAG      350
      ACGTAYTCTC AATCACTGGT CGTGGAAGTG TTGCAACTGG TCGTGTTGAA      400
      CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATTGCTGA      450
      AGAAACTGCT AAAACAAGTG TTACAGGTGT TGAATGTTC CGTAAATTGT      500
5     TGGATTACGC TGAAGCGGGC GACAACATTG GTGCATTATT ACGTGGTGT      550
      GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT      600
      CACTCCACAT ACAAATTCT CTGCAGAGT TTACGTTTTA ACTAAAGAAG      650
      AAGGCGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC      700
      TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA      750
10    AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC      800
      CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATT      835

```

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

```

30    CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
      GTGAACACAT CTTGTTATCT CGTAACGTAG GTGTTCTTA CATCGTTGTA      100
      TTCTTAAACA AAATGGATAT GGTGATGAC GAAGAATTAT TAGAATTAGT      150
      AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTC CCAGGCGATG      200
35    ACACTCCAGT TATTGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGATCCA      250
      GTTTACGAAG AAAAAATCTT CGAATTAATG GCTGCAGTTG ACGAATATAT      300
      CCCAACTCCA GAACGTGATA CTGAAAAACC ATTCATGATG CCAGTTGAGG      350
      ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
      CGTGGACAAG TTCGCGTTGG TGACGTTGTA GAAATCGTTG GTATCGACGA      450
40    AGAAACAGCT CAAACTACTG TAACAGGTGT TGAATGTTC CGTAAATTAT      500
      TAGACTACGC TGAAGCAGGC GATAACATCG GTGCTTTATT ACGTGGGGTT      550
      GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAC CAGGAACAAT      600
      CACTCCTCAT ACAAATTCTG TAGCTGAAGT TTACGTTTTA ACTAAAGAAG      650
      AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC      700
45    TTCCGTACAA CTGACGTAAC TGGTGTGTA GAATTACGCG AAGGTACTGA      750
      AATGGTAATG CCTGGTGACA ACGTAACTAT CGACGTTGAA TTAATCCACC      800
      CAATCGCTAT CGAAGACGGA ACTCGTTTCT CTATT      835

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50

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus solitarius*

(B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

```

GAGCTATCTT GGTAGTTTCT GCAGCTGATG GCCCAATGCC ACAAACTCGT      50
GAACATATTT TGTGTGTCACG TAATGTAGGT GTACCTTACA TCGTTGTGTT      100
CTTGAACAAA ATGGATATGG TTGATGACGA AGAATTACTT GAGTTAGTTG      150
10 AAATGGAAGT ACGTGATCTA TTATCTGAAT ACGACTTCCC AGGAGATGAT      200
ACTCCAGTTA TTTCCGGTTC AGCTTTGAAA GCTTTAGAAG GCGACGAAGA      250
ATATGAACAA AAAATTATGG ACTTAATGGA TGCAGTTGAT GACTACATTC      300
CAACTCCTGA ACGTGACCAT GACAAACCAT TCATGATGCC AATTGAAGAT      350
GTATTTTCAA TTACAGGCCG TGGTACTGTT GCTACAGGAC GTGTTGAACG      400
15 CGGGACTATC AAAGTCGGCG ATGAAGTTGA CATTATTGGT ATTCATGAAG      450
ACGTTAAAAA GACAACAGTT ACTGGTGTAG AAATGTTCCG TAAATTGTTG      500
GACTACGCTG AAGCAGGCGA TAACATTGGT ACTTTGTTAC GTGGTGTTC      550
TCGTGATGAT ATCGAACGTG GTCAAGTATT AGCTAAACCA GGTTCAATCA      600
CACCACATAC AAGATTCTCT GCTGAAGTTT ATGTTTTGAC TAAAGAAGAA      650
20 GCGCGACGTC ATACTCCATT CTTCTCAAAC TATCGTCCTC AATTCTACTT      700
CCGTACAAC TATATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA      750
TGGTAATGCC AGGTGATAAT GTAACAATGG ATGTTGAATT AATCCACCCA      800
GTCGCTATCG AAGAAGGAAC TCG                                823

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25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

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30 (A) LENGTH: 835 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: ATCC 25788

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

```

CGGTGCAATC TTGGTCGTAT CAGCGACAGA TGGCCCAATG CCACAAACAC      50
GGGAGCATAT TTTGCTTTCT CGTCAAGTGG GTGTGAAACA TTTGATCGTC      100
45 TTTTGAATA AGACGGACCT TGTCGATGAT GACGAGTTGA TCGATTTAGT      150
TGAAATGGAA GTCAGAGAAT TGCTGACTGA ATATGATTTT CCTGGCGACG      200
ACATTCTGT GATCAAGGGC TCTGCGTTAA AAGCCTTGA AGGGGACCCA      250
GATGCTGAAG CAGCGATCTT AACGCTGATG GATACAGTAG ATGAATATAT      300
CCCAACGCCA GAACGTGATA CTGACAAACC ATTGTTGTTA CCGATCGAAG      350
50 ATGTCTTTTC GATCACAGGA CGGGGGACCG TTGCTTCTGG TCGGATCGAT      400
CGCGGCATGG TAAAGTCGG GGATGAAGTA GAAATCGTCG GAATCAAACC      450
TGAAACACAA AAAGCAGTCG TGACAGGGGT AGAAATGTTC CGCAAAACGA      500
TGGACTTCGG AGAAGCTGGC GATAACGTAG GGGTATTGTT ACGGGGCATC      550
ACCCGTGATG AAATTGAACG TGGCCAAGTG TTAGCAAAAC CAGGTTCTAT      600
55 CACACCGCAT ACGAAATTCC AAGCGGAAGT CTATGTGTTG ACAAAGAAG      650
AAGGCGGTCG CCATACCCCA TTCTTTAATA ATTATCGCCC ACAATTTTAC      700
TTCCGTACAA CGGACGTAAC TGGAATATC GTTTTACCAG AAGGAACGGA      750
AATGGTGATG CCTGGTGACA ACGTAACGAT CGATGTGGAA TTGATCCATC      800
CGATCGCTGT AGAAAATGGA ACCACCTTCT CGATT                                835

```

60

2) INFORMATION FOR SEQ ID NO: 74

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus saprophyticus*
 15 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

	TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
20	AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
	ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
	AGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACTTGCTT	200
	TTTTAAGTAT	AGGTATAAAA	TACGATTGAT	TAAAACAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAATAA	GCCTTTATAC	TTTACCTAT	TACTTTTTAT	300
25	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAGGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT			380

30 2) INFORMATION FOR SEQ ID NO: 75

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG	TCGTATCAGC	GACAGATGGC	CCAATGCCAC	AAACACGGGA	50
	GCATATTTTG	CTTTCTCGTC	AAGTGGGTGT	GAAACATTTG	ATCGTCTTTT	100
	TGAATAAGAC	GGACCTTGTC	GATGATGACG	AGTTGATCGA	TTTAGTTGAA	150
	ATGGAAGTCA	GAGAATTGCT	GACTGAATAT	GATTTTCCTG	GCGACGACAT	200
50	TCCTGTGATC	AAGGGCTCTG	CGTTAAAAGC	CTTGGAAGGG	GACCCAGATG	250
	CTGAAGCAGC	GATCTTAACG	CTGATGGATA	CGGTAGATGA	ATATATCCCA	300
	ACGCCAGAAC	GTGATACTGA	CAAACCATTG	TTGTTACCGA	TCGAAGATGT	350
	CTTTTCGATC	ACAGGACGGG	GGACCGTTGC	TTCTGGTCCG	ATCGATCGCG	400
	GCATGGTAAA	AGTCGGGGAT	GAAGTAGAAA	TCGTCGGAAT	CAAACCTGAA	450
55	ACACAAAAAG	CAGTCGTGAC	AGGGGTAGAA	ATGTTCCGCA	AAACGATGGA	500
	CTTCGGAGAA	GCTGGCGATA	ACGTAGGGGT	ATTGTTACGG	GGCATCACCC	550
	GTGATGAAAT	TGAACGTGGC	CAAGTGTTAG	CAAAACCAGG	TTCTATCACA	600
	CCGCATACGA	AATTCCAAGC	GGAAGTCTAT	GTGTTGACAA	AAGAAGAAGG	650
60	CGGTCGCCAT	ACCCCA				666

2) INFORMATION FOR SEQ ID NO: 76

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus gallinarum*
 15 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

	TGGTGCGATT	TTAGTTGTAT	CCGCAACAGA	TGGTCCAATG	CCTCAAACCC	50
20	GGGAACATAT	CTTGCTTTTC	AGACAAAGTTG	GTGTGAAACA	TCTGATTGTT	100
	TTCTTGAACA	AAATCGATTT	AGTCGATGAC	GAAGAATTGA	TTGATTTAGT	150
	AGAAATGGAA	GTAAGAGAAC	TGCTATCTGA	ATATAATTTT	CCAGGGGATG	200
	ACATTCTGT	TATCAAAGGT	TGGCATTA	AAGCGTTGGA	AGGAGACCCT	250
	GATGCAGAA	CTGCCATCAT	GGAATTAATG	GATACAGTAG	ACAGCTATAT	300
25	CCCAACACCT	GAGCGTGATA	CAGACAAACC	ATTACTCTTG	CCAGTTGAAG	350
	ATGTCTTTTC	GATTACTGGA	CGAGGAACAG	TTGCTTCCGG	ACGGATCGAT	400
	CGGGGAACAG	TTCGGGTAGG	CGATGAAGTA	GAAATCGTCG	GTATCAAACC	450
	TGAAACCCAA	AAAGCTGTAG	TGACAGGCGT	CGAAATGTTC	CGCAAGACGA	500
	TGGACTTTGG	GGAAGCCGGT	GACAATGTAG	GTGTCTTGCT	GAGAGGGATC	550
30	ACTCGTGACG	AAATTGAACG	AGGACAAGTG	TTGGCTAAAC	CAGGTTCGAT	600
	CACACCACAT	ACAAAATTCC	AAGCAGAAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGTGGTCG	TCATACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTTTAT	700
	TTCCGTACAA	CGGATGTGAC	AGGGAACATT	ACATTGCCTG	AAGGAACAGA	750
35	A					751

2) INFORMATION FOR SEQ ID NO: 77

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Ehrlichia canis*
 50 (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

	TGCAGCAATA	TTAGTAGTGT	CTGCAACTGA	TGGAGCAATG	CCACAAACAA	50
55	GAGAACATAT	ATTATTAGCA	AAGCAAGTAG	GTGTAAAAGA	TATAGTAGTG	100
	TGGATGAATA	AGTGTGATGT	TGTAGATGAT	GAAGAAATGT	TGTCATTAGT	150
	TGAAATGGAA	ATAAGGGAAT	TGTTATCAA	ATATGGGTAT	CCTGGGGATG	200
	ATATAGATGT	AGTTAGAGGA	TCTGCAGTTA	AAGCATTAGA	AGAAGAAACA	250
	GGCTCAGGTG	TGTGGAGTGA	AAAAATAATG	GAATTGATGA	ATGCTTTAGA	300
60	AAAAATAAGT	TTACCAGTAA	GAGAAAAAGA	TAAGCCATTT	TTAATGTCAA	350

	TAGAAGATGT	GTTTTCAATA	CCTGGAAGAG	GTACAGTAGT	AACAGGAAGA	400
	ATAGAAAGAG	GAGTAATTAG	AGTAGGGGAT	AAAATAGAGA	TAGTAGGATT	450
	GCGTGAGATA	CAAAGTACAG	TATGTACAGG	TGTTGAAATG	TTTCATAAAG	500
	CATTAGATGC	AGGAGAAGCA	GGGGATAATG	CTGGAATATT	GTTAAGAGGG	550
5	ATAAAAAAAG	AAGATGTAGA	AAGAGGGCAA	GTATTGAGTG	CACCTGGACA	600
	GATACATTCA	TATAAGAGAT	TTAAGGCAGA	GGTATATATA	TTGAAAAAAG	650
	AAGAAGGAGG	AAGACATACT	CCATTTTCT	CAAATTACCA	GCCGCAATTT	700
	TATGTTAGAA	CAACAGATGT	AACAGGGAAT	ATAAAGTTAC	CAGAAGGAGT	750
	AGAAATGGTA	ATGCCAGGGG	ATAATATAAA	TATCGAAGTG	AGTTTGGATA	800
10	AGCCTGTTGC	TATTGATCAA	GGATTGAGAT	TTGC		834

2) INFORMATION FOR SEQ ID NO: 78

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
35	GAGTGGGAAG	CGAAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTAYAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
40	ACGAAGGCCG	TGCTGCTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
45	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGT				817

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```

5      CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
      CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTCCT      100
      GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA      150
      TGGAAGTTCG TGAAC TTCTG TCTCAGTACG ACTTCCCGGG CGACGACACT      200
10     CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG      250
      GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG      300
      AACCAGAGCG TGC GATTGAC AAGCCGTTCG TGCTGCCGAT CGAAGACGTG      350
      TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG      400
      TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC      450
15     AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAAC TCTGGACGAA      500
      GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA      550
      AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC      600
      ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT      650
      CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC      700
20     TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA      750
      TGCCGGGCGA CAACATCAAA ATGGTTGTGA CCCTGATCCA CCCGATCGCG      800
      ATGGACGACG GTCTGCGTTT CGCAA      825
  
```

25 2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 829 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

```

      GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
45     GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTC CGGGCGACGA      200
      CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
      AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC      300
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
      CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
50     GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT      450
      ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG      600
      CCKCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG      650
55     CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
      GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG      750
      GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
      CGCGATGGAC GACGGTCTGC GTTTCGCAA      829
  
```

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 20 TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT 150
 TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG 200
 ACACCCCGAT CATTCGTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT 250
 GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 25 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA 450
 TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGCTG 500
 ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA 600
 30 GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCATCCGA 800
 TCGCGATGGA CGACGG 816

35

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 50 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG 50
 55 CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT 100
 TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC 150
 GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CCGGCGACGA 200
 CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GGCGACAAAG 250
 AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC 300
 60 CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA 350

50

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAACA	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
5	GCGAGGAGAT	CGTTTCGCGG	CAGGTTCTCT	GCAAGCCCGG	TAGCGTGACC	600
	CCGCACACCG	AGTTTCGAGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCACCC	TTCCCGAGGG	CACCGAGATG	750
	GTCATGCCGG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
10	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

2) INFORMATION FOR SEQ ID NO: 83

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCCAATG	250
35	GAGAAATGGG	AGACAAGATT	GTAAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCCTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCTCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTG	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
40	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
45	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

```

5      GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
      GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA      100
      TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
      ATGGAAGTTC GYGAATTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT      200
10     CCCAGTTGTT AAAGGTTTCA CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT      250
      GGGAAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA      300
      GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT      350
      ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG      400
      GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT      450
15     GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGCACGA      500
      AGGCCGTGCT GGTGAGAACG TTGGTGTCTT GCTGCGTGGT ATCAAGCGTG      550
      AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTT AATCAAACCA      600
      CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG      650
      CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA      700
20     CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC      800
      GATGGATGAC GGTCTGCGTT TCGCAA      826
  
```

25 2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```

      TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT      100
      TTCTTAAACA AGTGTGACAT GGTGATGAT GAAGAGTTAT TAGAGCTAGT      150
45     TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG      200
      ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA      250
      GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT      300
      TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG      350
      ATGTATTCTC AATTTCAAGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG      400
50     CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTTCGTCC      450
      AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG      500
      ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTCT TGGACTTAAG      550
      AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA      600
      GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG      650
55     GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC      700
      CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT      750
      GGTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA      800
      TCGCTAGGAT GAAGGGTTAC GTTTTGCA      828
  
```

60

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC 50
 GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCKAG ACTGGTTGTA 100
 20 TTCATGAACA AGTGYGACAT GGTAGACGAC GCTGAAATGY TGGAACCTCGT 150
 TGAAATGGAA ATGCGTGAAC TGCTTTCAGC YTACGAATTC GAYGGYGACA 200
 ACACTCCKTT CATTACAGGT TCTGCTCTTG GTGCRTTGAA YGGCGTTGAA 250
 AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG ACACTTGGAT 300
 TCCTTTGCCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG 350
 25 ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCTACTGG TCGTATCGAA 400
 GCTGGTGTTA TCCATGTAGG TGACCAAGTT GAAATCCTCG GTTTGGGTGA 450
 AGACAAGAAG TCTGTTGTAA CTGGTGTGTA AATGTTCCGC AAGTTGCTGG 500
 ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTGCTCCG TGGTATCGAC 550
 AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAGCCCG GTCAGATTAA 600
 30 ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTTGAAG AAAGAAGAAG 650
 GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTATCTG 700
 CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT 750
 GGTAATGCCT GGTGATAACG TAGAAATCAG TGTAGAACTG ATCTACCCGG 800
 TAGCATTGAA CGTAGGTTTG CGTTTCGCT 829

35

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella haemolysans*
 50 (B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG 50
 55 CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT 100
 AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA 150
 TGGAAGTTCTG TGAACATTA TCTGAATACG GATTGACGAG AGATGAACTA 200
 CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC 250
 AGAAAAAGCT ATCATCGAAT TAATGGAAAC AGTTGACGAA TACATCCCAA 300
 60 CTCCAGAACG TGATAACGCT AAACCATTCA TGATGCCAGT TGAGGACGTA 350

```

      TTCTCAATCA CAGGTCGTGG TACAGTTGCT ACTGGACGTG TTGAACGTGG      400
      ACAAGTTAAA GTTGGAGACG TAGTAGAAAT CGTTGGATTA ACTGAAGAAC      450
      CAGCTTCAAC TACTGTAACA GGTGTTGAAA TGTTCCTGTA ATTATTAGAT      500
      TACGCTGAAG CAGGAGATAA CATCGGTGCA TTATTACGTG GTGTTGCTCG      550
5     TGAAGACATC GAACGTGGAC AAGTTTTAGC AGCTCCTAAA ACAATCACTC      600
      CACACACTCA ATTCGTAGCT GACGTGTACG TATTATCTAA AGAAGAAGGT      650
      GGACGTCACA CTCCATTCTT CACAAACTAC CGTCCTCAAT TCTACTTCCG      700
      TACTACTGAC GTAACGGTG TAGTTACTTT ACCAGAAGGT ACTGAAATGG      750
      TAATGCCTGG GGATAACGTA TCAATCAACG TAGAACTTAT TTCTCCAATC      800
10    GCGATCGAAG AAGGAACTCG TTTCTCAA      828

```

2) INFORMATION FOR SEQ ID NO: 88

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

```

30    TCTTAGTAAT CGCTGCTACA GATGGTCCTA TGGCTCAAAC TCGTGAACAC      50
      ATCCTATTAT CTCGTAACGT TGGAGTACCT AAAATTGTTG TATTCTTAAA      100
      CAAATGTGAT ATGGTTGATG ACGAAGAGTT ATTAGAATTA GTAGAAATGG      150
      AAGTTCGTGA ACTATTATCT GAATACGGAT TTGATGGAGA TGAAGTACCA      200
      GTAATCAAAG GTTCAGCTCT TAAAGCTCTT GAAGGAGATG CAGATGCTGA      250
35    AAAAGCTATC ATCGAATTAA TGGAAACAGT TGACGAGTAC ATCCCAACTC      300
      CAGAACGTGA TAACGCTAAA CCATTTATGA TGCCAGTTGA GGACGTGTTT      350
      TCAATCACAG GTCGTGGTAC AGTTGCTACT GGACGTGTTG AACGTGGACA      400
      AGTTAAAGTT GGTGACGTAG TAGAAATCGT TGGATTAACT GAAGAACCAG      450
      CTTCAACTAC TGTAACAGGT GTTGAAATGT TCCGTAAATT ATTAGATTAC      500
40    GCTGAAGCAG GAGATAACAT CGGTGCATTA TTACGTGGTG TTGCTCGTGA      550
      AGATATCGAA CGTGGACAAG TTTTAGCAGC TCCTAAAACA ATCACTCCAC      600
      ATACTCAATT CGTAGCTGAT GTGTACGTAT TATCTAAAGA AGAAGGTGGA      650
      CGTCACACTC CATTCTTCAC AACTACCGT CCACAATTCT ACTTCCGTAC      700
      TACTGACGTA ACTGGTGTAG TTACTTTACC AGAAGGTACT GAAATGGTAA      750
45    TGCCTGGGGA CAACGTATCA ATCAACGTAG AACTTATTTC TCCAATCGCT      800
      ATCGAAGAAG GAACTCGTTT CTC      823

```

50 2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
 (B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

```

5      GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA      50
      GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT      100
      TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA      150
      ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC      200
10     CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT      250
      GGAAGAAAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG      300
      GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT      350
      GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG      400
      GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT      450
15     GCAAAAACCA CCGTAACCGG TGTGAAATG TTCCGTAAAT TACTTGACGA      500
      AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG      550
      AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG      600
      CACACTGACT TCGAATCTGA AGTGACGTA TTGTCCAAAG AAGAAGGTGG      650
      TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA      700
20     CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT      750
      ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC      800
      GATGGACCAA GGTTTACGTT TCGCTATCG      829
  
```

25 2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 833 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus aphrophilus*
 (B) STRAIN: ATCC 33389

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

```

      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTCA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG      200
      ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACCTAG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC      600
      TCCGCACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAT      750
      GGTTATGCCT GGCATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

60

55

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

CGGCGCTATC TTAGTTGTAG CAGCAACTGA TGGTCCTATG CCTCAAACCTC 50
 GTGAACACAT CTTATTAGGC CGCCAAGTTG GTGTCCTTA CATCATCGTA 100
 20 TTCTTAAATA AATGCGATAT GGTAGATGAT GAAGAATTAT TAGAATTAGT 150
 TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGATTTC CCAGGTGACG 200
 ATACTCCTAT CGTTCGTGGT TCAGCATTAC AAGCATTAAA TGGTGTGCCT 250
 GAGTGGAAG AAAAAATCAT TGAATTAGCA CAACACTTAG ATTCTTATAT 300
 CCCTGAGCCT GAGCGTGCGA TTGATAAACC TTTCTTATTA CCAATCGAAG 350
 25 ACGTATTCTC AATTTCAGGT CGTGGTACAG TAGTAACCGG TCGTGTGAG 400
 CGTGGTATCA TCAAATCAGG TGAAGAAGT GAAATCGTAG GGATTAAAGA 450
 AACGACAAAA ACAACAGTAA CCGGTGTTGA GATGTTCCGT AAACATTAG 500
 ACGAAGGTCG TCGGGGTGAA AACGTAGGTG CTTATTACG TGGTACTAAA 550
 CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTACAATTAC 600
 30 ACCACACACT GATTTTGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ATCGTCCTCA GTTCTACTTC 700
 CGYACAACGG ACGTAACAGG AACGATTGAA TTACCTGAAG ATGTTGAGAT 750
 GGTAATGCCT GGTGATAATA TCAAGATGAC AGTAAGCTTA ATTCACCCTA 800
 TCGCGATGGA CGAAG 815
 35

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 50 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCAATG CCACAAACTC 50
 55 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCATA CATCATCGTA 100
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCAGGTGACG 200
 ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCATTAAA TGGCGTAGCA 250
 GAATGGGAAG AAAAAATCCT TGAGTTAGCA AACCCTTAG ATACTTACAT 300
 60 CCCAGAACCA GAGCGTGCAA TTGACCAACC GTTCCTTCTT CCAATCGAAG 350

	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGTA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
5	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTCGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTT	700
	CGTACAACCTG	ACGTAACCTG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
10	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 93

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTGCGTGA	ACTTCTTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
	GTAGTACGTG	GTTACGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGCGA	250
35	AGAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATTC	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGATAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAAA	GACACTGCGA	450
	AAACAACAGT	AACTGGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
40	CGTGCGGGTG	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCTGA	ATCAGAAGTG	TACGTATTAT	CAAAAGAAGA	AGGTGGTTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
	TGACGTAAC	GGTACTATTG	AATTACCAGA	AGGCGTAGAA	ATGGTAATGC	750
45	CAGGCGATAA	CATCAAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTTGC	GATT			824

50 2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

```

5      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCCTTA CATCATCGTG      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
      TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
10     ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT      300
      TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
      CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
15     GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
      GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
20     CGTACAACCTG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAT      750
      GGTTATGCCT GGTGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

25 2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 824 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus paraphrophilus*
 (B) STRAIN: ATCC 29241

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

```

      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCCTTA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
      ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCCTTGG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAT      750
      GGTAATGCCT GGCGATAACA TCAAAATGAC CGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTT      824
  
```

60

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
 (B) STRAIN: ATCC 33393

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

GCTATCTTAG TAGTAGCAGC AACTGATGGT CCTATGCCAC AAACCTCGTGA 50
 GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT 100
 20 TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA 150
 ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCAG GTGATGATAC 200
 TCCAATCATT CGTGGTTCTG CATTACAAGC GTTAAACGGC GTAGCAGAAT 250
 GGGAAAGAAA AATCCTTGAA TTAGCTCAAG CATTAGATAC TTACATTCCT 300
 GAACCTGAGC GTGCAATCGA CCAACCGTTC CTTCTTCCAA TTGAAGACGT 350
 25 GTTCTCAATC TCTGGTCGTG GTACTGTAGT AACAGGTCGT GTAGAGCGTG 400
 GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTTGGTAT CAAACCAACT 450
 GCGAAAACAA CCGTAACCGG TGTGAAATG TTCCGTAAAT TACTTGACGA 500
 AGGTCGTGCA GGTGAAAACA TCGGTGCATT ATTACGTGGT ACTAAACGTG 550
 AAGAAATCGA ACGTGGTCAA GTATTAGCGA AACC GG GTTC AATCACTCCA 600
 30 CACACTGACT TCGAATCTGA AGGTGACGTA TTATCTAAAG AAGAAGGTGG 650
 TCGTCATACT CCATTCTTCA AAGGTACCG TCCACAATTC TATTTCCTGA 700
 CAACTGACGT AACC GG TACT ATCGAGTTAC CGGAAGGCGT GGAAATGGTT 750
 ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATCC ACCCAATCGC 800
 GATGGACCAA GGTTTACG 818

35

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
 50 (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

CGGCGCTATC CTGGTTGTTG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50
 55 GTGAGCACAT CCTGCTGGGT CGTCAGGTG GCGTTCCTTW CATCATCGTR 100
 TTCCTGAACA AATGCGACAT GGTGATGAT GAAGAGCTGC TGGAAGTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCWGGYGATG 200
 ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGYGMACCT 250
 GAGTGGGAAG CTAAGATCGT AGAAGTGGCT GAAACTCTGG ATTCTTACAT 300
 60 YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCTGCTG CCAATCGAAG 350

ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTTACCGG TCGTG TAGAG 400
 CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA 450
 TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAAGTCTGG 500
 ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550
 5 CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA 600
 GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 CGTACAACCTG ACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAT 750
 GGTAATGCCA GGC 763
 10

2) INFORMATION FOR SEQ ID NO: 98

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Kingella kingae*
 25 (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC 50
 30 GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA 100
 TTCATGAACA AATGCGACAT GGTCGATGAT GCTGAGTTGT TGGAATTGGT 150
 TGAAATGGAA ATCCGTGACT TGTTGTCTAG CTACGATTTT CCAGGCGACG 200
 ATTGCCCAAT CGTTCAAGGT TCTGCATTGC GYGCATTGGA AGGCGACGCT 250
 GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT 300
 35 TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTTG CCAATCGAAG 350
 ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTG TAGAG 400
 CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA 450
 CACGCAAAAA ACCACTTGTA CTGGCGTGGA AATGTTCCGC AAATTGTTGG 500
 ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG 550
 40 CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC 600
 TCCGCACACT AAATTTGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG 650
 GTGGCCGTCA TACGCCATTG TTCGCTAACT ACCGCCACCA ATTCTACTTC 700
 CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAT 750
 GGTTATGCCA GGCGAAAACG TGAAAATCAC TGTTGAGTTG ATTGCACCTA 800
 45 TCGCTAGGAA AACGGTTTGC GTTTTGCG 828

2) INFORMATION FOR SEQ ID NO: 99

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

```

5  GGC GCG ATCC TGG TTG TTG C TGC GACT GAC GGC CCG ATGC CGC AGACT CG      50
   TGAG CAC ATC CTG CTG GGT C GTC AGGT AGG CGT TCC GTAC ATC ATC GTGT      100
   TCCT GAA CAA ATG CGA CAT G GTT GAT GAC G AAG AGCT GCT GGAG CTGG TT      150
   GAA ATG GAA G TCC GTG AGCT GCT GTCT CAG TAC GACT TCC CGGG CGAC GA      200
   CAC GCC GAT C GTT CGT GGT CCG CTCT GAA AGCG CTG GAA GGCG AAG CAG      250
10  ACT GGG AAG C GAA AAT CAT C GAA CTG GCT G TAC CTG GA TTCT TAC ATC      300
   CCG GA ACC AG AGCG TGCG AT TGACA AGCC G TTC CTG CTG C CGAT CGA AGA      350
   CGT ATT CTCC ATCT CCG GTC GTGG TACCG T GTT ACC GGT CGT GTAG AGC      400
   GCG GTAT CAT CAA AGT GGG C GAAGA AGTT G AAAT CGT TGG TAT CAA AGAG      450
   ACT GCG AAG T CTAC CTG TAC TGG CGT TGA ATG TTCC GCA AACT GCT GGA      500
15  CGA AGGCC GT GCT GGT GAG ACG TTGG TGT TCT GCT GCG T GGT ATCAA AC      550
   GTGA AGAA AT CGA ACG TGG CAG GTACT GG CTA AGCC GGG CTCT ATCA AG      600
   CCG CAC ACCA AGTT CGA ATC TGA AGT GTAC ATT CTGTCCA AAG ACCA AGG      650
   CGGCC GTC AT ACT CCG TTCT TCAA AGGCTA CCG TCC GCG AG TTCT ACT TCC      700
   GTACA ACTGA CGT GACT GGC ACC ATCG AAC TGCC GGA AGG CGT AGAG ATG      750
20  GTC ATGCC GG GCG ACA ACAT CAAA ATGG TT GTT ACCCT GA TTC ACCCG AT      800
   CGCG ATGG AC GAT GGT CTG C GTTTC GCA      828

```

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 749 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Klebsiella oxytoca
(B) STRAIN: ATCC 33496

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

```

40  GATGCCGCAG ACTCGTGAGC ACATCCTGCT GGGTCGTCAG GTAGGCGTTC      50
   CGTACATCAT CGTGTTCCTG AACAAAGTGCG ACATGGTTGA TGACGAAGAG      100
   CTGCTGGAAC TGGTTGAAAT GGAAGTTCGT GAACTTCTGT CTCAGTACGA      150
   TTTCCCGGGC GACGACACTC CGATCGTTCG TGTTTCTGCT CTGAAAGCGC      200
45  TGGAAGGCGA CGCWGAGTGG GAAKCKAAAA TCATCGAACT GGCTGGCTTC      250
   CTGGATTCTT ACATTCCGGA ACCAGAGCGT GCGATTGACA AGCCGTTCCCT      300
   GCTGCCGATC GAAGACGTAT TCTCCATCTC CGGTCGTGGT ACCGTTGTTA      350
   CCGGTCGTGT AGAGCGCGGT ATCATCAAAG TTGGCGAAGA AGTTGAAATY      400
   GTTGGTATYA AAGACACTGC TAAGTCTACC TGTACTGGCG TTGAAATGTT      450
50  CCGCAAAC TG CTGGACGAAG GCCGYGCTGG TGAGAACGTT GGTGTTCTGC      500
   TGCGTGGTAT CAAACGTGAA GAAATCGAAC GTGGTCAGGT ACTGGCTAAG      550
   CCGGGCTCTA TCAAGCCGCA CACCAAGTTC GAATCTGAAG TTTATATCCT      600
   GTCCAAAGAC GAAGGCGGCC GTCACACTCC GTTCTTCAA GGCTACCGTC      650
   CGCAGTTCTA CTTCCGTACA ACTGACGTGA CTGGCACCAT CGAACTGCCG      700
55  GAAGGCCGTAG AGATGGTTAT GCCGGGCGAC AACATCAAAA TGGTTGTTA      749

```

2) INFORMATION FOR SEQ ID NO: 101

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

```

15 TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
   GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCGTA CATCATCGTG      100
   TTCCTGAACA AATGCGACAT GGTGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
   TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG      200
   ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
20 GACTGGGAAG CGAAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
   CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG      350
   ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAAGG      400
   CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
   TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAAGTGTCTG      500
25 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
   CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA      600
   GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG      650
   GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
   CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
30 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATTCACCCRA      800
   TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830

```

35 2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```

50 CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
   TCCTGCTGGG TCGTCAGGTA GCGTTCGTA ACATCATCGT GTTCCTGAAC      100
   AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TTGAGATGGA      150
   AGTTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA      200
55 TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA      250
   GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC      300
   AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
   CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
   ATCAAAGTAG GTGAAGAAGT TGAATCGTTT GGTATCAAAG AAACCGCGAA      450
60 AACCACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500

```

GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC 600
 CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC 650
 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
 5 GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
 GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
 ACGACG 806

10

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA 50
 TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG 100
 GAACTGGTTG AGATGGAAGT TCGTGAACTG CTGTCTCAGT ACGATTTCCC 150
 30 GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG 200
 GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT 250
 ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC 300
 GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC 350
 GTGTAGAGCG CGGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT 400
 35 ATCAAAGAAA CCGCGAAAAC CACCTGTACT GGCGTTGAAA TGTTCCGCAA 450
 ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG 500
 GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC 550
 ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGATCA TCCTGTCCAA 600
 AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT 650
 40 TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC 700
 GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA 743

45 2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
 (B) STRAIN: ATCC 13884

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	150
5	TTCGTGAAC	RCTGTCTCAG	TACGATTTCC	CGGGCGACGA	CACCCCGATC	200
	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAACTGGCTG	GCCACCTGGA	TACCTATATC	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	400
10	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAA	ACCGCGAAAA	450
	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	CGGCCGTCAC	650
15	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGAAGTGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCATCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCAA				819

20

2) INFORMATION FOR SEQ ID NO: 105

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Kluyvera ascorbata*
(B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
40	TTCCTGAACA	AATGYGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGATGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAACGTGCTA	TCGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
45	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGCCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCTATCAA	600
50	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA	CC		832

55

2) INFORMATION FOR SEQ ID NO: 106

- 60 (i) SEQUENCE CHARACTERISTICS:

64

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
15	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGCTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
20	CCCAGAACCA	GAGCGTGCGA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCTGTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGCCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCCATCAA	600
	GCCGCACACC	AAATTGCAAT	CTGAAGTTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*
 (B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAAC TTC	TGCTCTAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
55	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCCTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACCGTTG	TTACCGGTTCG	TGTAGAACGC	400
	GGTATCATCA	AAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
60	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAACGT	550

65

GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGTT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGACAT TCTGTCCAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
 ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TTGAGATGGT 750
 5 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG 800
 CGAAGGACGA AGGTCTGCGT TTCGCA 826

10 2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus casei* subsp. *casei*
 (B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

25 GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACATATCT TACTTTCACG 50
 TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG 100
 TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA 150
 TTAAGTGAAT ATGAATTCCC TGGCGATGAC ATTCCTGTAA TCAAAGGTTC 200
 30 AGCTCTTAAA GCACTTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG 250
 AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT 300
 GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG 350
 TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG 400
 ACCAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA 450
 35 ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA 500
 CAACATTGGC GCACTTCTAC GTGGTGTGTC TCGTGAAGAT ATCCAACGTG 550
 GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAAA 600
 GCTGAACTT ATGTTTTAAC TAAAGAAGAA GGTGGACGTC ACACTCCATT 650
 CTTCAACAAC TACCGCCAC AATTCTATTT CCGTACTACT GACGTAAGT 700
 40 GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC 750
 ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC 800
 TAA 803

45

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
 (B) STRAIN: ATCC 19435

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

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CGGTGCAATC CTCGTTGTTG CTGCAACTGA TGGACCAATG CCACAAACTC      50
GTGAACACAT CTTGCTTTCA CGTCAAGTTG GTGTTAAATA CCTTATCGTC      100
TTCCTTAACA AGGCTGACCT TGTTGATGAT GAAGAATTGA TGGAACCTCGT      150
5  TGAAATGGAA GTTCGTGACC TCTTGAGCGA ATACGACTTC CCAGGTGACG      200
ATATTCTGT  AATCGCTGGT TCAGCACTTG GTGCTTTGAA CCGTGAACCA      250
CAATGGGTTG CTAAAGTTGA AGAATTGATG GACATCGTTG ATGAATACAT      300
CCCAACTCCA GAACGCGACA CTGACAAACC ACTCCTTCTT CCAGTCGAAG      350
ACGTATTCTC TATCACTGGT CGTGGTACAG TTGCTTCAGG ACGTATCGAA      400
10  CGTGGTACTG TTAAAGTTGG TGACGAAGTT GAAATCGTTG GTATCAAAGA      450
AGAAACTAAA AAAGCTGTTG TTACTGGTAT CGAAATGTTT CGTAAAACAC      500
TTACTGAAGG TCTTGCTGGT GATAACGTCG GTGCACTTCT CCGTGGTATC      550
CAACGTGACG AAATCGAACG TGGTCAAGTT ATTGCTAAAC CAGGTTCAAT      600
CACTCCACAC AAACTTTTCG AAGGTGAAGT TTACGTATTG AGCAAAGAAG      650
15  AAGGCGGACG TCACACTCCA TTCTTCGACA ACTACCGTCC TCAATTCTAC      700
TTCCACACAA CTGACGTTAC TGGTTCAGTT AAACCTCCAG AAGGAACTGA      750
AATGGTAATG CCTGGTGACA ACGTGCATAT CGACGTTGAA TTGATCCACC      800
CAGTTGCGAT CGAACAAGGT ACTAC                                     825

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20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 824 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Leclercia adecarboxylata
      (B) STRAIN: ATCC 23216

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

```

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCAATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTTC ATCATCGTGT      100
40  TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
GAGATGGAAG TTCGTGAAC TCTGTCCCAG TACGACTTCC CGGGCGACGA      200
-----
CACCCCAATC GTTCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
AGTGGGAAGA GAAAATCATC GARCTGGCTG GCTACCTGGA TTCCTACATC      300
CCAGAGCCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
45  CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
GCGGTATCAT CAARGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAGGAC      450
ACTGCTAAGT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCCGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CTAAGCCAGG CTCYATCAAG      600
50  CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGTCYA AAGACGAAGG      650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACKACTGA CGTGACCGGT ACCATCGARC TGCCAGAAGG CGTTGAGATG      750
GTAATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT      800
CGCAATGGAC GATGGTCTGC GTTC                                     824

```

55

2) INFORMATION FOR SEQ ID NO: 111

60 (i) SEQUENCE CHARACTERISTICS:

67

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella micdadei*
 (B) STRAIN: ATCC 33218

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
15	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
	TTCTTAAACA	AAGCTGACAT	GGTGCATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTAA	AAGCATTGGA	AGGCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTC	300
20	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
25	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AAC TGGTTCT	TGTGATTTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGCGTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

50	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTC	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATTGGA	AGGTGAAGAC	250
55	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTC	300
	ATACATTCCCT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTT	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAAGACGA	CTTGACGGG	TGTTGAGATG	TTCCGTAAAT	500
60	TACTTGATGA	AGGTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550

ACGAAGCGAG ATGAAGTGGG GCGTGGACAG GTATTGGCGA AGCCAGGAAC 600
 CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG 650
 AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC 700
 TATTTTCAGAA CCACTGACGT GACAGGTAAT TGTGACTTGC CATCAGGAGT 750
 5 TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG 800
 CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT 838

10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

25 GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC 50
 GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA TCATCGTATT 100
 CCTGAACAAG TGCGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG 150
 ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC 200
 30 ACTCCGGTAG TCCGCGGTTT AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA 250
 GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC 300
 CAGAACCTGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC 350
 GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG 400
 CGGCATCATC AAAGTCGGTG AAGAAGTGGA AATCGTCGGT ATCAAAGATA 450
 35 CCACCAAGAC CACCTGTACC GCGGTTGAAA TGTTCCGTAA GCTGCTGGAC 500
 GAAGGCCGTG CGGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG 550
 TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC 600
 CTCACACCCA GTTCGTGTCA GAAGTGTATA TCCTGAGCAA GGATGAAGGC 650
 GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG 700
 40 TACGACTGAC GTGACAGGCA CCATCGAAGT GCCGGAAGGC GTAGAGATGG 750
 TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TGCGCCGATC 800
 GCAATGGACG AAGGTCTGCG CTTCGCAA 828

45

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella richardii*
 (B) STRAIN: ATCC 33998

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

```

      GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA      50
      GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTC      100
      TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
5     ATGGAAGTTC GTGAACTTCT GTCTCAATAC GACTTCCCGG GCGACGATAC      200
      GCCGGTTGTT CGCGGTTTCA CGCTGAAAAGC GCTGGAAGGT GACGCGYAGT      250
      GGGAAACGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA      300
      GAGCCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCTA TCGAAGACGT      350
      TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG      400
10    GCATCATCAA AGTTGGTGAA GAAGTGAAA TCGTGGAAT CAAAGACACC      450
      ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA      500
      AGGCCGTGCA GGTGAGAACG TTGGTGTCTT GCTGCGYGGT ACTAAGCGTG      550
      ACGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT      600
      CACACAGAAAT TCGTGTGAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG      650
15    YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA      700
      CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCC AATCGC      800
      GATGGACGAA GGTCTGCGCT TCGCAA      826

```

20

2) INFORMATION FOR SEQ ID NO: 115

```

      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 843 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA
30

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Leptospira interrogans
      (B) STRAIN: ATCC 23581
35

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

```

      TCGCGCGATT CTTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA      50
      AAGAACATAT CCTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA      100
40    TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT      150
      CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC      200
      CAGGAGATAC AACTCCTATC GTTCAATGGTT CTGCGGTAAA AGCACATTGAG      250
      GGCGATGAAT CTGAAATTGG GATGCCGTGA ATTCTCAAAT TGATGGAAGC      300
      TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAATCGAC AAACCTTTCC      350
45    TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA      400
      ACTGGAAGAG TGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT      450
      TATCGGTATC CGCCCAACAA CAAAAACTGT TGTTACCGGT ATCGAAATGT      500
      TCAGAAAAC TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT      550
      CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA      600
50    GCCAGGTTCT ATCACTCCTC AAAAAAGTT TGCCGCTGAG GTGTATGTAT      650
      TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT      700
      CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC      750
      TAATGGTGTC GAAATGGTTA TGCCTGGTGA TAACGTTTCT TTGACGGTTG      800
      AATTGATTAG CCCGATCGCA ATGGACAAGG GTCTTAAGTT CGC      843
55

```

2) INFORMATION FOR SEQ ID NO: 116

60 (i) SEQUENCE CHARACTERISTICS:

70

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Megamonas hypermegale*
 (B) STRAIN: ATCC 25560

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
15	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTAC	AATTACTGGT	CGTGCTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAACCTGGTAT	CGAAATGTTT	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAAT	600
	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTAATA	CTGACGTTAC	TGGTGTGTTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mitsuokella multacida*
 (B) STRAIN: ATCC 27723

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCAGATG	CCGCAGACGC	50
	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTGCGGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
55	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCT	ATGAGTACAT	300
	CCCAGCGCCG	GTCCGCGACA	ACGCTAAGCC	GTTCTTGATG	CCGGTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTT	CGCAAGATGC	500
60	TTGATTTTCG	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550

```

GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT      600
TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG      650
AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC      700
TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAACTGCCGG AAGGCACGGA      750
5  GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC      800
   CGATCGCTAT CGAGAAGGGC                                820

```

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Mobiluncus curtisii subsp. holmesii
(B) STRAIN: ATCC 35242

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

```

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA      50
   AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC      100
   GCTCTGAACA AGTGCGATTG TTCCGATGTG GACGAAGACA TGCTCGAAAT      150
   CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG      200
30 ACTGCCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC      250
   GAGTGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCTG ATACCTACAT      300
   TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG      350
   ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA      400
   CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCTGCC      450
35 TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG      500
   ACGAAGCCTA CGCCGGCGAG AACTGTGGTC TGTGCTGCG TGGACCAAG      550
   CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCTCTG GCTCCGTGAC      600
   CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG      650
   GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCGCA GTTCTTCTTC      700
40 CGCACCACCG ACGTGACCGG TGTTATTAC CTGCCCCGAG GCACCGAAAT      750
   GGTTATGCCT GGCGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA      800
   TCGCTATGGA GGAAGGTCTC GGCTTCGCTA T

```

831

45

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 825 bases
50 (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Moellerella wisconsensis
(B) STRAIN: ATCC 35017

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

```

GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG      50
TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT      100
TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT      150
5  GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA      200
   CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG      250
   AGTGGGAAGC TAAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC      300
   CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCCTGTTAC CAATCGAAGA      350
   CGTATTCTCA ATTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTGAGC      400
10  GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT      450
   ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA      500
   CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAAC      550
   GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT      600
   CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAGG      650
15  TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC      700
   GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
   GTAATGCCAG GTGATAACAT CAAAATGATC GTTACTCTGA TCCACCCAAT      800
   TGCAATGGAT GCAGGTCTGC GTTTTT                                825

```

20

2) INFORMATION FOR SEQ ID NO:120

```

(i) SEQUENCE CHARACTERISTICS:
25  (A) LENGTH: 827 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
30

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Branhamella catarrhalis
    (B) STRAIN: ATCC 43628
35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

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```

TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA      100
40  TTCATGAACA AGTGCGATAT GGTGATGAT GAAGAGCTAC TAGAATTGGT      150
   TGAAATGGAA GTTCGTGAAC TTCTATCTGA CTATGATTTC CCTGGTGATG      200
   ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCTGAT      250
   GGTAAATATG GCGAGCCTGC AGTTC TAGAA CTGCTAGACA CACTAGACAG      300
   CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA      350
45  TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT      400
   GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT      450
   CAAACCAACT GCTAAAACCA CCTGTACTGG TGTGAAATG TTCCGTAAAC      500
   TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCCTGGT      550
   ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GTACTTGCAA AACCAGGTTC      600
50  AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAG      650
   AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC      700
   TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC      750
   CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC      800
   ACCCAATCGC CAGGATAAAG GTCTACG                                827
55

```

2) INFORMATION FOR SEQ ID NO: 121

```

(i) SEQUENCE CHARACTERISTICS:
60

```

(A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
15	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAACTGGCA	GGTTTCCTGG	ATTCTTACAT	300
20	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GTTCAATCAA	600
	ACCACAYACC	AAATTTGAAT	CAGAAAGTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATT	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACCACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGAT	CGTCACCCTG	ATCCACCCAA	800
30	TCGCAA					806

2) INFORMATION FOR SEQ ID NO: 122

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: TB 299

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

50	GGTGGGATCC	TGGTGGTTCG	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
55	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCCG	TCGAGGACGT	350
	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCCGGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
60	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550

GCGAGGACGT CGAGCGTGGC CAGGTTGTCA CCAAGCCCGG CACCACCACG 600
 CCGCACACCG AGTTCGAAGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG 650
 CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC 700
 GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG 750
 5 GTGATGCCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT 800
 CGCCATGGAC GAAGGTCTGC GTTTC 825

10 2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25 CCGTGCGATC TTGGTATGTT CCGCAGCTGA CGGTCCTATG CCGCAAACCTC 50
 GCGAACACAT CCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTG 100
 TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAGCTGT TGGAGCTGGT 150
 TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGTGACG 200
 30 ACTGCCCCGAT CGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGACGCA 250
 GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT 300
 CCCAACACCT GAGCGTGCAG TGGACAAACC TTTCTTGTTG CCTATCGAAG 350
 ACGTATTCTC TATTTCCGGT CGCGGTACAG TAGTAACCGG TCGGTAGAG 400
 CGCGGTATCA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
 35 AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGG 500
 ACGAAGGTCA AGCTGGTGAC AACGTAGGTG TATTGCTGCG TGGTACTAAA 550
 CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACTATCAC 600
 TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG 650
 GTGGTCTGCA CACTCCGTTT TTCGCTAACT ACCGTCCACA ATTCTACTTC 700
 40 CGTACTACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTAGAAAT 750
 GGTAATGCCG GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA 800
 TCGCTA 806

45

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

75

```

      CGGCGCAATC TTGGTATGTT CCGCTGCTGA CCGTCCTATG CCGCAAACCTC      50
      GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG      100
      TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAAGTGC TGGAAGTGGT      150
5     TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG      200
      ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA      250
      GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT      300
      CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG      350
      ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG      400
10    CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA      450
      AACCCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTGTTG      500
      ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CCGTACCAAA      550
      CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC      600
      TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG      650
15    GTGGTCGTCA TACTCCGTTC TTCGCTAACT ACCGTCCACA ATTCTACTTC      700
      CGTACTACCG ACGTAACCGG TCGGTTACT TTGGAAGAAG GTGTAGAAAT      750
      GGTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAAGT ATTGCACCTA      800
      TCGCTATGGA AGAAGGTCTG CG                                822

```

20

2) INFORMATION FOR SEQ ID NO: 125

```

      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 820 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA
30
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Neisseria flavescens
      (B) STRAIN: ATCC 13120
35

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

```

      CGGCGCGACT TGGTATGTTT CGCAGCTGAC GGTCTCTATG CCGAAACCCG      50
      CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT      100
40    TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAAGTGGTT      150
      GAAATGGAAA TTCGTGACTT GTTGTCAGC TACGACTTCC CAGGCGACGA      200
      CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG      250
      CTTACGAAGA AAAAACTTTC GAATTGGCTG CTGCCTTGGA CAGCTACATC      300
      CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA      350
45    CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC      400
      GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA      450
      ACTCAAAAAA CCACTTGTA CCGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC      550
      GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT      600
50    CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG      650
      TGGTCGTAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC      700
      GTACTACCGA CGTAAGTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG      750
      GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAAGTGA TTGCGCCAAT      800
      CGCTATGGAA GAAGTCTGCG                                820
55

```

2) INFORMATION FOR SEQ ID NO: 126

```

60      (i) SEQUENCE CHARACTERISTICS:

```


(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 49226

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

	GGTGCAATCC	TGGTATGTT	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
15	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCAGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGGAA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAACTGGCTA	CCGCATTGGA	CAGCTACATC	300
20	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTTCTCC	ATTTCGGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAAC	550
25	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGGAAAAAGG	TGTGGAAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*
 (B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	GTTCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTGCA	GATGTTCCGC	AAACTGCTGG	500
60	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550

CGTGAAGAAG TGGAAACGCGG TCAGGTATTA GCCAAACCGG GTACCATCAC 600
 TCCGCACACC AAGTTCAAAG CAGAAGTGTA TGTATTGAGC AAAGAAGAGG 650
 GCGGTCGTCA CACTCCGTTT TTCGCCAACT ACCGTCCGCA ATTCTACTTC 700
 CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GCGTGGAAAT 750
 5 GGTAATGCCG GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA 800
 TCGCTATGGA AGAAGG 816

10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: ATCC 13077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

25 CCGGTGCAATC CTGGTATGTT CCGCAGCCGA CCGTCCTATG CCGCAAACCC 50
 GCGAACACAT CCTGCTGGCC CGTCAAGTAG GCGTACCTTA CATCATCGTG 100
 TTCATGAACA AATGCGACAT GGTGCGACGAT GCCGAGCTGT TGGAAGTGGT 150
 TGAAATGGAA ATCCGCGACC TGCTGTCCAG CTACGACTTC CCCGGCGACG 200
 30 ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGATGCC 250
 GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT 300
 CCCGACTCCC GAGCGTGCCG TGGACAAAC TTTCTTGTTG CCTATCGAAG 350
 ACGTATTCTC TATTTCGGT CGTGGTACAG TAGTAACCGG TCGGTAGAG 400
 CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTCG GTCTGAAAGA 450
 35 AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGG 500
 ACGAAGGTCA AGCAGGCGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA 550
 CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACAATCAC 600
 TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG 650
 GCGGCCGCCA TACCCCGTTC TTCGCCAACT ACCGTCCCCA ATTCTACTTC 700
 40 CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTGGAAAT 750
 GGTAATGCCG GGCGAGAACG TAACCATCAC CGTAGAACTG ATTGCGCCTA 800
 TCGCTATGGA AGAAGGTTTG CGCTTTGCGA T 831

45

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

78

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CGGCGCAATC TTGGTATGTT CTGCTGCTGA CGGTCCTATG CCGCAAACCC 50
GYGAACACAT CCTGTTGGCC CGTCAAGTAG GYGTAACCTTA CATCATCGTG 100
TTCATGAACA AATGCGACAT GGTGACGAT GCCGAAYTGT TGGAAGTGGT 150
5  TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCTGGYGACG 200
ACTGCCCCGAT TGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGATGCC 250
GCTTACGAAG AAAAAATCTT CGAACTGGCT GCCGCATTGG ACAGCTACAT 300
CCCGACTCCC GAGCGTGCCG TAGACAAACC GTTCCTGTTG CCTATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACAG TAGTAACCGG CCGTGTAGAG 400
10 CGCGGTGTTA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
AACCCTAAAA ACCACATGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGGT 500
ACGAAGGTCA AGCCGGTGAC AACGTAGGCG TATTGCTGCG CCGTACCAAA 550
CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
TCCGCACACC AAATTCAAAG CAGAAGTGTA CGTATTGAGC AAAGAAGAGG 650
15 GTGGTCGTCA TACTCCGTTT TCGCTAACT ACCGTCCTCA ATTCTACTTC 700
CGTACTACCG ACGTAACCGG TCGGGTACTT TTGGAAGAAG GTGTAGAAAT 750
GGTTATGCCT GGTGAGAAAG TAGCCATYAC TGTAGAACTG ATTGCGCCTA 800
TYGCTATGGA AGAAG 815

```

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

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25 (A) LENGTH: 829 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Neisseria sicca
    (B) STRAIN: ATCC 9913

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

```

GGCGCAATCT TGGTATGTTT CGCTGCTGAC GGTCTCTATGC CGCAAACCCG 50
CGAACACATC CTGTTGGCCC GCCAAGTAGG CGTACCTTAC ATCATCGTGT 100
40 TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAAGTGGTT 150
GAAATGGAAA TCCGTGACTT GCTGTCAAGC TACGACTTCC CTGGTGACGA 200
CTGCCCGATC GTACAAGGTT CTGCACTGAA AGCCTTGGA GCGGACGCCG 250
CTTACGAAGA AAAAATCTTC GAACTGGCTG CTGCATTGGA CAGCTACATC 300
CCGACTCCTG AGCGTGCCGT GGACAAACCG TTCCTGTTGC CTATTGAAGA 350
45 CGTATTCTCC ATCTCCGCTC GCGGTACCGT AGTAACCGGC CGTGTAGAGC 400
GCGGTGTTAT CCACGTTGGT GACGAGATTG AAATCGTAGG TCTGAAAGAA 450
ACCCAAAAAA CCACTTGTAC CGGTGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGTCAA GCCGGTGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC 550
GTGAAGAAGT GGAACGCGGT CAAGTATTGG CTAAACCGGG TACCATCACT 600
50 CCTCACACTA AATTCAAAGC AGAAGTTTAC GTATTGAGTA AAGAAGAGGG 650
TGGTCGTCAT ACTCCGTTCT TCGCTAACTA CCGTCCTCAA TTCTACTTCC 700
GTACTACCGA CGTAACCGGC GCGGTTACTT TGGAAGAAGG TGTAGAAATG 750
GTTATGCCTG GTGAGAACGT AGCCATCACT GTAGAACTGA TTGCACCGAT 800
CGCTATGGAA GAAGGTCTGC GCTTTGCGA 829
55

```

2) INFORMATION FOR SEQ ID NO: 131

60 (i) SEQUENCE CHARACTERISTICS:

79

- (A) LENGTH: 814 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
- (B) STRAIN: ATCC 14221

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

```

15  CGGCGCGACT TGGTATGTTT CGCAGCTGAT GGTCCCTATGC CTCAAACTCG      50
    CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT      100
    TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAAGCTGTT      150
    GAAATGGAAA TCCGTGACCT GTTGTCAAGC TACGACTTCC CAGGCGACGA      200
    CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGACGCTG      250
    GTTACGAAGA GAAAATCTTC GAATTGGCTG CTGCTCTGGA CAGCTACATC      300
20  CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA      350
    CGTATTCTCT ATCTCTGGCC GTGGTAGACG AGTAACTGGT CGTGTAGAGC      400
    GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA      450
    ACCCAAAAAA CCACTTGTA CCGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
    CGAAGGTCAA GCTGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACCAAAC      550
25  GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATTACT      600
    CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG      650
    TGGTCGTCAC ACTCCATTCT TCGCTAACTA CCGTCCACAA TTCTACTTCC      700
    GTACTACTGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG      750
    GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT      800
30  CGCTATGGAA GAAG                                         814

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2) INFORMATION FOR SEQ ID NO: 132

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
- (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

```

50  GCCATCTTGG TATGTTCTGC TGCTGACGGT CCTATGCCGC AAACCCGTGA      50
    GCACATCCTG TTGGCTCGTC AAGTAGGTGT ACCCTACATC ATCGTATTCA      100
    TGAACAAATG CGATATGGTT GATGATGCAG AGCTGCTGGA ATTGGTAGAA      150
    ATGGAAATCC GTGATCTGCT GAGCAGCTAC GATTTCCCTG GCGATGATTG      200
    YCCAATCGTG CAAGGTTCTG CTTTGAAAGC TTTGGAAGGT GATGCCGCTT      250
55  ACGAAGAAAA AATCTTTGAA TTAGCTGCTG CATTGGATAG CTATATTCCA      300
    ACWCCTGAGC GYGCTGTTGA TAAACCATT CTTTGCCGA TTGAAGATGT      350
    ATTCTCAATT TCAGGTCGTG GTACAGTAGT AACTGGTCGT GTAGAGCGCG      400
    GTATTATTCA CGTAGGCGAT GAAATTGAAA TTGTAGGTTT GAAAGARACY      450
    CAAAAAATA CTTGTACCGG CGTTGAAATG TTCCGTAAAT TGCTGGATSA      500
60  AGGTCAGGCT GGTGATAACG TAGGCGTATT GTTGCCTGGT ACCAAACGTG      550

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AAGACGTTGA GCGTGGTCAA GTATTGGCTA AGCCTGGTWC TATTACTCCG 600
 CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCGG 650
 TCGTCATACT CCGTTCTTCG CTAACATATCG TCCGCAATTC TATTTCCGTA 700
 CTACAGACGT TACCGGTGCK GTRACTTTAG AAGAAGGTGT GGAAATGGTA 750
 5 ATGCCTGGTG AGAAYGTTGC CATTACTGTW GARYTGATYG CTCCGATTGC 800
 KATGGAAGAA GGYTGCGT 818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ochrobactrum anthropi*
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25 CGGCGCAATT CTGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTCGCT CGTCAGGTTG GCGTTCCGGC AATCGTCGTG 100
 TTCCTGAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT 150
 TGAAGTGGAA GTTCGCGAAC TTCTGTGCGAA ATACGATTTC CCGGGCGACG 200
 30 AAGTTCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG 250
 AAGGAAGTGG GCGAAGACGC CGTTCGTTTCG CTGATGGCCG CTGTTGACGA 300
 CTACATTCCG ACCCCGGAAC GTCCGATCGA CCAGCCGTTT CTGATGCCGA 350
 TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTCGC 400
 GTTGAGCGCG GTATCGTCAA GGTTGGTGAA GAAAGTGAAA TCGTCGGCAT 450
 35 CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC 500
 TGCTCGAYCA GGGCCAGGCT GCGGACAACA TCGGCGCTCT GATCCGCGGC 550
 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTT 600
 TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG 650
 ACGAAGGTGG CCGTCATACG CCGTTCTTTA CGAACTACCG TCCGCAGTTC 700
 40 TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC 750
 GGAAATGGTT ATGCCTGGCG ACAACGTGCG TATGGACGTC ACCCTGATCG 800
 TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA 836

45

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

81

CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTT GCGGTTCCCT ACATCATCGT GTTCCTGAAC 100
 AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAACTGG TAGAGATGGA 150
 5 AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA 200
 TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA 250
 GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCCGGATCC 300
 AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT 350
 CAATCTCTGG CCGTGGTACC GTTGTACCG GTCGTGTTGA GCGCGGCATC 400
 10 GTTAAAGTCG GCGACGAAGT TGAATCGTG GGTATCAAAG ATACTGCCAA 450
 ATCAACCTGT ACCGGTGTG AGATGTTCCG TAAGCTGCTG GACCAGGGTC 500
 AGGCAGGCGA AAACGTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC 550
 ATCCAGCTGG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC 600
 CCAGTTCGAG TCAGAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC 650
 15 ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAAC 700
 GATGTAACCG GTTCAGTAGA GCTGCCAGAA GCGGTTGAGA TGGTCATGCC 750
 AGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG 800
 ACGAA 805

20

2) INFORMATION FOR SEQ ID NO: 135

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 30 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

CGCGATCCTG GTTGTGCTG CGACTGATGG CCCAATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 40 CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
 GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA 200

 CCCAATCGT ACGCGGTTCT GCGCTGAAAG CGCTGGAAGG CGACGCTGAG 250
 TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC 300
 AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 45 TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTGAGCGC 400
 GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC 450
 TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAA CTGCTGGACC 500
 AGGGTCAGGC AGGCGAGAAC TGTGGTGTTC TGCTGCGCGG TATCAAGCGT 550
 GAAGAGATCC AGCGTGGTCA GGTCTGGCT AAGCCAGGCA CCATCAAGCC 600
 50 ACACACCAAG TTCGTATCAG AAGTGACGT ACTGTCTAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTAATTCCGT 700
 ACYACTGATG TGACCGGCAM CATMGAAGT CCAGAAGGCG TTGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG 800
 CGATGGACCA GGGTCTGCGT TTCGC 825

55

2) INFORMATION FOR SEQ ID NO: 136

- 60 (i) SEQUENCE CHARACTERISTICS:

82

(A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

	CACAAACACG	TGAGCACATC	CTTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
15	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
	AGAATTAGTT	GAAATGGAAG	TGCGTGAAC	TCTTTCTCAA	TATGATTTC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAAC	200
	GGYGTAGCTG	AGTGGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCTTCTTC	300
20	CGATTGAAGA	CGTGTTCTCA	ATTTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
	CGTGTTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAARC	GTGAAGAAAT	CGAACGTGGT	CAAGTGTTAG	CGAAACCGGG	550
25	TTCAATYACG	CCACACACTG	ATTTTGAATC	AGAAGTTTAC	GTGTTATCAA	600
	AAGAAGAAGG	TGGTCGTCAT	ACACCATCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACGGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTTGA	750
	TTCACCCAAT	CG				762

30

2) INFORMATION FOR SEQ ID NO: 137

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
50	GAGAACACAT	CTTATTATCA	AGACAAGTAG	GAGTACCATA	TATCGTAGTA	100
	TATTTGAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAAT	TACTATCTGA	ATATGGATTC	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAA	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
55	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTTAC	AATTACAGGA	AGAGGAACTG	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAGTT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACCTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTRAG	AGGAACCAAG	550
60	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAG	GAACAATTCA	600

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TCCTCATACA AACTTCAGTG GAGAAGTATA TGTATTGACA AAAGAAGAAG      650
GAGGAAGACA TACTCCATTC TTCTCAGGAT ACAGACCACA ATTTTACTTT      700
AGAACCACAG ATATTACAGG AGCAGTAACA TTACCAGAAG GAGTAGAAAT      750
GGTAATGCCR GGAGATAATA TCACAATGAC AGTAGAATTG ATTCACCCAA      800
5  TTGCAATGGA AACAGGATTA CGATTTGCAA TT                               832

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2) INFORMATION FOR SEQ ID NO: 138

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

```

25 TAGTATGTTT AGCAGCAGAY GGTCCAATGC CACAAACAAG AGAACACATT      50
   CTACTAGCAA GACAAGTTGG TGTACCAAAG ATAGTAGTAT TCCTAAACAA      100
   AGAAGACCAA GTAGACGATC CAGAACTAAT TGAATTAGTA GAGATGGAAA      150
   TCAGAGACCT ACTATCAGAA TATGACTTCG AYGGAGACAA CACACCAATC      200
   GTAGTAGGAT CAGCATTAAT AGCCCTAGAC GATCCAGACG GAGAATGGGG      250
30 AGACAAAATC GTAAACTAA TGGAAGMAGT AGACGAATAC ATCCCAACAC      300
   CAGTAAGAGA TACAGAACAC CCATTTCCTAA TGCCAATCGA AGACRTATTC      350
   TCAATYACAG GAAGAGGAAC AGTAGCAACA GGAAGAGTAG AACAAGGTGT      400
   AGTAAAAGTA GGMGACACAG TAGAACTAGT AGGCTTAACA GACGAAAAGCA      450
   GACAAGTAGT AGTAACAGGT GTAGAAATGT TTAGAAAACA ACTAGACCTA      500
35 GCAGAAGCMG GAGACAACAT TGGAGCCCTA CTAAGAGGAG TACAAAGAGA      550
   AGAATCCAA AGAGGACAAG TACTAGCAGC ACCAGGAACA ATCAAACCAC      600
   ACACAAAATT TGAAGCAGAA GTATACGTAC TAACAAAAGA AGAAGGTGGA      650
   AGACACACAC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTCAGAAC      700
   AACAGACGTA ACAGGAGACA TCCAAC TAGC AGACGGAGTA GAAATGGTAA      750
40 TGCCAGGAGA CAACTCAACA TTTACAGTAA CACTAATCAC ACCAATCGCA      800
   ATGGACGAAG GACTAAGATT CGC                               823

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45 2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60


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CTATCATCGT AGTATCTGCA GCAGACGGTC CAATGCCCAA ACAGAGAGAA      50
CACATCCTAC TAGCAAGACA AGTAGGCGTT CCAAAAATCG CAGTATTCCT      100
AAACAAAGAA GACCAAGTAG ACCGATCCAGA ACTAATCGAA TTAGTAGAAA      150
TGGAAATCAG AGACCTACTT TCAGAATACG ACTTCGATGG AGACAACGCT      200
5  CCGAGTAGTAG TAGGATCTGC TCTTAAATCA CTAGAAGAAG GCGGAGAAGG      250
   CCCATGGTCA GACAAAATCC TTGACCTAAT GGCACAAGTA GACGAATACT      300
   TCGACATCCC AGAAAGAGAC AACGACCAAC CATTCCTAAT GCCAGTAGAA      350
   GACGTAATGA CAATCTCAGG ACGTGGAACA GTAGCAACAG GAAGAGTTGA      400
   AAGAGGAACA CTAAAAGTTG GTGATACAGT AGAAATCGTA GGAATAACAG      450
10  AAGATACAAA AGAAACAGTA GTAACCTGGAG TAGAAATGTT CCACAAATCM      500
   CTAGACCAAG CAGAATCTGG AGATAACGTA GGACTACTAC TAAGAGGAGT      550
   AACAAGAGAT CAAATCTCAA GAGGACAACT ACTAGCAAAA CCAGGWTGAG      600
   TAAACCCACA CACAGAATTC GAAGGTCAAG TATACGTACT AACAAAAGAA      650
   GAAGGTGGAC GTCACACACC ATTCTTCAGT GGATATAGAC CACAATTCTT      700
15  CTTTGAACA ACAGACGTAA CAGGAGACAT CGAACTAGAA GAAGGCGTAG      750
   AAATGGTAAT GCCAGGAGAC AACGCAACAT TCAAAATCAC ACTCCAAAAA      800
   CCAATCGCTC TAGAAGAAGG ACTAAGATTC GC                        832

```

20

2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

```

CGGTGCTATC ATCGTAGTTG CTGCAACTGA TGGTCCTATG CCTCAGACGC      50
GTGAGCACAT CCTACTAGCA CGTCAGGTCA ACGTACCTCG TCTAGTTGTC      100
TTTATGAACA AGTGCGACCT TGTGTATGAC GAGGAGATGC TCGAGCTCGT      150
40  AGAGATGGAT ATGCGTGAGC TACTAAGCTT CTATGACTTT GACGGCGACA      200
   ACACTCCTGT CATCCGTGGT TCTGCTCTTG GTGCTCTCAA TGGTGAGCCT      250
   AAGTGGGTAG AGAAGGTTAT GGAGCTCATG GAGGCTGTAG ACACCTGGAT      300
   CCCACTACCT GAGCGCGACA TCGACAAGCC TTTCCTAATG CCTGTAGAGG      350
   ACGTATTCTC TATCACAGGT CGTGGTACTG TCGCTACTGG TCGTATCGAG      400
45  ACTGGTGTCT TTAAGGTCAA CGATGAGGTT CAGATCATCG GTCTAGGTGC      450
   TGAGGGTAAG AAGAGCGTCG TAACTGGCGT GGAAATGTTT CGCAAGATCC      500
   TTGATGAGGG TGAAGCTGGT GATAACGTAG GTCTCCTACT CCGTGGTATC      550
   GACAAGGACG AGATCAAGCG CGGTATGGTC CTAGCACACC CAGGTCAGGT      600
   CAAGCCTCAC GATCACTTCA AGGCTGAGGT CTATATCCTG AAGAAGGAAG      650
50  AGGGTGGTCT TCACACACCA TTCCACAACA AGTACCGTCC TCAGTTCTAC      700
   ATCCGTACGC TAGACGTAA CCGCGAGATC AACTCCAGAG AGGGTGTAGA      750
   GATGGTTATG CCTGGTGATA ACGTCACCAT CGATGTCAAG CTCATCTCTC      800
   CAGTAGCTTG TAGCGTAGGT CTACGCTTCG C                        831

```

55

2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 818 bases

85

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: ATCC 33277

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

	CGGTGCTATA ATCGTTGTAG CAGCTACAGA CGGTCCTATG CCTCAGACTC	50
	GCGAGCACAT CCTTTTGGCT CGCCAGGTAA ACGTTCCTCG TCTGGTTGTT	100
15	TTCATGAACA AATGTGACAT GGTAGACGAT GAAGAGATGC TCGAGCTTGT	150
	TGAAATGGAC ATGCGCGAAC TCCTTTCTTT CTACGATTTC GATGGTGACA	200
	ATACCCCTAT CATCCGTGGT TCTGCTCTGG GCGCTTTGAA TGGAGAGCCT	250
	CAGTGGGAAG ACAAGGTGAT GGAGCTTATG GAAGCTGTTG ACAACTGGGT	300
	TCCCTGCGCT GAGCGCGATA TCGACAAACC GTTCTTGATG CCGGTTGAAG	350
20	ACGTGTTCTC TATCACGGGT CGTGGTACGG TCGCTACAGG ACGTATCGAA	400
	ACCGGTATTG TGAAGACCGG TGACGAAGTT CAAATCATCG GCCTCGGTGC	450
	AGAAGGAATG AAGTCGGTTG TTACGGGTGT TGAAATGTTT CGTAAGATTG	500
	TTGACGAAGG TCAGGCTGGT GACAACGTTG GTCTCCTCCT GCGTGGTATC	550
	GATAAGGATC AGATCAAGCG TGGTATGGTT ATCTCTCACC CGGGTAAGAT	600
25	TACTCCTCAC AAGAGATTTA AGGCCGAGGT TTATATCTTG AAGAAAGAAG	650
	AAGGTGGTCG CCACACTCCT TTCCACAACA AATATCGTCC GCAGTTCTAC	700
	ATCCGTACGC TTGACGTGAC CGGTGAAATC ACTCTTCCCG AAGGAACAGA	750
	AATGTTATG CCCGGTGACA ACGTAACGAT CACTGTAGAA CTCATCTACC	800
	CGGTTGCATG TAATGTAG	818
30		

2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pragia fontium*
 45 (B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

	CGGCGCTATT CTGGTTGTTG CTGCAACTGA TGGTCCTATG CCTCAAATC	50
50	GTGAGCACAT CCTGTTAGGY CGCCAGGTTG GCGTACCATA CATCATTGTG	100
	TTCCTGAACA AGTGTGACAT GGTTGAYGAT GAAGAGCTGT TAGAACTGGT	150
	TGAAATGGAA GTTCGTGAGC TTCTGTCTCA GTACGATTTC CCAGGTGATG	200
	ATACTCCAGT TGTTCGTGGT TCTGCGCTGA AAGCGTTTGA AGGCGAAGCT	250
	GAGTGGGAAG CTAAAATCAT TGAATTGGCT GACTCCCTGG AYAGCTACAT	300
55	TCCACAGCCA GAGCGTGCAA TTGATAAGCC GTTCCTGCTG CCAATCGAAG	350
	ACGTTTTCTC AATCTCTGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG	400
	CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	TACTGTGAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AARTTACTGG	500
	ATGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAG	550
60	CGTGATGAAA TCGAACGTGG TCAAGTATTA GCAAAACCAG GTTCAATCAA	600

```

      CCCGCACTACT  AACTTCGTAT  CAGAAGTTTA  TATCCTGAGC  AAAGATGAAG      650
      GTGGTCGTCA  TACTCCATTC  TTCAAAGGCT  ACCGTCCACA  GTTYTACTTC      700
      CGTACAACCTG  ACGTGACCGG  TACCATCGAA  CTGCCAGAAG  GCGTAGAGAT      750
      GGTAAATGCCA  GGTGATAACA  TTCAGATGAC  TGTAACCTCTG  ATTGCCCCAA      800
5  TCGCGATGGA  CGAAGGTTTA  CGCTTCGCTA                                830

```

2) INFORMATION FOR SEQ ID NO: 143

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

```

25  TGGTGCTATC  TTGGTTGTAG  CTGCTACTGA  TGGTCCTATG  CCTCAGACTC      50
      GTGAGCACGT  ATTGCTCGCT  CGTCAGGTAA  ACGTACCTCG  CTTGGTTGTA      100
      TTCTTGAACA  AGTGTGATAT  GGTTCACGAT  GCTGAGATGC  TTGACCTCGT      150
      TGAGATGGAG  GTTCGTGAGA  TCCTCGAGCA  GTACGGTTAT  GAGGAGGATA      200
      CTCCTATTAT  TCGTGGTTCT  GCACTCGGTG  CTTTGAACGG  TGTGAGAAG      250
30  TGGGTAGACT  CTGTAATGGA  GCTCATGGAT  ACTGTTGACA  CTTGGATTGA      300
      AGAGCCAGAG  CGTGAGATTG  ACAAGCCATT  CTTGATGCCT  GTTGAGGACG      350
      TATTCTCTAT  CACAGGTCGT  GGTACTGTAG  CTACTGGTCG  TATCGAGACT      400
      GGTATCTGTA  AGGTAGGTGA  TGAGGTTTCAG  TTGCTCGGTC  TCGGTGAGGA      450
      CAAGAAGTCT  GTTATCACTG  GTGTTGAGAT  GTTCCGTAAG  AACCTTCCAA      500
35  CAGGTCAGGC  TGGTGACAAC  GTAGGTCTCC  TCCTTCGTGG  TATCGATAAG      550
      GCTGAGGTTA  AGCGTGGTAT  GGTGTTGTG  CACCCAGGTG  CTATTACTCC      600
      TCACGATCAC  TTCAAGGCAT  CTATCTATGT  ATTGAAGAAG  GAAGAGGGTG      650
      GTCGTCATAC  TCCATTCGGT  AACAAGTATC  GTCCACAGTT  CTACCTCCGT      700
      ACAATGGACT  GTACAGGTGA  AATCCACCTC  CCAGAGGGCG  TTGAGATGGT      750
40  TATGCCAGGT  GACAACGTAG  AGATTGAAGT  TGTATTGATC  TATAAGGTTG      800
      CTTTGAACGA  GGGTCTTCGT  T                                821

```

45 2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Prevotella oralis*
 (B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

60

TGGTGCTATT CTTGTAGTAG CTGCTACTGA CGGTCCTATG CCTCAAACCTC 50
 GTGAACACGT GCTTCTTGCT CGTCAGGTGA ACGTACCTCG TTTGGTCGTT 100
 TTCTTGAACA AGTGCGATAT GGTGACGAT GAAGAAATGC TTGAGCTCGT 150
 AGAAATGGAG CTTTCATGAAC TTCTCGAGCA GTATGAATAT GAGGAGGATA 200
 5 CTCCTATTGT TCGTGGTTCC GCACTTGGCG CTCTGAATGG AGTAGAGAAG 250
 TGGGTTGACA GCGTGATGAA GTTGATGGAT ACCGTTGATG AATGGATACA 300
 GGAACCAACG CGTGATCTTG ATAAGCCTTT CTTGATGCCG GTAGAGGATG 350
 TATTTTCTAT TACTGGTCGT GGAACGGTTG TTACAGGCCG TATTGAAACT 400
 GGTAAGGTTA AGGTGGGCGA TGAAGTTCAA CTTCTTGGTC TCGGTGAAGA 450
 10 TAAGAAGTCC GTTGTGACAG GCGTTGAGAT GTTCCGTAAG ATTCTTGACG 500
 AAGGTGAAGC TGGTGATAAT TAGGCTTGC TGCTTCGTGG TATCGATAAG 550
 ACGGAAGTAA AGCGTGGTAT GGTGTCGTA CATCCGGGGG CTATTACTCC 600
 TCACGATCAT TTCAAGGCTT CAGTTTACGT ATTGAAGAAA GAAGAAGGCG 650
 GTCGCCATAC TCCGTTTGGT AMCAAGTATC GTCCACAGTT CTATCTTCGT 700
 15 ACCATGGACT GTACTGGTGA AATTACTCTT CCGGAAGGAG TTGAGATGGT 750
 AATGCCGGGT GATAACGTCG AAATTGAAGT TAAGTTGATC TATCCGGTAG 800
 CTTTGAACGA GGGACTTCGT TTCGCTA 827

20

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Propionibacterium acnes*
 (B) STRAIN: ATCC 6919

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

CGGCGCCATC CTCGTGGTTG CTGCTACCGA CGGCCCGATG CCTCAGACTC 50
 GCGAGCACGT TCTGCTCGCT CGTCAGGTGG GCGTGCCCGC CATCGTCGTC 100
 GCCCTCAACA AGTGCGACAT GGTGACGAT GAGGAGCTCA TTGAGCTCGT 150
 40 CGAGATGGAG GTCCGCGAGC TGCTGACCTC GCAGGAGTTC GACGGCGACA 200
 ACTGCCCTGT CGTTCGCATC TCCGCCTTCC AGGCCCTCCA GGGTGATGAG 250
 AAGTGACCC AGTCGATCCT CGACCTCATG GACGCCGTGG ACGAGTACAT 300
 CCCGCAGCCT GAGCGCGATC TCGACAAGCC CTTCTTATG CCGATCGAGG 350
 ACGTCTTCAC CATCACCGGC CGTGGCACCG TTGTCACCGG TCGTGTCGAG 400
 45 CGCGGCGTCG TCAAGACTGG CGAAGAGGTC GAGATCGTCG GTATCCACGA 450
 GAAGACCCAG AAGACCACCG TTACCGGTGT CGAGATGTTT CGCAAGATCC 500
 TCGACGAGGG CCGCGCTGGT GAGAACGTCG GCGTTCTGCT CCGTGGCACC 550
 AAGAAGGAGG ATGTCGTTCC CGGCATGGTC CTCTCCAAGC CTGGTTCCAC 600
 CACCCCCCAC ACCGACTTCG AGGCCCAGGT CTACGTCCTC AAGAAGGATG 650
 50 AGGGTGGCCG CCACAAGCCG TTCTTCTCCC ACTACAGCCC CCAGTTCTAC 700
 TTCCGTACCA CGGACGTGAC TGGCACTGTT GAGCTCCCCG AGGGCACCAG 750
 GATGGTCATG CCTGGCGACA ACACCGACAT GACTGTGCAC CTGATTACAC 800
 CGGTTGCCAT GGAGGATCAG CTCAAGTTCC CTA 833

55

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 745 bases

88

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 35659

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
20	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGACCA	600
25	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

30

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGTTACT	GGAATTAGTM	150
50	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTTCAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
	ACAGCGAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
60	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	750
GTAATGCCAG	GTGACAACAT	CAACATGATC	GTTGAACTGA	TTCACCCAAT	800
CGCGATGGAC	GACGGTTTAC	GTTTCGCTA			829

5

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
GTGAGCACAT	CCTGTTAGGT	CGCCAGGTTG	GTGTACCTTA	CATCATCGTA	100
25 TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAACTGC	TGGAATTAGT	150
AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
ACACTCCAGT	AATCCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
GAGTGGGAAG	CAAAAATTGT	TGAATTAGCA	GAAGCACTGG	ATTCTTACAT	300
CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCTTGCTG	CCTATCGAAG	350
30 ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTAGAG	400
CGTGGTGTG	TTAAAGTTGG	TGAAGAAGTT	GAGATTGTTG	GTATTAAAGA	450
CACAGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAATTACTTG	500
ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	TTCTTCTGCG	TGGTACTAAA	550
CGTGAAGAAA	TCGAACGTGG	ACAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
35 GCCACACACT	AAATTCTGAAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
GTGGTCGTCA	CACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
CGTACAACCTG	ACGTAACCTG	TACTATCGAA	TTACCAGAAG	GCGTAGAAAT	750
GGTAATGCCA	GGTGACAACA	TCAACATGAT	CGTTGAACTG	ATTCACCCTA	800
TCGCGTAGGA	CGACGTTTGA	CGTT			824

40

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GCCAAAGTAGG	TGTTTCCTTAC	50
60 ATCATCGTTT	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAACTGTT	100

90

	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	150
	CAGGCGATGA	CACTCCAGTT	GTTTCGCGTT	CAGCACTGAA	AGCGCTGGAA	200
	GGCAACCCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	GTTACCTGGA	250
	TTCTTACATC	CCAGAACCAG	AGCGTGCAAT	TGACAAGCCA	TTCCTGCTGC	300
5	CAATCGAAGA	CGTATTCTCA	ATCTCTGGTC	GTGGTACAGT	AGTAACAGGC	350
	CGTGTGAGC	GTGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	400
	TATTCAAGCG	ACTGCGAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	450
	AACTGCTGGA	TGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	500
	GGTACTAAAC	GTGAAGAAAT	TCAACGTGGT	CAAGTACTGG	CTAAACCAGG	550
10	TTCAATCAAG	CCACACACTC	AATTCGAATC	AGAAGTATAT	ATTCTGAGCA	600
	AAGATGAAGG	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	700
	CGTAGAGATG	GTAATGCCAG	GCGACAACAT	CAACATGATC	GTGAC	745

15

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 830 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia rettgeri*

(B) STRAIN: ATCC 9250

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGY	CGCCAAGTAG	GTGTWCCTTA	CATCATCGTT	100
35	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAAGTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTCCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCAACCCA	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCA	GGTCACTTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCTGCTG	CCAATCGAAG	350
40	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACGGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
	ACGAAGGTCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAA	550
	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCAAAACCAG	GTTCAATCAA	600
45	GCCACACACT	AAATTGCAAT	CAGAAGTCTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACTCCATT	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGATAACA	TCAACATGAT	CGTTACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTTTA	CGTTTCGCAA			830

50

2) INFORMATION FOR SEQ ID NO: 151

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 5 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

```

CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC      50
10 GTGAGCACAT CCTGTTAGGT CGCCAAGTAG GTGTTCTTA CATCATCGTT      100
TTCCTGAACA AATGTGACAT GGTGACGAC GAAGAACTGT TAGAATTAGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG      200
ACACTCCAGT TGTTTCGYGGT TCAGCACTGA AAGCGCTGGA AGGTATCCCT      250
GAGTGGGAAG CGAAAATTGT TGAATTAGCC GGTTACCTGG ACAGCTACAT      300
15 CCCAGAACCA GAGCGCGCAA TTGACCGTCC ATTCCTGCTG CCAATCGAAG      350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG SCGTGTTGAG      400
CGTGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA      450
CACRGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTCTTG      500
ACGAAGGTCG TGCTGGTGAG AACGTTGGTG TTTTACTGCG TGGTACTAAG      550
20 CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCTAAACCAG GTTCAATCAA      600
GCCACACACT ACTTTTGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG      650
GTGGTCGTCA TACTCCATTG TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTAACCGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GGCGACAACA TCAACATGAT CGTGACACTG ATTCACCCAA      800
25 TCGCGATGGA TGATGGTTTA CGTTTC      826

```

2) INFORMATION FOR SEQ ID NO: 152

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*
 40 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

```

45 CGGTGCAATC CTAGTTGTTG CGGCAACAGA TGGCCCAATG CCACAAACTC      50
GTGAGCACAT CCTGTTAGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTG      100
TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAGCTGC TGGAAGTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTC CCAGGTGATG      200
ACACTCCAGT TATCCGTGGT TCAGCGCTGA AAGCGTTGGA AGGCAACCCA      250
50 GAGTGGGAAG CGAAAATCGT TGAAGTAGCA GAAGCACTGG ACAGCTACAT      300
CCCAGAGCCA GAGCGTGCAA TTGACAAGCC ATTCCTGCTG CCAATCGAAG      350
ACGTATTCTC AATCTCAGGT CGTGGTACAG TAGTCACAGG CCGTGTGAG      400
CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTAG GTATCAAAGA      450
GACTGCGAAA ACCACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTCTTG      500
55 ACGAAGGCCG TGCGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTACTAAG      550
CGTGAAGAAA TCGAACGTGG TCAAGTTCTG GCGAAACCAG GTTCAATCAA      600
GCCACACACA ACTTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG      650
GTGGTCGTCA CACGCCATTG TTCAAAGGYT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTAACAGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT      750
60 GGTAATGCCA GGCGACAACG TGAACATGAA AGTAACTCTG ATTCACCCAA      800

```


TCGCGATGGA CGATGGTTTG CGTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCAT GCCGCAGACC CGCGAGCACA 50
 TCCTGCTGTC CCGCCAGGTA GCGTTCCTT ACATCGTCGT GTTCCTGAAC 100
 AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAAGTGG TCGAGATGGA 150
 AGTTCCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GACACTCCGA 200
 25 TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC 250
 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT 300
 TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG 350
 ACGTGTTCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG 400
 CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC 450
 30 GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 500
 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG 550
 CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG 650
 GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC 700
 35 CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGGACAACA TCAAGATGGT TGTCACCCTG ATCGCTCCGA 800
 TCGCCATGGA AGATGGCTGC GTTCGCG 827

40

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*
 (B) STRAIN: ATCC 13525

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC 50
 GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCCGTA CATCGTGGTT 100
 TACCTGAACA AGGCTGACCT GGTAACGAC GCTGAGCTGC TGGAAGTGGT 150
 60 TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG 200

```

          ACACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC      250
          GACAACGAAA TGGGCACCAC GTCCGTTCGT AAAGTGGTTG AAAGTCTGGA      300
          CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC      350
          CAATCGAAGA CGTGTTCCTG ATCTCCGGTC GCGGTACTGT TGTGACTGGT      400
5         CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG      450
          TCTGCGTGAC ACTACCGTCA CCACCTGCAC CCGGTGTTGAA ATGTTCCGTA      500
          AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT      550
          GGTACCAAGC GTGACGACGT TGAGCGTGGC CAGGTTCTGG TTAAGCCAGG      600
          TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA      650
10        AAGAAGAAGG CCGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG      700
          TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCGGAAGG      750
          CGTTGAAATG GTTATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA      800
          TCAAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T              841

```

15

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:

```

          (A) LENGTH: 841 bases
20         (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

          (A) ORGANISM: Pseudomonas stutzeri
          (B) STRAIN: ATCC 17588

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

```

          CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC      50
          GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTCGTG      100
          TTCCTGAACA AGGCCGACAT GGTGATGAC GCCGAGCTGC TCGAGCTGGT      150
35        CGAGATGGAA GTTCGYGACC TGCTGTCGAC CTACGACTTC CCGGGTGAYG      200
          ACACTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC      250
          GACAACGAGC TCGGCACCAC TGCGGTGAAG AAGCTGGTCG AGACCCTGGA      300
          CAGCTACATT CCCGAGCCGG TTCGTGCCAT CGACAAGCCG TTCCTGATGC      350
          CGATCGAAGA CGTGTTCCTG ATCTCCGGTC GCGGCACSGT GGTAACCGGT      400
40        CGCGTAGAGC GCGGCATCGT CAAGGTTTCA GAAGAGATCG AGATCGTCCG      450
          TCTGCGTCCG ACCACCAAGA CTACCTGCAC CGGCGTTGAG ATGTTCCGCA      500
          AGCTGCTCGA YGARGGTCGT GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT      550
          GGCACCAAGC GTGACGAAGT GGAGCGTGGT CAGGTTCTGG CCAAGCCGGG      600
          CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGATC GTGCTGTCCA      650
45        AGGAAGAAGG TGGTCGTCAC ACCCGTTTCT TYAAGGGCTA CCGTCKKAG      700
          TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCGGAAGG      750
          CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA      800
          TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T              841

```

50

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:

```

55        (A) LENGTH: 833 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

```

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Psychrobacter phenylpyruvicus*

(B) STRAIN: ATCC 23333

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

	GCTATTCTAG	TAGTATCAGC	AACTGACGGT	CCAATGCCAC	AAACACGTGA	50
	GCACATTCTA	TTATCACGTC	AGGTGTTGGT	ACCATACATC	ATCGTATTCA	100
10	TGAACAAATG	TGACATGGTA	GATGACGAAG	AGTTACTAGA	GCTAGTAGAA	150
	ATGGAAGTGC	GTGAATTACT	TTCAGACTAC	GACTTCCCAG	GTGATGACAC	200
	TCCAATCATC	AAAGGTTTCA	CTTTAGAAGC	GTAAATGGT	AACGACGGTA	250
	AGTACGGTGA	GCCAGCAGTT	ATCGAACTAC	TAAACACTCT	AGACACTTAC	300
	ATTCCAGAGC	CAGAGCGTGA	CATCGATAAG	CCATTCTCTA	TGCCAATCGA	350
15	AGACGTATTC	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGCCGTGTTG	400
	AATCTGGTAT	CATCAAAGTT	GGTGACGAAA	TCGAAATCGT	TGGTATCAAA	450
	GACACAGTTA	AAACAACCTG	TACTGGTATC	GAGATGTTCC	GTAAGTTACT	500
	AGACGAAGGT	CGTGCTGGTG	AGAACTGTGG	TGTACTATTA	CGTGGTACTA	550
	AGCGTGAAGA	CGTACAACGT	GGTCAAGTAC	TTGCTAAGCC	AGGTTCAATC	600
20	ACTCCACACA	CCAACCTTCG	CGCAGAAGTA	TACGTACTAT	CAAAAGAAGA	650
	AGGTGGTTCG	CACACTCCAT	TCTTAAATGG	TTACCGTCCA	CAGTTCTACT	700
	TCCGTACTAC	TGACGTAAAC	GGTGCAATCA	CGTTACAAGA	AGGTACTGAA	750
	ATGGTAATGC	CAGGCGATAA	CGTTGAGATG	AGCGTAGAGC	TAATCCACCC	800
	AATCGCTAGG	ACAAAGGTTT	ACGTTTCGCA	ATC		833

25

2) INFORMATION FOR SEQ ID NO: 157

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rahnella aquatilis*

40 (B) STRAIN: ATCC 33071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

	GGCGCTATCC	TGGTTGTTGC	TGCAACTGAC	GGCCCTATGC	CTCAGACTCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATAC	ATGATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTAGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	TCTGTCTGCT	TACGAATTCC	CAGGCGACGA	200
	CATCCCGGTC	ATCAAAGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGATGCTA	250
	CTTGGGAAGC	GAAAATCATC	GAAGTGGCAG	AAGCACTGGA	CAGCTACATT	300
50	CCATTGCCAG	AGCGTGCTAT	CGATAAGCCA	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACAGT	GGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTGGGC	GAAGAAGTTG	AAATCGTCGG	TATCAAGGAC	450
	ACTGTTAAGT	CTACTTGTA	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCGGGCGAGA	ACGTGGGTGT	TCTGCTGCGT	GGTATCAAGC	550
55	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCAATCAAA	600
	CCACACACCA	AGTTTGATT	CGAAGTGTAC	ATCCTGAGCA	AAGATGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTTATGCCTG	GTGACAACGT	GAACATGGTT	GTTACCCTGA	TCCACCCAAT	800
60	CGCGATGGAT	GACGGTCTGC	GTTTC			825

95

2) INFORMATION FOR SEQ ID NO: 158

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

```

20  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
25  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG      500
30  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCCG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT      750
35  GGTAATGCCG GCGGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

40 2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

```

55  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
60  TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
  
```

```

ACACGCCGAT CGTTCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGTGACGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
5 CGCGGTATCA TCAAAGTGGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTG 500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
10 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

```

15

2) INFORMATION FOR SEQ ID NO: 160

```

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 807 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Salmonella choleraesuis subsp. diarizonae
        (B) STRAIN: ATCC 43973

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

```

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATTATCGT GTTCCTGAAC 100
35 AAATGCCACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150
AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCAA 200
TCGTTCTGTTG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250
GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
40 CCATCTCCGG TCGTGGTACC GTTGTACCAG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAARCTGCTG GACGAAGGCC 500
GTGCWGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
45 CAAGTTCGAA TCTGAAGTGT ATATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGCG AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGTAATGCC 750
GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

```

50

2) INFORMATION FOR SEQ ID NO: 161

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Heidelberg
 (B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

```

10  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACGTCCGAT  CGTTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
15  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGGT      500
20  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA YACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGAAGTG CACCATCGAA TTGCCGGAAG GCGTAGAGAT      750
25  GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                      832
  
```

30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

```

45  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA      150
    AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACGCCGA      200
50  TCGTGCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAATGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCTACCTG GATTCTTACA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAAC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CTATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA      450
55  GTCGACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
    GTGCTGGCGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
    ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC      600
    CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC      650
    ATACTCCGTT CTTCAAAGGC TACCGTCCGC AATTCTACTT CCGTACGACT      700
60  GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC      750
  
```

GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

5

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
25 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TGTAAGAGCGC 400
30 GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
AAGGCCGTGC CCGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GATGAAGGCG 650
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGAAGGACAC CATCGAAGTG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGTTGTG TACCCTGATC CATCCGATCG 800
CRATGGACGA CCGTCTGCGT TTCGCAA 827

40

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCIGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC 100
60 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150

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AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCGA 200
TCGTGCGTGG TTCCGCTCTG AAAGCGCTGG AAGGCGAMGC TGAGTGGGAA 250
GMGAAAATCA TCGAACTGGC TGGCTWCCTG GATTCTTACA TTCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
5 CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCCGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
10 CAAGTTCGAA TCTGAAAGTG ACATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807
15

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2) INFORMATION FOR SEQ ID NO: 165

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
30 serotype Typhi
    (B) STRAIN: ATCC 10749

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

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35 CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
40 GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTG 500
45 ACGAAGGCCG TGCNNGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACY AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
50 GGTAAATGCC GCGGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

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55 2) INFORMATION FOR SEQ ID NO: 166

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    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 817 bases
    (B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Double

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100

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10 CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA 100
 TTCATGAACA AATGCGACAT GGTGATGAT GAAGAGCTGC TGGAACTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG 200
 15 ACCTGCCGGT TGTTCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250
 GAGTGGGAAG CTAAAATCAT CGAGCTGGCC GGTCACCTGG ATTCCTACAT 300
 CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTTGAG 400
 CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 20 CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG 500
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGACA TCGAACGTGG TCAGGTACTG GCTAAACCAG GTTCCATCAA 600
 GCCGCACACT CAGTTCGATT CAGAAGTGTA TATCCTGAGC AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 25 CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
 GGTAATGCCA GGCATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA 800
 TCGCTATGGA CCAAGGC 817

30

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia liquefaciens*

(B) STRAIN: ATCC 27592

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG 50
 TCGTCAGGTT GGC GTTCCTT TCATCATCGT ATTCATGAAC AAATGCGACA 100
 TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAAATGGA AGTTCGTGAA 150
 50 CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCTGTTG 200
 TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAAATCA 250
 TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCAGAACCC AGAGCGTGCT 300
 ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG 350
 TCGTGGTACC GTTGTACCG GTCGTGTTGA GCGCGGTATC GTTAAAGTTG 400
 55 GCGAAGAAGT TGAAATCGTT GGTATCAAAG ACACCGTTAA GTCTACCTGT 450
 ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC GTGCTGGTGA 500
 GAACGTTGGT GTTCTGCTGC GTGGTATCAA GCGTGAAGAC ATCGAACGTG 550
 GTCAGGTACT GGCTAAACCA GGTTCAATCA AGCCACACAC CAAGTTCGAC 600
 TCAGAAAGTGT ACATCCTGAG CAAAGAAGAA GGTGGTCGTC ATACTCCATT 650
 60 CTTCAAAGGC TACCGTCCAC AGTTCCTACT CCGTACAACCT GACGTGACCG 700

GTACCATCGA ACTGCCAGAA GCGTTGAAA TGGTAATGCC AGGTGACAAC 750
 GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA 787

5

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GCGGTTTCCTT 50
 TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100
 YTGGAAGCTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
 25 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200
 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
 GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
 30 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
 CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
 35 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
 GCGGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

40 2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

GGCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTCCT CTGGCGACGA 200
 60 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250

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AGTGGGAAGC TAAGATTGTA GAACTGGCTG AAGCGCTGGA TTCTTACATC      300
CCAGAACCAG AGCGTGCTAT CGACAAGCCG TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTGAGC      400
GCGGTATCAT CAAAGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAC      450
5  ACCGTTAAGT CTACCTGTAC CGGTGTAGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC      550
GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCTATCAAG      600
CCGCACACCA AATTGCACTC AGAAGTGTAC ATCCTGAGCA AAGAAGAAGG      650
TGGTCGTCAC ACGCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
10 GTACTACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      750
GTAATGCCAG GCGATAACGT GAACATGGTT GTTACCCTGA TTCACCCAAT      800
CGCAATGGAC GACGGTCTGC GTTTCGCAA      829

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15

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

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20  (A) LENGTH: 830 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Serratia plymuthica
      (B) STRAIN: DSM 4540

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

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CGGCGCAATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTT CATCATCGTA      100
TTCATGAACA AATGCGACAT GGTGATGAT GAAGAGCTGC TGGAACCTGGT      150
35  AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTACGACTTC CCTGGTGATG      200
ACCTGCCGGT TGTTCTGTTG TCAGCGCTGA AAGCACTGGA AGGCGAACCA      250
GAGTGGGAAG CTAAAATCAT CGAGCTGGCT GGTTCCTGCTG ATTCTTACAT      300
CCCAGAACCA GAGCGTGCTA TCGACAAGCC GTTCCTGCTG CCAATCGAAG      350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTGAG      400
40  CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTGG GTATCAAAGA      450
CACCGTTAAG TCTACCTGTA CCGCGCTTGA AATGTTCCGC AAAGTGTCTG      500
ACGAAGGCCG TGCTGGTGAG AACGTGGGTG TTCTGCTGCG TGGTATCAAG      550
CGCGAAGATA TCGAACGTGG TCAGGTCCCTG GCTAAACCAG GTTCAATCAA      600
GCCACACACC AAGTTTGACT CAGAAGTGTA CATCCTGAGC AAAGAAGAAG      650
45  GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GGTGACAACG TGAACATGGT TGTAACCCTG ATCCACCCAA      800
TCGCGATGGA CGACGGCCTG CGTTTCGCAA      830

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50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

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55  (A) LENGTH: 829 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

GGCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCAATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTACCTTAC ATCATCGTAT 100
 10 TCATGAACAA ATGCGACATG GTAGATGATG AAGAGCTGCT GGAAGCTGGTA 150
 GAGATGGAAG TTCGCGAACT GCTGTCTGCT TACGACTTCC CAGGCGACGA 200
 CCTGCCGGTA ATCCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCCG 250
 AGTGGGAAGC GAAAATCGTT GAGCTGGCAG AAGCGCTGGA CAGCTACATC 300
 CCAGAGCCAG AGCGTGCTGT AGACAAGCCG TTCCTGCTGC CAATCGAAGA 350
 15 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
 GCGGTATCAT CAAAGTTGGT GAAGAAGTAG AAATCGTAGG TATCAAAGAC 450
 ACCGTTAAGT CTACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAGC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CGAAGCCAGG TTCAATCAAG 600
 20 CCGCACACCC AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
 GTACAACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG 750
 GTAATGCCAG GCGACAACGT GAACATGAAA GTTACTCTGA TTCACCCAAT 800
 CGCAATGGAC GACGGTCTGC GTTTCGCAA 829

25

2) INFORMATION FOR SEQ ID NO: 172

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 40 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

CGGCGCGATC YTGGTAGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACTC 50
 45 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 TTCCTGAACA AATGCGACAT GGTGTATGAC GAAGAGCTGC TGGAAGCTGGT 150
 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
 ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
 GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTACAT 300
 50 TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGGT 500
 ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
 55 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCTGTCC AAAGATGAAG 650
 GCGGCCGTC TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACTACTG ACGTGAAGTG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
 50 TCGCGATGGA CGACGGTCTG CGTTTC 826

2) INFORMATION FOR SEQ ID NO: 173

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20 TGGTAGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC 50
 CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
 ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG 150
 TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC 200
 GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGC GACGCAG AGTGGGAAGC 250
 25 GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCYTAYATT CCGGAACCAG 300
 AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
 ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC GCGGTATCAT 400
 CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACYCAGAAGT 450
 CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
 30 GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
 CGAACGTGGT CAGGTACTGG CGAAGCCRGG CACCATCAAG CCGCACACCA 600
 AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT 650
 ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA 700
 CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
 35 GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC 800
 GACGGTCTGC GTTTCGCA 818

40 2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55 CCTGGTAGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTA GGC GTTCCGT ACATCATCGT GTTCCTGAAC 100
 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TTGAAATGGA 150
 AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GAACTCCGA 200
 60 TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250

GCGAAAATCC TGGAACTGGC TGGCTTCCTG GATTCTTACA TTCCGGAACC 300
 AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
 CCATCTCCGG TCGTGGTACC GTTGTACC CGTGTGTAGA ACGCGGTATC 400
 ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
 5 GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
 GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
 CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGMCCTC 650
 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
 10 GACGTGACTG GTACCATCGA ACTGCCGGAA GGCCTAGAGA TGGTAATGCC 750
 GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
 ACGACG 806

15

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 TTCCTGAACA AATGCGACAT GGTGTATGAC GAAGAGCTGC TGGAACCTGGT 150
 35 TGAAATCGTAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
 AACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
 GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTACAT 300
 TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 40 CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG 500
 ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCCG GCACCATCAA 600
 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
 45 GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACTACTG ACGTGAAGT TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC 832

50

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

106

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 13301

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

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TCTGCTGCTG ACGGTCCAAT GCCACAACT CGTGAACACA TTCTTTTATC      50
ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC AAAGTTGACA      100
10 TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC      150
TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG TAATCGCTGG      200
TTCAGCATT AAGCTTTAG AAGGCGATGC TCAATACGAA GAAAAAATCT      250
TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC AGAACGTGAT      300
TCTGACAAAC CATTATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG      350
15 TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG      400
GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA ACAAAGTGT      450
ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG AAGCTGGTGA      500
CAACATTGGT GCATTATTAC GTGGTGTTGC TCGTGAAGAC GTACAACGTG      550
GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC TGAATTCAAA      600
20 GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC ACACTCCATT      650
CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT GACGTAACCTG      700
GTGTTGTTCA CTTACC                                     716

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25

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 29247

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

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TTCTTTTATC ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC      50
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA      100
AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG      150
45 TAATCGCTGG TTCAGCATT AAGCTTTAG AAGGCGATGC TCAATACGAA      200
GAAAAAATCT TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC      250
AGAACGTGAT TCTGACAAAC CATTATGAT GCCAGTTGAG GACGTATTCT      300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      350
ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA      400
50 AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      450
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTGC TCGTGAAGAC      500
GTACAACGTG GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC      550
TGAATTCAAA GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC      600
ACACTCCATT CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT      650
55 GACGTAACCTG GTGTTGTTCA CTTACCAGAA GGTMCTGAAA TGGTAATGCC      700
TGGTGATAAC GTTGAAATG                                     719

```

60 2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

15 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50
 TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT 100
 AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150
 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 200
 20 CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT 250
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 300
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 350
 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400
 CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450
 25 ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTGCT 500
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550
 ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600
 GTGGACGTCA CACTCCATTC TTCTC 625

30

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 704 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 43300

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

GTTGGTGAC CAGCATTAGT AGTATTCTTA AACAAAGTTG ACATGGTTGA 50
 CGATGAAGAA TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAA 100
 50 GCCAATATGA CTTCCCAGGT GACGATGTAC CTGTAATCGC TGGTTCAGCA 150
 TTAAAGCTT TAGAAGCGA TGCTCAATAC GAAGAAAAAA TCTTAGAATT 200
 AATGGAAGCT GTAGATACTT ACATTCCAAC TCCAGAACGT GATTCTGACA 250
 AACCATTGAT GATGCCAGTT GAGGACGTAT TCTCAATCAC TGGTCGTGGT 300
 ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG TTGGTGAAGA 350
 55 AGTTGAAATC ATCGGTTTAC ATGACACATC TAAAACAACT GTTACAGGTG 400
 TTGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG TGACAACATT 450
 GGTGCATTAT TACGTGGTGT TGCTCGTGAA GACGTACAAC GTGGTCAAGT 500
 ATTAGCTGCT CCTGGTTCAA TTACACCACA TACTGAATTC AAAGCAGAAG 550
 TATACGTATT ATCAAAAGAC GAAGGTGGAC GTCACACTCC ATTCTTCTCA 600
 60 AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA CTGGTGTTGT 650

TCACCTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700
TGAC 704

5

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
(B) STRAIN: ATCC 6538

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT 100
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150
25 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 200
CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT 250
TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 300
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 350
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400
30 CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450
ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT 500
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600
GTGGACGTCA CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTC 650
35 CGTACTACTG ACGTAACTGG TGTGTTCAC TTACCAGAAG GTACTGAAAT 700
GGTAATGCCT GGTGATAACG TTGAAATGAC 730

40 2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
(B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG 200
60 ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA 250

```

GAATACGAAC AAAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300
TCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGAAAGA 450
5 CGGTTTCAAA AAAACAACAG TTACTGGTGT AGAAATGTTT CGTAAATTAT 500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT 550
TCACGTGAAG AAGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
TACACCACAC ACTAAATTCA CTGCAGAAGT TTACGTATTA TCTAAAGATG 650
AAGGTGGACG TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAT 700
10 TTCCGTACTA CTGACGTAAC AGGTGTGTGT ACTTTACCAG AAGGTACAGA 750
AATGGTAATG CCTGGCGATA ACGTTAAAAT GGAAGTTGAA TTAATTTCTC 800
CAATCGCTAT CGAAGACGGT ACTCGTTTCT CAAT 834

```

15

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

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20 (A) LENGTH: 835 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Staphylococcus capitis subsp. capitis
    (B) STRAIN: ATCC 27840

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

```

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
35 TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG 200
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
CAATAACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT 300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 400
40 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA 450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC 600
ACCACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
45 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCACA ATTCTATTTT 700
CGTACTACTG ACGTAACTGG TGTGTGTTAA TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCACAAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA 800
TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA 835

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50

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 804 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macrococcus caseolyticus*
 (B) STRAIN: ATCC 13548

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

GTATCTTAGT AGTATCTGCT GCTGACGGTC CAATGCCACA AACTCGTGAA 50
 CACATCCTTT TATCACGTAA CGTTGGTGTA CCAGCATTAG TAGTATTCTT 100
 10 GAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTTGAAA 150
 TGGAAGTTCG TGAATTATTA TCTGAATATG ACTTCCCTGG TGACGATGTA 200
 CCTGTAATCG CTGGATCTGC TTTAAAAGCA TTAGAAGGCG TTGAAGAATA 250
 CGAAGACAAA ATCATGGAAT TAATGGACGC AGTTGATGAG TACATCCCAA 300
 CTCCAGAACG TGATTCTGAC AAACCATTC A TGATGCCAGT TGAGGACGTA 350
 15 TTCTCAATCA CTGGTCGTGG TACAGTTGCA ACTGGACGTG TTGAGCGTGG 400
 ACAAGTTAAA GTTGGTGAAG AAGTTGAAAT CATTGGTTTA ACTGAAGAAC 450
 CAGCAAAAAC TACAGTTACA GGTGTAGAAA TGTTCGTA A ATTATTAGAT 500
 TACGCTGAAG CTGGAGATAA CATCGTGCT TTATTACGTG GTGTTTCTCG 550
 TGAAGACGTA CAACGTGGAC AAGTATTAGC TAAACCAGGT TCAATTACTC 600
 20 CACATACTAA ATTCAAAGCT GAAGTTTACG TATTATCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CACTAACTAC CGCCCTCAGT TCTACTTCCG 700
 TACAACGAC GTAACGTGGT TAGTTAACTT ACCAGAAGGT ACTGAAATGG 750
 TAATGCCTGG AGATAACATC GAAATGAACG TTGAATTAAT TTCTCCAATC 800
 GCGA 804
 25

2) INFORMATION FOR SEQ ID NO: 184

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 40 (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
 45 GTGAACATAT CCTTTTATCA CGTAACGTTG GTGTTCCAGC ATTAGTTGTA 100
 TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 200
 ATGTACCTGT AATCTCTGGT TCAGCATTA AAGCTCTTGA AGGCGACGCT 250
 GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTTCAT 300
 50 TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG GCGTGTTGAA 400
 CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGCAAGA 450
 AGATTCAAGC AAAACAACCTG TTAAGTGGTGT AGAAATGTTT CGTAAATTAT 500
 TAGACTACGC TGAAGCTGGT GACAACATTG GTGCGTTATT ACGTGGTGT 550
 55 GCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
 TACACCACAC ACAAACCTTA AAGCGGAAGT TTACGTTTTA TCAAAAGATG 650
 AAGGTGGCCG TCATACGCCA TTCTTCAGTA ACTATCGCCC ACAATTCTAT 700
 TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACTGA 750
 AATGGTTATG CCTGGCGACA ACGTAGAAAT GGAAGTTGAA CTAATTTCTC 800
 60 CAATCGCTAT CGAAGACGGT ACACGTTTCT CT 832

2) INFORMATION FOR SEQ ID NO: 185

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	ATCTTATTAT	50
	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	100
	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	AAGTTCGTGA	150
	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	GTAATCGCTG	200
	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	ACAAAAAATC	250
25	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	CAGAACGTGA	300
	TTCTGACAAA	CCATTTCATGA	TGCCAGTTGA	GGACGTATTC	TCAATCACTG	350
	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTT	400
	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	AAACAACCTGT	450
	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCTGGTG	500
30	ACAACATCGG	TGCTTTATTA	CGTGGTGTTG	CACGTGAAGA	CGTACAACGT	550
	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	CAAAATTCAA	600
	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	CACACTCCAT	650
	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	TGACGTAAC	699

35

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

55	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAATA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
60	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400

CGTGGGCCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG ~~GTATCCATCA~~ 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600
 5 ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATT CTTACAAACT ATCGTCCACA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG TGTGTGTTAAC TTACCAGAAG GTACTGAAAT 750
 GGTTATGCCT GGCGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

10

2) INFORMATION FOR SEQ ID NO: 187

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus warneri*
 25 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

CACAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50
 30 TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100
 AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150
 CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAG AGCTTTAGAA 200
 GGCGACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250
 TGAATACATT CCAACTCCAG AACGTGATTG TGACAAACCA TTCATGATGC 300
 35 CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350
 CGTGTGTAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400
 TTTACATGAC ACTTCTAAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450
 AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500
 GGTGTTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550
 40 TTCAATTACA CCACATAACA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600
 AAGACGAAGG TGGACGTCAC ACTCCATTCT TCAGTAACTA CCGCCACAA 650
 TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTCAT TACCAGAAGG 700
 TACTG 705

45

2) INFORMATION FOR SEQ ID NO: 188

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 23

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

      TTTTATCACG TAACGTTGGT GTACCAGCAT TAGTAGTATT CTAAACAAA      50
      GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTTG AAATGGAAGT     100
5    ACGTGACTTA TTATCTGAAT ACGACTTCCC AGGTGACGAC GTACCTGTAA     150
      TCGCTGGTTC AGCTTTAAAA GCTTTAGAAG GCGATGCTCA ATACGAAGAA     200
      AAAATCTTAG AATTAATGCA AGCAGTTGAT GATTACATTC CAACTCCAGA     250
      ACGTGACTCT GATAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA     300
      TCACTGGTCG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGTCAAATC     350
10   AAAGTTGGTG AAGAAGTTGA AATTATTGGT ATCAAAGAAA CTTCTAAAAC     400
      AACTGTTACT GGTGTAGAAA TGTTCCTGTA ATTATTAGAC TACGCTGAAG     450
      CTGGTGACAA CATCGGTGCT TTATTACGTG GTGTTGCTCG TGAAGATGTA     500
      CAACGTGGTC AAGTATTAGC TGCTCCAGGT TCAATTACAC CTCACACAAA     550
      ATTCAAAGCA GACGTATACG TTTTATCAAA AGATGAAGGT GGACGTCATA     600
15   CTCCATCTTT CACTAACTAT CGTCCACAAT TCTATTTCCG TACTACTGAC     650
      GTAACGTGGT TTGTAACTT ACCAGAAG                                678

```

20 2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

```

35   ACCAGCATTA GTAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
      AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC     100
      GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC     150
      TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG     200
10   CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC     250
      ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC     300
      TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA     350
      TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG     400
      TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT     450
15   ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG     500
      CTCCAGGTTT AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT     550
      TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG     600
      TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC     650
      CAGAAGGTAC TGAAATGG                                668

```

20 2) INFORMATION FOR SEQ ID NO: 190

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 5 (B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

```

10 AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TTGAAATGGA      50
   AGTACGTGAC TTATTATCTG AATACGACTT CCCAGGTGAC GATGTACCTG      100
   TAATCGCTGG TTCAGCATT AAGGCTTTAG AAGGCGATGC TCAATACGAA      150
   GAAAAAATCT TAGAATTAAT GCAAGCAGTT GATGATTACA TTCCAACCTCC      200
   AGAACGTGAT TCTGACAAAC CATTCTATGAT GCCAGTTGAG GACGTATTCT      250
   CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      300
15 ATCAAAGTTG GTGAAGAAGT TGAAATCATT GGTATCCATG ACACTTCTAA      350
   AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG      400
   AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTGTC TCGTGAAGAC      450
   GTACAACGTG GTCAAGTATT AGCTGCTCCA GGTTCATCA CACCTCACAC      500
   AAAATTTAAA GCAGACGTAT ACGTTTTATC TAAAGACGAA GGTGGACGTC      550
20 ACACTCCATT CTTCAACAAAC TATCGTCCAC AATTCTATTT CCG          593

```

2) INFORMATION FOR SEQ ID NO: 191

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

```

40 CGGCGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC      50
   GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      100
   TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT      150
   TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG      200
   ACGTACCTGT AATCGCTGGT TCAGCTTTAA AAGCTTTAGA AGGCGATGCT      250
45 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTATAT      300
   TCCAACCTCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG      350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA      400
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATTATTG GTATCAAAGA      450
   AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG      500
50 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT      550
   CGTGAAGATG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATTAC      600
   ACCTCACACA AAATTCAAAG CAGACGTATA CGTTTTATCA AAAGATGAAG      650
   GTGGACGTCA TACTCCATTC TTCTCTAACT ATCGTCCACA ATTCTATTTT      700
   CGTACTACTG ACGTAACTGG TGTGTTAAAC TTACCAGAAG GTACTGAAAT      750
55 GGTAATGCCT GGTGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA      800
   TCGCGATTGA AGACGGTACT CGTTTCTC          828

```

60 2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

15 ATGGTCCAAT GCCACAACT CGTGAACACA TTCTTTTATC ACGTAACGTT 50
 GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA 100
 CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG 150
 AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATT A 200
 20 AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT 250
 GCAAGCAGTT GATGACTACA TTCCAACCTC AGAACGTGAT TCTGACAAAC 300
 CATTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT 350
 GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT 400
 TGAAATCATC GGTTTACATG ACACTTCTAA AACAACTGTT ACTGGTGTAG 450
 25 AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT 500
 GCTTTATTAC GTGGTGTTCG TCGTGAAGAC GTACAACGTG GTCAAGTATT 550
 AGCTGCTCCT GGTTC AATTA CACCACATAC AAAATTCAAA GCGGAAGTTT 600
 ACGTTTTATC TAAAGACGAA 620

30

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA 50
 ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGAATTATTA TCTGAATACG 100
 50 ACTTCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTAAAAGCT 150
 TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC 200
 AGTTGATGAT TATATTCCAA CTCCAGAACG TGA CTGAT AAACCATTCA 250
 TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT 300
 ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT 350
 55 TATTGGTATC AAAGAACTT CTA AAACAAC TGTTACTGGT GTAGAAATGT 400
 TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CGGTGCTTTA 450
 TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC 500
 TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT 550
 TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT 600
 60 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTA ACTTACC 650

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCTTTTA TCACGTAACG TTGGTGTAAC AGCATTAGTA GTATTCTTAA 50
 ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
 TGTAATCGCT GGTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC 250
 CCAGAACGTG ACTCTGATAA ACCATTCATG ATGCCAGTTG AGGACGTATT 300
 CTCAATCACT GGTCTGGTGA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAAACTTCT 400
 AAAACAAC 450
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTT GCTCGTGAAG 500
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
 ACAAATTCA AAGCAGACGT ATACGTTTGA TCAAAAGATG AAGGTGGACG 600
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
 CTGACGTAAC TGGTGTTGTT AACTTACCAG AAGG 684
 35

2) INFORMATION FOR SEQ ID NO: 195

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 50 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
 55 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
 GACTTCCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAGC 150
 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GACTGTGTC 300
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

TTATTGGTAT CAAAGAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400
 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450
 ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500
 CTCCAGGTTC AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550
 5 TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAACATCG 600
 TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC 650
 CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50
 TGGTTCAGCT TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA 100
 TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150
 30 GACTCTGATA AACCATTTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200
 TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250
 TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAACT 300
 GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350
 TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400
 35 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC 450
 AAAGCAGACG TATATGTTTT ATCAAAAAGAT GAAGGTGGAC GTCATACTCC 500
 ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA 550
 CTGGTGTTGT TAACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600
 AACGTTGAAA T 611

40

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*
 35 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAACTC 50
 50 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA 100

	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGATT	TATTAAGTGA	ATATGACTTC	CCAGGTGACG	200
	ATGTGCCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	CTAAAATCTT	AGAATTAATG	GATGCAGTTG	ATAACTACAT	300
5	TCCAACCTCCA	GAACGTGACT	CTGACAAACC	ATTTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATTATTG	GTATCCACGA	450
	TACTACTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CGTTATTACG	TGGTGTGCT	550
10	CGTGAAGATG	TACAACGTGG	ACAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACT	AAATTTAAAG	CTGACGTATA	TGTTTTATCT	AAAGATGAAG	650
	GTGGACGTCA	TACACCATTC	TTCTCAAAC	ACCGCCACA	ATTCTATTTC	700
	CGTACTACAG	ACGTAACTGG	TGTTGTTAAT	TTACCAGAAG	GTACAGAAAT	750
	GGTTATGCCT	GGCGACAACG	TGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
15	TCGCTATCGA	AGACGGAAC	CGTTTCTC			828

2) INFORMATION FOR SEQ ID NO: 198

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

35	AGTAGTATCT	GCTGCTGATG	GCCCAATGCC	ACAAACTCGT	GAACACATTC	50
	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	CTTAAACAAA	100
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	GTACCTGTAA	200
	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	CTATGAGCAA	250
40	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	CAACACCAGA	300
	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTCAAATC	400
	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	AATCAAGCAA	450
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
45	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	ACGTGATGAC	550
	GTACAACGTG	GTCAAGTTT	AGCTGCTCCT	GGTACTATTA	CACCACATAC	600
	AAAATTCAAA	GCGGATGTT	ACGTTTTATC	TAAAGATGAA	GGTGGTCGTC	650
	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT		690

50

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG 83

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

```

GCATTAGTTG TATTCTTAAA CAAAGTTGAC ATGGTTGACG ATGAAGAATT      50
ATTAGAATTA GTAGAAATGG AAGTTCGTGA TTTATTAAGC GAATATGACT      100
10 TCCCAGGTGA CGATGTACCT GTAATCTCTG GTTCTGCATT AAAAGCTTTA      150
GAAGGCGACG CTGACTATGA GCAAAAAATC TTAGACTTAA TGCAAGCTGT      200
TGATGACTTC ATTCCAACAC CAGAACGTGA TTCTGACAAA CCATTCATGA      250
TGCCAGTTGA GGACGTATTC TCAATCACTG GTCGTGGTAC TGTTGCTACA      300
GGCCGTGTTG AACGTGGTCA AATCAAAGTC GGTGAAGAAA TCGAAATCAT      350
15 CGGTATGCAA GAAGAATCAA GCAAAACAAC TGTTACTGGT GTAGAAATGT      400
TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT TGGTGCATTA      450
TTACGTGGTG TTTCACGTGA TGACGTACAA CGTGGTCAAG TTTTAGCTGC      500
TCCTGGTACT ATTACACCAC ATACAAAATT CAAAGCGGAT GTTTACGTTT      550
TATCTAAAGA TGAAGGTGGT CGTCATACAC CATTCTTCAC TAACTACCGC      600
20 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTTG TTAACCTACC      650
AGAAGGTACT GAAATGGTTA TGCCTGGCGA TAACGTTGAA ATGGATGTTG      700
AATTAATTTT TCCAATCGCT ATT                                723
  
```

25

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSsa 18

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

```

CGTTGGTGTT CCAGCATTAG TTGTATTCTT AAACAAAGTT GACATGGTTG      50
ACGATGAAGA ATTATTAGAA TTAGTAGAAA TGGAAAGTTCG TGACTTATTA      100
AGCGAATATG ACTTCCCAGG TGACGATGTA CCTGTAATCT CTGGTTCTGC      150
45 ATTAAAAGCT TTAGAAGGCG ACGCTGACTA TGAGCAAAAA ATCTTAGACT      200
TAATGCAAGC TGTTGATGAC TTCATTCCAA CACCAGAACG TGATTCTGAC      250
AAACCATTCA TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG      300
TACTGTTGCT ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTCGGTGAAG      350
AAATCGAAAT CATCGGTATG CAAGAAGAAT CAAGCAAAAC AACTGTTACT      400
50 GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG CTGGTGACAA      450
CATTGGTGCA TTATTACGTG GTGTTTCACG TGATGACGTA CAACGTGGTC      500
AAGTTTTAGC TGCTCCTGGT ACTATTACAC CACATACAAA ATTCAAAGCG      550
GATGTTTACG TTTTATCTAA AGATGAAGGT GGTGTCATA CACCATCTCT      600
CACTAACTAC CGCCACAAT TCTATTTCCG TACTACTGAC GTAACGGTGG      650
55 TTGTTAACTT ACCAGAAGGT ACTGAAATGG TTATGCCTGG CGATAAC      697
  
```

60

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

15 CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAATC 50
   GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCCCTGC ATTAGTAGTA 100
   TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 150
   TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG 200
   ACGTTCCTGT AATTGCTGGT TCAGCATTAA AAGCATTAGA AGGCGACGAA 250
20 GCTTACGAAG ACAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT 300
   CCCAATCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
   CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA 450
   AGAATCTTCT AAAACAACCTG TAACTGGTGT TGAAATGTTC CGTAAATTAT 500
25 TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTT 550
   GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT 600
   CACACCTCAC ACTAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG 650
   AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT 700
   TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA 750
30 AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTTAC 800
   CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA 835

```

35 2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50 CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAATC 50
   GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA 100
   TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
   AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG 200
55 ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
   AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
   TCCAATCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 450
60 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500

```

ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 556
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTT 700
 5 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCAA C 831

10

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 50

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA 100
 TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 30 AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG 200
 ACGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGACGAA 250
 AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 400
 35 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 40 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTT 700
 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

45

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium longum*
 60 (B) STRAIN: ATCC 15707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

	TGGCGCTATC	CTCGTTGTGG	CCGCCACCGA	CGGCCCCGATG	GCCCAGACTC	50
	GCGAGCACGT	GCTGCTCGCC	CGTCAGGTTG	GCGTTCCGAA	GATCCTCGTC	100
5	GCCCTGAACA	AGTGCGACAT	GGTCGACGAT	GAAGAGCTCA	TCGAGCTCGT	150
	CGAAGAAGAG	GTCCGCGACC	TCCTCGACGA	GAACGGCTTC	GACCGTGA	200
	GCCCGGTCAT	CCACACCTCC	GCTTACGGTG	CTCTGCACGA	CGACGCTCCG	250
	GACCACGAGA	AGTGGGTCCA	GTCCGTTAAG	GACCTCATGG	ACGCTGTCGA	300
	CGACTACATC	CCGACCCCGG	TTCACGACCT	GGACAAGCCG	TTCCTGATGC	350
10	CGATCGAGGA	CGTCTTCACC	ATCTCCGGCC	GTGGTACCGT	TGTCACCGGT	400
	CGTGTGAGC	GTGGCCAGCT	GGCCGTCAAC	ACCCCGGTTCG	AGATCGTTGG	450
	TATCCGTCCG	ACCCAGCAGA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGACCATGGA	CGCCTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTTCTGCGT	550
	GGTCTCGGCC	GTGACGATGT	CGAGCGTGGC	CAGGTTGTGG	CCAAGCCGGG	600
15	CTCCGTCACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGC	CGGCCGTAC	TCGCCGTTCT	TCTCCAATA	CCGTCCGCAG	700
	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	GTCATCGAGC	TGCCGGAAGG	750
	CGTCGAGATG	GTTCAGCCGG	GCGACCACGC	TACCTTCACC	GTTGAGCTGA	800
	TTCAGCCCAT	CGCTATGGAG	GAAGGCCTGA	CCTTCGCTG		839

2) INFORMATION FOR SEQ ID NO: 205

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stenotrophomonas maltophilia*
- (B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

	CGGCGCGATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCGATG	CCGCAGACCC	50
40	GTGAGCACAT	CCTGCTGTCG	CGCCAGGTCG	GCGTGCCGTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TCGAGCTGGT	150
	CGAGATGGAA	GTGCGCGAAC	TGCTGAGCAA	GTACGAGTTC	CCGGGCGACG	200
	ACACCCCGAT	CATCGCCGGT	TCGGCCCGCC	TGGCGCTGGA	AGGCGACCAG	250
	AGCGACATCG	GCGTGCCGGC	CATCCTGAAG	CTGGTCGACG	CGCTGGACAG	300
45	CTGGATTCCG	GAGCCGGAGC	GTGCGATCGA	CAAGCCGTTC	CTGATGCCGG	350
	TGGAAGACGT	GTTCTCGATC	TCGGGCCGCG	GCACCGTGGT	GACCGGTCGT	400
	ATCGAGCGCG	GCGTGATCAA	GGTTGGCGAC	GAAATCGAAA	TCGTCCGGCAT	450
	CCGTCCGGTG	CAGAAGACCA	CCGTGACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	GGGTCAGGCA	GGCGACAACG	CTGGCCTGCT	GCTGCGCGGC	550
50	ACCAAGCGTG	ATGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGCAC	600
	GATCAAGCCG	CACACCAAGT	TCGAAGCGGA	AGTGTACGTC	CTGTCAAGG	650
	ACGAGGGCGG	CCGCCACACC	CCGTTCTTCA	ACGGCTACCG	TCCGCAGTTC	700
	TACTTCCGCA	CCACCGACAT	CACCGGCGCC	GCTGCACTGC	CGGAAGGCGT	750
	CGAA					754

2) INFORMATION FOR SEQ ID NO: 206

50 (i) SEQUENCE CHARACTERISTICS:

123

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

	TGGTGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
15	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACTAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCG	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500
50	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550

TGATGAAATC GAACGTGGTC AAGTTCCTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
 TACAACCTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 5 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25 CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG 50
 CACATCCTTC TTTCACGTCA AGTTGGTGTT AAACACCTTA TCGTATTCAT 100
 GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA 150
 TGGAAATTCG TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT 200
 30 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCA CTTGAAGGCG ATGAAAAATA 250
 CGAAGACATC ATCATGGAAT TGATGAGCAC TGTTGATGAG TACATTCCAG 300
 AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT CGAAGATGTA 350
 TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
 TACTGTTCTG GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA 450
 35 TCCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500
 GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG 550
 TGATGAAATC GAACGTGGTC AAGTTCCTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
 40 TACAACCTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

45

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

```

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
5  AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC      200
   TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
   TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
   AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
   TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
10  GGTACTGTTC GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
   TATCCAAAAA GCAGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAACCTG      500
   ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCAA      550
   CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
   CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
15  GTGGACGTCA TACTCCATTC TTCAACAAC ACTCGTCCACA ATTCTACTTC      700
   CGTACAACCTG ACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
   GGTATGCCT GGTGATAACG TTAATATCGA AGTTGAATTG ATTCACCCAA      800
   TCGCCGTAGA ACAAGGTACT AC          825

```

20

2) INFORMATION FOR SEQ ID NO: 210

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(i) SEQUENCE CHARACTERISTICS:
25  (A) LENGTH: 825 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Streptococcus agalactiae
     (B) STRAIN: CDCss-1073

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

```

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTAAACA CCTTATCGTA      100
40  TTCATGAACA AAGTTGACCT TGTGATGAT GAAGAATTGC TTGAATTGGT      150
   TGAAATGGAA ATTTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
   ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
   AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
   TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
15  ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
   CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
   AGATATCCAA AAAGCAGTTG TTAAGTGGTG TGAAATGTTT CGTAAACAAC      500
   TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
   CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
50  CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
   AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
   TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA      750
   AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTCACC      800
   CAATCGCCGT AGAACAAGGT ACTAC          825

```

55

2) INFORMATION FOR SEQ ID NO: 211

60 (i) SEQUENCE CHARACTERISTICS:

126

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
15	TGAACACATC	CTTCTTTCAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCTTCTT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCAATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCAATCG	AACCTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTGTAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
50	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	GTGTTCTTCT	TCGTGGTATC	550

CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
 CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
 5 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTACC 800
 CAATCGCCGT TGAACAAGGT ACTACAT 827

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus* (deposited as
Streptococcus constellatus)
 (B) STRAIN: ATCC 27823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACCTCGTGA 50
 ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
 TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
 30 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCCAG GTGATGAAAT 200
 CCCAGTTATC CAAGGTTTCA CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
 ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
 GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT 350
 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
 35 GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
 ATCCAAAAAG CAGTTGTTAC TGGTGTTGAA ATGTTCCGTA AACAATTGGA 500
 CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
 GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTTCAT 600
 CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
 40 TGGACGTCAT ACTCCATTCT TCAACAATA CCGTCCTCAA TTCTACTTCC 700
 GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
 GTAATGCCTG GTGATAACGT AACAATTGAT GTTGAGTTGA TCCACCCAAT 800
 TGCCGTAGAA CAAGGAACTA C 821

45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cricetus*
 60 (B) STRAIN: ATCC 19642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

```

5   GCTATCCTTG TAGTAGCTTC TACAGACGGA CCAATGCCAC AAAC TCGTGA      50
    ACACATCTTG CTTTCACGCC AAGTTGGTGT TAAGAGCCTT ATCGTCTTCA      100
    TGAACAAGGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA      150
    ATGGAAATCC GTGATCTTCT TTCAGAATAC GATTTC CCGAG GTGATGATAT      200
    CCCTGTTGTT CAAGGTT CAG CTCTTAAAGC CCTTGAAGGT GATACAGCTG      250
    CCGAAGACAA GATCATGGAA TTGATGGACA TCGTTGATGA CTACATTCCA      300
    GAACCAAAAC GTGATACTGA TAAGCCATTG CTTCTTCCAG TCGAAGACGT      350
10  ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG      400
    GTACTGT TAA GGTCAATGAC GAAGTTGAAA TCGTTGGTAT CAAGGACGAA      450
    ATCCAAAAG CGGTTGTTAC CGGAGTTGAA ATGTTCCGTA AACAATTGGA      500
    TGAAGGTCTT GCAGGGGATA ACGTTGGTGT GCTTCTTCGT GGTATCCAAC      550
    GTGATGAAAT CGAACGTGGT CAAGTATTGG CTGCACCTGG TTCAATCCAT      600
15  CCACACACTA AATTCAAGGG TGAAGTTTAC ATCCTTTCTA AAGATGAAGG      650
    TGGACGTCAC ACTCCATTCT TCAACAATA CCGTCCACAG TTCTACTTCC      700
    GTACAACTGA CGTAACTGGT TCAATCGAAT TGCCAGCAGG TACTGAAATG      750
    GTTATGCCTG GTGATAACGT TACTATCGAC GTTGAATTGA TCCACCCAAT      800
    CGCTGTTGAA AAAGGTACTA C                                821
20

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2) INFORMATION FOR SEQ ID NO: 215

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cristatus*
 (B) STRAIN: ATCC 51100

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

```

40  TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
    ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG      100
    AACAAGATCG ACTTGGTTGA TGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
    GGAAATCCGT GACCTCTTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
    CAGTTATCCA AGGTT CAGCT CT TAAAGCTC TTGAAGGTGA TACTAAGTAC      250
    GAAGACATCA TCATGGAATT GATGAACACT GTTGATGAGT ACATCCCAGA      300
45  ACCAGAACGT GATACTGACA AACCTCTTCT TCTTCCAGTC GAAGACGTAT      350
    TCTCAATCAC TGGTCGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
    ACTGTTCTGT TCAACGATGA AATCGAAATC GTTGGTATCA AAGAAGAAAT      450
    CCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAGCTTGACG      500
    AAGGTCTTGC AGGGGACAAC GTAGGTGTAC TTCTTCGTGG TATCCAACGT      550
50  GATGAAATCG AACGTGGTCA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
    ACACACTAAA TTCAAGGGTG AAGTTTACAT CCTTACTAAA GAAGAAGGTG      650
    GACGTCACAC TCCATTCTTC AACAAC TACC GTCCACAGTT CTACTTCCGT      700
    ACAACTGACG TTACAGGTTT AATCGA ACTT CCAGCAGGTA CTGAAATGGT      750
    AATGCCTGGT GATAACGTAA CTATCGACGT TGAGTTGATC CACCCAATCG      800
55  CCGTTGAACA AGGTACTCCT T                                821

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60

2) INFORMATION FOR SEQ ID NO: 216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Streptococcus downei*
 (B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

```

15 AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
   TTTACGTC A GGTGGTGTT AAGAACCTTA TCGTCTTCAT GAACAAGGTT      100
   GACTTGGTTG ACGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG      150
   TGACCTGCTT TCAGAATACG ATTTCCAGG TGATGATATC CCTGTTGTTC      200
   AAGGTTGAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG      250
20 ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG      300
   TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA      350
   CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTAAAG      400
   GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC      450
   AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG      500
25 CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC      550
   GAACGTGGTC AAGTGTGGC TGCGCCTGGT TCGATTCACC CACACACTAA      600
   GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA      650
   CTCCATTCTT TAACAACTAC CGTCCACAGT TCTACTTCCG TACAACGTAC      700
   GTAACGGTT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG      750
30 TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC              792

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2) INFORMATION FOR SEQ ID NO: 217

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

```

50 GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
   CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTT ATGAACAAAA      100
   TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC      150
   CGTGACCTTC TTTCAGAATA CGATTTCCCA GGTGATGACC TTCCAGTTAT      200
   CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA      250
55 TCATCATGGA ATTGATGGAT ACTGTTGATT CATAATTCC AGAACCAGAA      300
   CGTGACACTG ACAAACCAT TCTTCTTCCA GTCGAAGACG TATTCTCAAT      350
   CACAGGTCGT GGTACAGTTG CTTCAGGACG TATCGACCGT GGTACTGTTC      400
   GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA      450
   GCTGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAACCTG ACGAAGGTCT      500
50 TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAG CGTGACGAAA      550

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	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATTC	TTCAACAACCT	ATCGTCCACA	ATTCTACTTC	CGTACAACCTG	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

2) INFORMATION FOR SEQ ID NO: 218

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus equi* subsp. *equi*
 (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTGTAAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCTGTGAC	TTCTTTTCAGA	ATATGATTTT	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTCGTGTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTT	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

45 2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Streptococcus ferus*
 (B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

60

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CGGTGCAATC CTTGTAGTAG CTTCTACAGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAGGTAG GTGTAAACA CCTTATCGTC      100
TTCATGAACA AAGTTGACTT GGTGACGAT GAAGAATTGC TTGAATTGGT      150
TGAAATGGAA ATCCGTGACC TGCTTTCAGA ATATGATTTC CCAGGTGATG      200
5 ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCGCTTGA AGGTGATACT      250
GCTCAAGAAG ATGTTATCAT GGAATTGATG AAAACCGTTG ATGAGTACAT      300
CCCAGAACCA GAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCAAG      350
ATGTATTCTC AATCACAGGT CGTGGTACTG TAGCTTCAGG ACGTATCGAT      400
CGTGGTACTG TAAGAGTCAA CGATGAAGTT GAAATCGTTG GTATCAAAGA      450
10 CGAAATCACT AAAGCAGTTG TTACCGGTGT TGAAATGTTT CGTAAACAAT      500
TGGACGAAGG TCTTGCTGGT GATAACGTTG GTGTGCTTCT CCGTGGTGTG      550
CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCAAT      600
CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT ACTAAAGAAG      650
AAGGTGGACG TCATACACCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC      700
15 TTCCGTACAA CTGACGTAAC TGGTTCAATC GAATTGCCAG CAGGTACTGA      750
AATGGTTATG CCTGGTGATA ACGTGACTAT CGACGTTGAA TTGATCCACC      800
CAATCGCCGT TGAACAAGGT ACTAC      825

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20

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*
(B) STRAIN: ATCC 10558

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

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CGGAGCTATC CTTGTAGTAG CTTCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCACAT CCTTCTCTCA CGCCAAGTTG GTGTAAACA CTTGATCGTG      100
TTCATGAACA AAGTTGACTT GGTGACGAT GAAGAATTGC TTGAGTTGGT      150
40 TGAAATGGAA ATCCGTGACC TCTTGTCAGA ATACGACTTC CCAGGTGACG      200
ATCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA AGGTGACTCT      250
AAATATGAAG ATATCATCAT GGAATTGATG AACACTGTTG ATGAGTACAT      300
CCCAGAACCA GAACGCGACA CTGACAAACC ATTGCTTCTT CCAGTCAAG      350
ACGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
15 CGTGGTATCG TTAAAGTCAA TGACGAAATC GAAATCGTTG GTATCAAAGA      450
AGAAATCCAA AAAGCAGTTG TTACTGGTGT TGAAATGTTT CGTAAACAGC      500
TTGACGAAGG TCTTGAGGG GACAACGTTG GTGTGCTTCT TCGTGGTATC      550
CAACGTGATG AAATCGAACG TGGACAAGTT ATTGCTAAAC CAGGTTCAAT      600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTATATCCTT ACTAAAGAAG      650
50 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC      700
TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA      750
AATGGTAATG CCTGGTGATA ACGTAACTAT CGACGTTGAG TTGATCCACC      800
CAATCGCCGT TGAACAAGGT ACTACT      826

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55

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 799 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*

(B) STRAIN: ATCC 27335

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

	TG TAG TAG CT	TCA ACT GAC G	GAC CA ATG CC	TCA AACT CGT	GA ACAT ATCC	50
	TT CTTT CAC G	TCA AGT AGG T	GT TAA ATAC C	TT ATT GTCT T	CAT GAAC AAA	100
15	GT TGA CT TGG	TTG ACG ATG A	AGA ATT GCT T	GA ATT GGT TG	AA ATGG AAA T	150
	CC GTG ATCT T	CTT TCAG AAT	ACG ATT TCC C	AG GTG ATG AT	ATT CCAG TAA	200
	TCC AAG GTT C	AG CACT TAA A	GCT CTT GAAG	GTG ATG AAA A	AT ATGA AGAC	250
	AT CAT CAT GG	AAT TGAT GAA	TACT GTT GAT	GA ATAT ATTC	CAG AAC CAG A	300
	AC GTG ATACT	GAC AAAC CAT	TG CTT CTT CC	AG TCG AAG AT	GT ATT CTCAA	350
20	TC ACT GGAC G	TGG TACT GTT	GCT TCAG GAC	GT ATCG ACCG	TGG TACT GTT	400
	AA AGT CAAC G	AT GAAG TTG A	AAT CGT TGG T	AT CCG CGAG G	AA ATCC AAA A	450
	AG CAG TTGT T	ACT GGT GTT G	AA ATGT TCC G	TAA ACA ATT G	GAC GAAG GTC	500
	TT GCT GGAG A	TA ACG TAGG G	GTT CTT CTTC	GT GGT ATCCA	AC GTG ACG AA	550
	ATT GAAC GTG	GAC AAG TTCT	TG CTAA ACCA	GG TTCA ATTC	AT CCAC ACAC	600
25	TAA ATT CAAA	GGT GAAG TTT	AC ATC CTT AC	TAA AGA AGAA	GG TGG ACG TC	650
	ATA CTCC ATT	CTT CAACA AC	TAC CGT CCT C	AAT TCT ACT T	CC GTACT ACA	700
	GAC GTTAC AG	GTT CAAT CGA	ACT TCCT GCA	GG TACT GAAA	TGG TAAT GCC	750
	TGG TGATA AC	GTA ACA ATT G	AT GTT GAG TT	GAT CCACCCA	ATT GCCG TA	799

30

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus macacae*

(B) STRAIN: ATCC 35911

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

	TGG TGCT ATT	CTT G TAG TAG	CTT CA ACT GA	CGG TCCA ATG	CCT CAA ACG C	50
	GT GAAC ATAT	CCT TCT TTT CA	CGC CAAG TAG	GT GTT AAA AA	CCT TATT GTT	100
50	TT CAT GAATA	AAG TTG ACT T	AG TTG ATG AT	GA AGA ATT GC	TT GAATT GGT	150
	TG AAAT GGAA	AT CCG TGAT C	TT CTT ACAG A	AT ATG ATT TC	CC AGG CGAT G	200
	AA CTT CCAG T	TAT CCA AGG T	TC AGC ACT TA	AAG CTCT TGA	AG GTG ATACT	250
	AAG TAC GAAG	AT ATT ATCAT	GGA ATT GTT G	GATA CTGT AG	AT GATT ACAT	300
	CCC AGA ACCA	CA ACG TGATA	CTG ACA AGCC	ATT GCT TCT T	CC AGT CGA AG	350
55	AT GTTTT CTC	TATT ACT GGA	CG TGG TACT G	TTG CTT CAG G	AC GTATT GAC	400
	CG TGG TACT G	TTA AGG TTAA	TG ATGA AGTT	GAA ATCG TTG	GT ATT CGT GA	450
	CG ATATT CAA	AA AGC AGT TG	TT ACT GGT GT	TG AAAT GTTC	CG TAA ACAG C	500
	TT GAC GAAG G	TCT TGCT GGT	GATA ACG TCG	GT GTC CTT CT	TC GTGG TAT C	550
	CA ACG TGAT G	AA ATT GAAC G	CGG TCA AGTT	CTT GCT AAAC	CAG GAT CAAT	600
60	TC ATCC ACAT	ACT AAATT CA	AAG GTGA AGT	TT ATATT CTT	ACT AAAGA AG	650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii* (deposited as *Streptococcus mitis*)
- (B) STRAIN: ATCC 33399

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTTGAC	500
35	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
- (B) STRAIN: ATCC 25175

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

50

	CCCTGGTGCT	ATCCTTGTAG	TAGCTTCAAC	TGATGGACCA	ATGCCACAAA	50
	CTCGTGAACA	CATTCTTCTT	TCACGTCAAG	TTGGTGTTAA	ATACCTCATT	100
	GTCTTCATGA	ATAAAGTTGA	TTTGGTTGAC	GATGAAGAAT	TGCTTGAATT	150
	GGTTGAAATG	GAAATCCGTG	ATCTTCTTTC	AGAATATGAT	TTCCCAGGTG	200
5	ATGATATTCC	AGTTATTCAA	GGTTCAGCTC	TTAAAGCTCT	TGAAGGCGAT	250
	ACTGCTCAAG	AAGATATCAT	CATGGAATTA	ATGCATACTG	TTGATGACTA	300
	CATTCCAGAT	CCAGAACGTG	ATACTGACAA	GCCGCTCCTT	CTTCCAGTCG	350
	AAGATGTTTT	CTCAATCACT	GGTCGTGGTA	CTGTTGCTTC	AGGACGTATT	400
	GATCGTGGTA	CTGTTAAAAGT	TAACGATGAA	GTTGAAATCG	TTGGTATCCG	450
10	TGATGACATT	CAAAAAGCTG	TTGTTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	AATTGGATGA	AGGTATTGCA	GGGGATAATG	TTGGTGTTCT	CCTTCGTGGT	550
	ATCCAACGTG	ATGAAATCGA	ACGTGGTCAA	GTTCTTGCTA	AACCAGGTTC	600
	AATTCACCCA	CATACTAAAT	TCAAAGGTGA	AGTTTATATC	CTTACTAAAG	650
	AGGAAGGTGG	ACGTCATACA	CCATTCTTCA	ATAACTATCG	TCCACAATTC	700
15	TACTTCCGTA	CAACTGACGT	AACTGGTTCA	ATTGAGTTGC	CAGCAGGTAC	750
	TGAAATGGTT	ATGCCTGGTG	ATAACGTTAC	TATTGACGTT	GAATTGATCC	800
	ATCCAATCGC	TGTTGAACAA	GGTACTA			827

20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus parasanguinis*
 (B) STRAIN: ATCC 15912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

	AGCTATCCTT	G TAGTAGCTT	CAACTGACGG	ACCAATGCCA	CAAACACGTG	50
	AACACATCCT	TCTTTCACGT	CAGGTTGGTG	TTAAACACTT	GATCGTCTTC	100
	ATGAACAAAG	TTGACTTGGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
40	AATGGAAATC	CGTGACCTTC	TTTCAGAATA	CGATTTCCTA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	TGACTCTAAA	250
	TATGAAGATA	TCATCATGGA	ATTGATGGAT	ACTGTTGATG	AGTACATCCC	300
	AGAACCAGAA	CGCGATACTG	ACAAACCATT	GCTTCTTCCA	GTCGAAGACG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
45	GGTGTTGTTC	GTGTCAATGA	TGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	450
	AATCCAAAAA	GCAGTTGTGA	CTGGTGTTGA	AATGTTCCGT	AAACAACCTG	500
	ACGAAGGTCT	TGCAGGGGAT	AACGTTGGTG	TGCTTCTTCG	TGGTATCCAA	550
	CGTGATGAAA	TCGAACGTGG	ACAAGTTATC	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTCAAAG	GTGAAGTTTA	CATCCTTACT	AAAGAAGAAG	650
50	GTGGACGTCA	TACTCCATTC	TTCAACAAC	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC	ACGTAAC	ATCTATCGAA	CTTCCACCAG	GAAGTGAAT	750
	GGTAATGCCT	GGTGATAACG	TGACTATCGA	CGTTGAGTTG	ATCCACCCAA	800
	TCGCCGTTGA	ACAAGGTACT	ACAT			824

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus rattii*
 (B) STRAIN: ATCC 19645

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTGCTTAG	CTTCAACTGA	TGGACCAATG	CCGCAAACCTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGTTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTGT	TGAACAAGGT	ACTA			824

30

2) INFORMATION FOR SEQ ID NO: 227

35 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus sanguinis*
 (B) STRAIN: ATCC 10556

45

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTTCACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGTCTTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550
50	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GTTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

2) INFORMATION FOR SEQ ID NO: 228

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus sobrinus*
- (B) STRAIN: ATCC 33478

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TGTAGTAGCT	TCTACTGACG	GACCAATGCC	ACAAACTCGT	GAACACATCT	50
25 TGCTTTCACG	CCAAGTTGGT	GTTAAGAACC	TCATCGTCTT	CATGAACAAG	100
GTTGACTTGG	TTGATGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCT	AGGTGACGAC	ATTCCTGTTG	200
TTCAAGGTTT	AGCTCTTAAG	GCTCTTGAAG	GTGATACAGC	TGCCGAAGAC	250
AAGATTATGG	AATTGATGGA	CATCGTTGAT	GATTACATTC	CAGAACCAAA	300
30 ACGCGATACT	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GTATTCTCAA	350
TCACTGGTCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT	400
AAGGTTAACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAAA	450
AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC	500
TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA	550
35 TTTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTCAATCC	ACCCACACAC	600
TAAAGTTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTAAC	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC	750
40 TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC	795

40

2) INFORMATION FOR SEQ ID NO: 229

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
- (B) STRAIN: ATCC 43765

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

TGTAGTAGCT	TCAACTGACG	GTCCAATGCC	ACAAACTCGT	GAGCACATCC	50
50 TTCTTTCACG	TCAGGTTGGT	GTAAACACC	TTATCGTCTT	CATGAACAAA	100

	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAGTTGGTTG	AAATGGAAAT	150
	CCGTGACCTT	CTTTCAGAAAT	ACGATTTCCC	AGGTGATGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	GTACGAAGAC	250
	ATCGTTATGG	AATTGATGAA	CACTGTTGAT	GAGTACATTC	CAGAACCAGA	300
5	ACGCGACACT	GACAAACCAT	TGTTGCTTCC	AGTCGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTA	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	CGTGTCAACG	ACGAAATCGA	AATCGTTGGT	CTTCAAGAAG	AAAAATCTAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAACCT	GACGAAGGTC	500
	TTGCCGCGCA	TAACGTTGGT	GTGCTTCTTC	GTGGTGTACA	ACGTGATGAA	550
10	ATCGAACGTG	GTCAAGTTAT	CTCTAAACCA	GGTTCCTATCA	ACCCACACAC	600
	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCGACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAACCT	700
	GACGTAACCT	GTTCAATCAA	ATTGCCAGAA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGCCG	797

2) INFORMATION FOR SEQ ID NO: 230

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 793 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus uberis*

(B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

	TTGTTGTTGC	ATCAACTGAT	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
35	CTTCTTTTAC	GCCAAGTTGG	TGTTAAACAC	CTTATCGTTT	TCATGAACAA	100
	AATCGACCTT	GTTGACGATG	AAGAATTGCT	TGAATTAGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTCC	CAGGTGATGA	CCTACCAGTT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GAATTGATGA	AAACTGTTGA	TGAGTATATT	CCAGAACCAG	300
40	AACGTGATAC	AGACAAACCA	TTACTTCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCACAGGTC	GTGGTACTGT	AGCTTCAGGA	CGTATCGATC	GTGGTACTGT	400
	TCGTGTCAAC	GACGAAATTG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	450
	AAGCAGTTGT	TACTGGTGTG	GAAATGTTCC	GTAAACAACCT	TGACGAAGGT	500
	CTTGCAGGAG	ATAACGTAGG	TATCCTTCTT	CGTGGTGTTC	AACGTGACGA	550
45	AATCGAACGT	GGACAAGTTA	TTGCTAAACC	AGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGATGA	AGGTGGACGT	650
	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTATT	TCCGTACAAC	700
	TGACGTAACA	GGTTCAATCG	AACTTCCAGC	TGGTACTGAA	ATGGTAATGC	750
50	CTGGTGATAA	CGTGACAATC	AGCGTTGAGT	TGATCCACCC	AAT	793

2) INFORMATION FOR SEQ ID NO: 231

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus vestibularis*
 5 (B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

```

10 TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC      50
   CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA      100
   AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA      150
   TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA TATTCCAGTT      200
   ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
   CATCATCATG GACTTGATGA ACACTGTTGA CGAATACATT CCAGAACCAG      300
15 AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA      350
   ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTGTG      400
   TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA      450
   AAGCAGTTGT TACTGGTGTG GAAATGTTCC GTAAACAACT TGACGAAGGT      500
   ATTGCCGAGG ATAACGTCGG TGTCCTTCTT CGTGGTATCC AACGTGATGA      550
20 AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCACACA      600
   CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT      650
   CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTCTACT TCCGTACAAC      700
   TGACGTAACA GGTTCATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC      750
   CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG      798
25

```

2) INFORMATION FOR SEQ ID NO: 232

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tatumella ptyseos*
 40 (B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

```

45 GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACCCG      50
   TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
   TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAAGTGGTA      150
   GAAATGGAAG TCCGTGACCT GCTGTCACAG TACGACTTCC CGGGTGACGA      200
   CACGCCAATC GTTCGCGGTT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG      250
   AGTGGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC      300
50 CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCCTGCTGC CAATCGAAGA      350
   CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGTGTAGAGC      400
   GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT      450
   ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA      500
   CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC      550
55 GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAA      600
   CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG      650
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
   GTACAACTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
   GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT      800
60 CGCGATGGAC GATGGTCTGC GTTTCGCAA      829

```

2) INFORMATION FOR SEQ ID NO: 233

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20 GCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCGATGC CGCAGACTCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTC CGGGCGATGA 200
 CACGCCGATC GTACGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 25 AGTGGGAAGC GAAAATCATC GAACTGGCAG GTTTCCTGGA TTCTTACATT 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 CGTATTCTCC ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
 GCGGTATCAT CAAAGTGGGT GAAGAAGTAG AAATCGTTGG TATCAAAGAG 450
 ACTGCGAAGT CAACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA 500
 30 CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC 600
 CCGCACACCA AGTTCAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG 650
 CGGCCGTAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 35 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCGATGGAC GACGGTCTGC GTTTCGCAA 829

40 2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
 (B) STRAIN: ATCC 10790

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

55

CGGCGCTATC TTGGTTGTAT CCGCAGCTGA CGGCCCTATG CCTCAAACCTC 50
 GCGAACACAT CTTGTTGGCT CGCCAAGTTG GTGTTCCTGC AATCGTAGTA 100
 TTCTTGAACA AAGCTGACAT GGTGACGAT GAAGAATTGA TCGAATTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTTTCTTC CTACGAATTC CCTGGCGACG 200
 60 AAGTACCTAT CGTTGTAGGT TCCGCGTTGA AAGCTTTGGA AGGCGATGCT 250

	CAATATGTAG	CTAAAATTGA	CGAATTGATG	GACGCTGTAG	A [~] CTCCTACAT	300
	CCCAACACCA	GTTCTGTACA	CTGATAAACC	ATTCTTGATG	CCTGTGGAAG	350
	ATGTTTTTAC	AATCACTGGT	CGTGGTACAG	TAGCAACTGG	CCGTGTTGAA	400
	CGTGGTCAAG	TAAACGTTGG	TGATACTGTT	GAAGTAGTAG	GCTTGAAAGA	450
5	AAAAGCTGAA	CAATACGTAG	TAACAGGTCT	TGAAATGTTT	CGTAAAGTGT	500
	TGGATTCTGC	AGTAGCAGGT	GACAACGTAG	GTGCATTGCT	TCGTGGTGT	550
	GATCGTAAAG	ACATYGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCCAT	600
	CAACCCACAY	ACAAAATTCA	AAGCAGAAGT	ATACGTATTG	ACTAAAGAAG	650
	AAGGTGGTCG	TCATACTCCA	TTCTTCTCCA	ACTACCGTCC	ACAATTCTAC	700
10	TTCCGTACAA	CAGACGTAAC	AGGTGTTGTA	AACCTTCCTG	AAGGTGTAGA	750
	AATGTGTATG	CCTGGCGATA	ACGTAACAAT	GGAAATCGAA	TTGATTACTC	800
	CAATCGCTAT	CGAAGAAGGT	CTTCG			825

15

2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

	CGCTATCCTG	GTTGTTGCTG	CAACTGATGG	CCCAATGCCA	CAGACTCGTG	50
	AGCACATCCT	GTTGGGTCGT	CAGGTTGGTG	TTCCTTACAT	CATCGTATTC	100
	ATGAACAAAT	GTGACATGGT	TGACGATGAA	GAGCTGCTAG	AACTGGTAGA	150
35	AATGGAAGTG	CGCGATCTTC	TGTCTACCTA	CGATTTCCTA	GGCGATGATA	200
	CGCCAGTTGT	TCGTGGTTCC	GCGCTGAAAG	CATTGGAAGG	CGAACCTGAG	250
	TGGGAAGCAA	AAATTATCGA	ACTGGCTGGC	TACCTGGATT	CTTACATCCC	300
	AGAACCAGAG	CGTGCTATCG	ATAAGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCTAT	CTCTGGTCGT	GGTACTGTTG	TAACGGGTCTG	TGTAGAGCGC	400
40	GGTATCGTTA	AAGTTGCTGA	AGAAGTCGAA	ATTGTTGGCC	TGAAAGATAC	450
	CGTTAAATCT	ACTTGACTGT	GCGTTGAAAT	GTTCCGCAA	CTGCTGGATG	500
	AAGGCCGTGC	AGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGATATCG	AACGTGGTCA	AGTTCTTGCT	AAACCAGGTT	CGATTAAACC	600
	ACACACCAAA	TTTGAATCAG	AAGTTTATAT	TCTGAGCAA	GATGAAGGTG	650
45	GTCGCCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCTCAGTT	CTACTTCCGT	700
	ACAACCTGATG	TAACCGGTAC	TATTGAACTG	CCAGAAGGCG	TTGAGATGGT	750
	GATGCCAGGT	GATAACATTC	AAATGATTGT	TAACCTGATT	GCTCCTATCG	800
	CAATGGATGA	CGGCTTGCGC	TTTGC			825

50

2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

141

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*
 (B) STRAIN: ATCC 33641

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

```

GGCGCGATCC TGGTTGTTGC TGCCACTGAT GGCCCGATGC CACAGACTCG      50
CGAGCACATT CTGTTAGGGC GTCAGGTGGG TGTTCCTTAC ATCCTGGTCT      100
10 TCCTGAACAA ATGTGACATG GTTGACGACG AAGAGCTGCT GGAAGCTGGTA      150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCCT CTGGCGACGA      200
CACTCCAGTT ATCCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCTG      250
AGTGGAAGC AAAAATCATC GAATTGGCTG AGGCGCTGGA TAGCTATATT      300
CCACAGCCAG AGCGTGCGAT TGATAAACCA TTCCTGCTGC CAATCGAAGA      350
15 CGTATTCTCA ATCTCTGGCC GTGGTACTGT TGTACCGGT CGTGTAGAGC      400
GCGGTATCGT TAAAGTCGGC GAAGAAGTCG AAATCGTTGG TATCATTGAT      450
ACCATCAAGA CTACCTGTAC TGGTGTTGAA ATGTTCCGCA AATTGCTGGA      500
CGAAGGCCGT GCGGGTGAGA ACGTTGGTGT TCTGCTACGT GGTACTAAAC      550
GTGATGACGT ACAACGTGGT CAGGTATTGG CAAAACCAGG TTCTATCAAG      600
20 CCACACACCA AATTTGAATC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
TGGTCGCCAT ACTCCGTTCT TCAAAGGTTA TCGTCCTCAG TTCTACTTCC      700
GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
GTGATGCCAG GTGATAACAT TCAAATGATT GTTAACCTGA TTGCTCCTAT      800
CGCAATGGAT GACGGTCTGC GCTTTGCG      828
25

```

2) INFORMATION FOR SEQ ID NO: 237

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*
 40 (B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

```

CTTGTTGTC GCTGCAACTG ATGGTCCTAT GCCACAGACT CGCGAGCACA      50
45 TCCTGCTAGG TCGTCAGGTG GGTGTTCTT ACATCCTGGT CTTCTGAAC      100
AAGTGTGACA TGGTTGACGA TGAGGAGTTG CTGGAATTGG TAGAAATGGA      150
AGTCCGCGAA CTTCTGTCTC AATATGATTT CCCTGGCGAT GATACTCCTG      200
TTATCCGTGG TTCAGCGCTG AAGGCGTTGG AAGGCGAGCC TGAATGGGAA      250
GCAAAAATTA TCGAATTAGC TGAGGCGCTG GATAGTTATA TTCCACAGCC      300
50 AGAGCGCGCG ATTGATAGAC CATTCTTGCT GCCAATCGAA GACGTATTCT      350
CTATCTCAGG TCGTGGTACA GTCGTCACTG GTCGTGTAGA GCGTGGGATC      400
GTTAAAGTTG GCCAAGAAGT TGAAATCGTT GGTATTATCG ATTCCATTAG      450
AACAACATGT ACTGGCGTTG AAATGTTCCG CAAATTGCTG GACGAAGGCC      500
GCGCGGGTGA GAACGTGGT GTTCTACTGC GTGGGACTAA ACGTGATGAC      550
55 GTACAGCGTG GTCAGGTATT AGCTAAGCCA GGTTCTATCA AGCCACATAC      600
TAAATTCGAA TCCGAAGTTT ATATTCTGAG CAAAGATGAA GGCGGGCGTC      650
ACACGCCGTT CTTCAAAGGC TACCGTCCTC AGTTCTACTT CCGTACAACG      700
GATGTAACCG GTACTATTGA ATTGCCAGAC GGCGTTGAGA TGGTGATGCC      750
AGGTGATAAC ATTCAAATGA TTGTTAACCT GATTGCACCT ATTGCGATGG      800
60 ATGATGGTCT GCG      813

```

2) INFORMATION FOR SEQ ID NO: 238

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

```

20 GGAGCGATCT TGGTTGTTGC TGCAACCGAT GGCCCTATGC CGCAGACTCG      50
   TGAGCATATC CTGCTGGGCC GCCAGGTTGG TGTCCCATAC ATTATTGTCT      100
   TCCTGAACAA ATGTGACATG GTTGACGATG AAGAGTTGCT AGAGTTGGTT      150
   GAAATGGAGG TTCGTGAGCT TCTGTCTCAA TACGATTTCC CAGGCGACGA      200
   CACTCCAGTC ATCCGTGGTT CAGCGTTGAA AGCCCTGGAA GGTGACGCTG      250
25 AGTGGGAAGC TAAAATTATC GAGTTGGCAG AAGCTCTGGA TAGCTATATT      300
   CCGCAACCAG AACGCGCTAT TGATAGACCA TTCCTATTGC CAATTGAAGA      350
   CGTATTCTCT ATTTCTGGTC GTGGTACTGT AGTTACTGGT CGTGTAGAAC      400
   GTGGTATTGT TAAGGTCGGC GAAGAAGTTG AAATCGTTGG TATTATCGAT      450
   ACGATTAAAA CAACTTGTA TGGCGTTGAA ATGTTCCGCA AGCTGCTGGA      500
30 TGAAGGCCGT GCTGGTGAAA ATGTTGGTGT TCTGCTGCGT GGTACTAAGC      550
   GTGACGATGT TCAGCGTGGT CAAGTACTGG CGAAACCAGG TTCTATCAAG      600
   CCACACACGA AGTTTGAGTC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
   CGGCCGTCAT ACACCGTTCT TCAAGGGCTA CCGTCCTCAG TTCTACTTCC      700
   GTACAACTGA CGTGACCGGT ACCATTGAGC TGCCAGAAGG CGTTGAAATG      750
35 GTCATGCC TGACCAACGT AAACATGGTT GTTAACCTAA TTGCTCCTAT      800
   CGCAATGGAT GATGGTCTGC GCTTCGCAA      829

```

40 2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

```

55 TGGAGCGATC TTGGTTGTTG CTGCAACCGA TGGCCCTATG CCGCAGACTC      50
   GTGAGCATAT CCTGCTGGGC CGCCAGGTTG GTGTCCCATC CATTATTGTC      100
   TTCCTGAACA AATGTGACAT GGTGACGAT GAAGAGTTGC TAGAGTTGGT      150
   TGAATGGAG GTTCGTGAGC TTCTGTCTCA ATACGATTTT CCAGGCGACG      200
60 AACTCCAGT CATCCGTGGT TCAGCGTTGA AAGCCCTGGA AGGTGACGCT      250

```

GAGTGGGAAG CTAAAATTAT CGAGTTGGCA GAAGCTCTGG ATAGCTATAT 300
 TCCGCAACCA GAACGCGCTA TTGATAGACC ATTCCTATTG CCAATTGAAG 350
 ACGTATTCTC TATTTCTGGT CGTGGTACTG TAGTTACTGG TCGTGTAGAA 400
 CGCGGTATTG TTAAGGTCGG CGAAGAAGTT GAAATCGTTG GTATTATCGA 450
 5 TACGATTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGC AAGCTGCTGG 500
 ATGAAGGCCG TGCTGGTGAA AATGTTGGTG TTCTGCTGCG TGGTACTAAG 550
 CGTGACGATG TTCAGCGTGG TCAAGTACTG GCGAAACCAG GTTCTATCAA 600
 GCCACACACG AAGTTTGAGT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 GCGGCCGTCA TACACCGTTC TTCAAGGGCT ACCGTCCTCA GTTCTACTTC 700
 10 CGTACAACTG ACGTGACCGG TACCATTGAG CTGCCAGAAG GCGTTGAAAT 750
 GGTGATGCCT GGTGACAACG TAAACATGGT TGTTAACCTA ATTGCTCCTA 800
 TCGCAATGGA TGATGGT 817

15

2) INFORMATION FOR SEQ ID NO: 240

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCAATG CCACAGACTC 50
 GCGAGCACAT CCTGTTGGGT CGTCAAGTGG GTGTTTCCTTA CATCTTAGTC 100
 TTCCTGAACA AGTGTGACAT GGTGACGAC GAAGAGTTGC TGGAAGTGGT 150
 35 TGAAATGGAA GTTCGTGAGC TTCTGTCTCA ATACGATTTC CCTGGCGATG 200
 AACTCCGGT TATTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAGGCC 250
 GAGTGGGAAG CCAAAATTAT TGAAGTTGCT GAAGCACTGG ATAGCTACAT 300
 TCCACAGCCA GAGCGCGCGA TTGATAAACC ATTCTTGCTG CCAATCGAAG 350
 ACGTATTCTC TATCTCAGGC CGTGGAACAG TTGTTACCGG GCGTGTGAG 400
 40 CGCGGTATCG TCAGAGTGGG CGAAGAAGTT GAAATCGTGG GTATCATCGA 450
 CACCATTAAC ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGCTG 500
 ACGAAGGCCG TGCCGGTGAG AACGTTGGTG TTCTGCTGCG CGGTACTAAA 550
 CGCGATGACG TGCAACGTGG TCAAGTGTG GCTAAACCAG GTTCTATTAA 600
 GCCGCATACC AAATTTGAGT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 45 GTGGTCGTCA TACTCCGTTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
 CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGACG GTGTTGAGAT 750
 GGTGATGCCA GGTGATAACA TTCAAATGAT TGTTAACCTG ATTGCGCCTA 800
 TTGCAATGGA TGACGGTCTA CGATTGCA 829

50

2) INFORMATION FOR SEQ ID NO: 241

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 804 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 10 TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG 200
 AACTCCGAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA 250
 GAGTGGGAAG CTAAATCGT TGAGCTGGCT GGCTTCCTGG ATTCTTACAT 300
 CCCAGAACCA GTTCGTGCTA TCGACCTGCC GTTCCTGCTG CCGATCGAAG 350
 15 ACGTATTCTC CATCTCCGGT CGTGGCACCG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 GACTGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGG 500
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GTTCCATCAA 600
 20 GCCGCACACC AAATTCGAAT CTGAAGTTTA TATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACAACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGGACAACA TCAAAATGGT TGTACCCTG ATCCACCCGA 800
 TCGC 804
 25

2) INFORMATION FOR SEQ ID NO: 242

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp.
 40 *denitrificans*
 (B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45 TCAGTTCCCC CGCGATCACA TGCCCAAGAT CTACGAAGCG CTTACTCTGG 50
 CCGACGAGGG TTCCTCGTTC GCCGAAAAGG GTCTGACGCT GGAAGTGCAG 100
 CAACAGCTGG GCGACGGCGT GGTGCGTACC ATCGCGCTGG GCTCCAGCGA 150
 CGGCCTGCGC CGCGGTATGA AGGTCACCGG TACGGGCGCG CCGATCTCGG 200
 TGCCGGTTCG CACCGGCACG CTGGGCCGCA TCATGGACGT GCTGGGTCGT 250
 50 CCCATCGACG AAGCCGGCCC GATCCAGCAC GAAGAAAAGC GTGGCATTCA 300
 CCAGCCGGCT CCCCCTTTCG ACGAACTGTC GCCGTCGGTG GAACTGCTGG 350
 AAACCGGCAT CAAGGTTATT GACCTGGTCT GCCCGTTCGC CAAGGGCGGC 400
 AAGGTCGGCC TGTTCGGCGG CGCCGGCGTG GGCAAGACCG TCAACATGAT 450
 GGAAGTATGC AACAACATCG CCAAGCAGCA CAGCGGCTTG TCGGTGTTTCG 500
 55 CCGGCGTGGG CGAGCGTACC CGCGAAGGCA ACGACTTCTA CCACGAAATG 550
 GAAGAGTCGA ACGTTCTGGA CAAGGTTGCG ATGGTGTTTCG GTCAGATGAA 600
 CGAACCCCCG GGCAACCGTC TGCGCGTGGC GCTGACCGGC CTGACCATGG 650
 CCGAGAAGTT CCGCGACGAA GGCCGCGACA TCCTGTTCTT CGTGGACAAC 700
 ATCTACCGCT ACACCCTGGC CGGTACGGAA GTGTCCGCGC TGCTGGGCCG 750
 60 TATGCCGTCG GCAGTGGGCT ACCAGCCCAC GCTGGCCGAA GAAATGGGCA 800

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

20 TGAAACTACT TTAGAAGTTC AGCAACAACT TGGTGATGGT GTTGTTCGTA 50
CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAACT 100
AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150
TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200
25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
TTGCCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTCGGT GGTGCTGGTG 350
TTGGTAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
30 TAATGACTTC TATCACGAAA TGAAAGATTC TAACGTTCTT GACAAAGTAG 500
CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600
AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAAC ATCTACCGTT 650
ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
35 GCGGTAGGTT ACCAACCTAC ACTTGACAGAA GAAATGGGTG TTCTTCAAGA 750
GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

40 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
(B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAACCTACATT 50
AGAAGTTCAG CAACAACCTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100
GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150
CCGATTTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
50 TCTTGGTCGC CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTAT	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTCGC	350
	TAAAGTGGT	AAAGTTGGTC	TGTTCCGGTG	TGCCGGTGTT	GGTAAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTTC	CTGGTGTGTT	TGAGCGTACT	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTTC	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTAAGTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG-197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCT	GTTGGTGTATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
40	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAACCT	AAAGGATCTG	TAACGTC		837

50

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

147

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis*
 (B) STRAIN: ATCC 15554

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

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TTCCCCCGCG ACAGCATCCC TAAAGTCTAC GAAGCATTGA CGCTCGTTGA      50
CGAAAGTTCG GCTTTCGCAG AAAAAGGCCT GACTTTTGAA GTACAGCAAC      100
10 AATTGGGTGA CGGTGTAGTT CGCACCATCG CCATGGGTTC CAGCGACGGC      150
CTGCGCCGCG GTATGGAAGT GGCCGGTTCG GCGCTCCCA TCTCCGTTCC      200
CGTGGGTGTC GGCACCCTGG GTCGCATTAT GGACGTTCTG GGTGCCCCTA      250
TTGACGAAGT CGGTCCATT CAGTCCGACG AGCGTCGCGC CATTACCCAG      300
CCTGCGCCTA CTTTCGACGA ACTGTCGCCT TCCGTAGAGC TGCTGGAAAC      350
15 CGGTATTAAA GTGATTGACC TGTTTGCCC GTTCGCCAAG GGTGGTAAGG      400
TTGGTCTGTT CGGTGGTGCC GGTGTGGGCA AGACCGTGAA CATGCTGGAG      450
CTGATCAACA ACATCGCCAA GGCACACAGC GGTCTGTCCG TGTTTGCCGG      500
TGTGGGTGAG CGTACCCGTG AAGGTAACGA CTTCTACCAC GAAATGGCCG      550
ATGCTGGCGT TATCCAGATG GACAACCTGA GCGAGTCCAA AGTGGCCATG      600
20 GTGTTTCGTC AGATGAACGA ACCTCCAGGC AACCGTCTGC GTGTGGCACT      650
GTCCGGCCTG ACCATGGCCG AGAAGTTCCG TGACGAAGGC CGTGACATCC      700
TGTTCTTTGT GGACAACATC TACCGCTACA CGCTGGCCGG TACAGAAGTG      750
TCCGCTCTGC TGGGTCGTAT GCCTTCCGCA GTGGGTACC AGCCTACGCT      800
GGCCGAGGAA ATGGGTAAGC TGCAAGAGCG CATTACCTCC ACCAAGACCG      850
25 G

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2) INFORMATION FOR SEQ ID NO: 247

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

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15 GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAGAG      50
CAACGAAAAC GGAACAAGCA TTAACCTAAC ATTTGAAGTT GCACTTCATT      100
TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGTCTTCCAC AGATGGACTT      150
GTTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT      200
TGGTGATGCA ACACTTGGTC GTGTATTTAA CGTATTAGGT GATGCAATTG      250
50 ACTTAGATGG TGAGGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT      300
CAAGCACCTG CATTCAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC      350
TGGTATTTAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA      400
TCGGTCTATT CGGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA      450
TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTCGCTGG      500
55 TGTAGGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG      550
ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTCGGACA AATGAACGAG      600
CCACCTGGAG CACGTCAACG TGTTGCGTTA ACAGGTTTAA CAATGGCTGA      650
GCATTTCCGT GATGAGCAAG GACAAGATGT ACTTCTGTTC ATCGATAATA      700
TCTTCCGTTT CACGCAAGCA GGTCTGAAG TATCTGCCCT TCTTGCCCGT      750
60 ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA      800

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5 2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCGTGG CACAGAAGTA 150
GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
25 ACGTGTATTC AACGTATTAG GTGATGCAAT TGACTTAGAT GGTGAACTTC 250
CTGCGGATGT ACACCGTGAT CCAATTCACC GTCAAGCACC TGCATTTCGAA 300
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
CCGGCGTAGG TAAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
30 CAAGAGCACG GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
AAACTGCGAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
CGTGTTGCAT TAACAGGTTT AACAAATGGCT GAGCATTTCC GTGATGAGCA 650
AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
ATCTACAAAT 810

10 2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
50 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TGCCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCG	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTG	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGCTAC	CTTGGTATTC	GGGCAGATGA	ACGAACCGCC	GGGCGCCCCG	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

2) INFORMATION FOR SEQ ID NO: 250

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAAATACTG	GTTGTAGAAG	TTCAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTCAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAT	400
	CGGTTTGTTT	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTTGCCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACCTGGA	TCTTTCGAAA	GTGGATTATA	ACGAACTGGA	GAAATCGCAA	650
	GTGTCTCTGA	TTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGACTGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTTCT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTACA	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

55

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 833 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*
 (B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

	CGAATTCCCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTTC	50
	AGAATGGTAA	TGAGAGCCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
15	GGTATTGTGC	GTACCATCGC	CATGGGTTCT	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCAAT	CGAAGTACCA	GTAGGTAAAG	200
	CAACCCTGGG	CCGTATCATG	AACGTCCTGG	GTCAGCCGAT	CGACATGAAA	250
	GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGTT	CAGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	350
20	TTATCGACCT	GATGTGTCCG	TTCGCGAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GTGTAGGTAA	AACCGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTA CTCTGTA	GGGTAACGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCAGGAAA	600
25	CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAGTTCCGTG	650
	ACGAAGGTCG	TGACGTACTG	CTGTTTCGTTG	ACAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CGGAAGTATC	CGCACTGCTG	GGTCGTATGC	CATCAGCAGT	750
	AGGCTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGTGTTCTG	CAGGAACGTA	800
	TCACCTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

30

2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

	GTGTACGACG	CACTGAAGGT	GGAAAACACC	GAGATCACCC	TCGAAGTCCA	50
50	GCAGCAGCTG	GGCGACGGCG	TGGTGCGTAC	CATCGCCCTC	GGTTCCACCG	100
	ACGGCCTGAA	GCGCAACCTG	GTTGCCGTCA	ACACCGGCCG	TGGCATCTCG	150
	GTGCCGGTCG	GCGCCGGCAC	CCTGGGCCGC	ATCATGGACG	TGCTGGGCCG	200
	TCCGATCGAC	GAAGCCGGCC	CGGTCGCTGC	CAGCGACAAC	TGGGAAATCC	250
	ACCGCGCTGC	GCCGTGCTAT	GAAGACCAGT	CCCCGGCCAC	CGAGCTGCTG	300
55	GAAACCGGCA	TCAAGGTCAT	CGACCTGATG	TGCCCCGTTG	CCAAGGGCGG	350
	CAAGGTCGGC	CTGTTCCGGC	GCGCCGGCGT	CGGCAAGACC	GTCAACATGA	400
	TGGAAGTATG	CAACAACATC	GCCAAGGCGC	ACAGCGGCCT	GTCCGTGTTC	450
	GCCGGCGTGG	GTGAGCGTAC	CCGTGAGGGC	AACGACTTCT	ACCACGAGAT	500
	GAAGGACTCC	AACGTCCTGG	ACAAGGTGGC	GATGGTGTAC	GGCCAGATGA	550
60	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTCG	CCCTGACCGG	CCTGACCATG	600

	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTC	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCCGC	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGTTTCGATC	ACCTCGATC				819

2) INFORMATION FOR SEQ ID NO: 253

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTTGG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTTGG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGCACG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATTT	TCCGTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

45

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

	TTCCCGGTGG	GCCACCTGCC	CGACATTTAC	AATGCACTTA	CCGTTGAACT	50
	GKCCAAACACC	GGYGTCCACG	AASAGGGCGA	GACCACCAAG	AAGATCACCC	100
	TTGMSGTTGA	ACAGCATCTT	GGCGATTCCA	CCGTGCGTAC	CGTCGCTCTG	150
5	AAGCCGACTG	ACGGCCTTGT	GCGTGCGGCC	ACCGTGTATG	ACACCGGCGG	200
	CCCGATCTCT	GTGCCGGTTG	GCGATGTCAC	CAAGGGCCAC	GTATTCGACG	250
	TGTCCGGCAA	CATCCTCAAC	AAGAAGGCCG	ACGAGACCGT	TAAGGTTACC	300
	GAACGTTGGT	CTATCCACCG	TAACCCGCCG	GCATTCGACC	AGCTGGAGTC	350
	CAAGACCCAG	ATGTTGAAA	CCGGTATCAA	GGTCATCGAT	TTGCTGACCC	400
10	CGTATGTGCA	GGGCGGCAAG	ATCGGTCTGT	TCGGCGGCGC	AGGCGTCGGC	450
	AAGACCGTGC	TGATCCAGGA	AATGATTCAG	CGTGTGGCTC	AGAACCACGG	500
	CGGTGTGTCC	GTGTTCCGAG	GCGTCGGCGA	GCGTACCCGT	GAGGGTAACG	550
	ATCTGATCGG	CGAAATGGAC	GAAGCCGGCG	TGCTCGAGAA	GACCGCACTG	600
	GTCTTCGGCC	AGATGGATGA	GCAGCCGGGT	ACCCGTCTGC	GCGTGCCGCT	650
15	GACCGCACTG	ACCATGGCAG	AGTACTTCCG	TGACGTACAG	AATCAGGACG	700
	TGCTGCTGTT	CATCGATAAC	ATCTTCCGTT	TCACCCAGGC	TGGTTCCGAG	750
	GTGTCCACCC	TGCTCGGCCG	TATGCCGTCC	GCACTGGGCT	ACCAGCCGAA	800
	CCTGGCCGAT	GAGATGGGCG	CGCTGCAGGA	GCGAATCACT	TCGACCCGTG	850
	GACACTCCAT	CACCTC				866
20						

2) INFORMATION FOR SEQ ID NO: 255

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
 - (B) STRAIN: S2308
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

	AAGGCCAGCT	GCCGCTGATC	CTGAACGCGC	TTGAAGTGGA	CAATCAGGGC	50
40	CATCGTCTGG	TTCTCGAAGT	TGCCCAGCAC	CTCGGCGAAG	ACACCGTGCG	100
	CACCATCGCC	ATGGACGCGA	CCGAAGGTCT	CGTTCGCGGT	CAGGAAGCAC	150
	GCGACACTGG	CGAACCGATC	ATGGTGCCGG	TCGGCGTCGA	AACGCTTGGC	200
	CGCATCATGA	ACGTCATCGG	CGAGCCGGTT	GACGAAGCAG	GCCCCATCAA	250
	GACCAAGGCA	ACCCGCGCCA	TCCACCAGAA	CGCGCCGGAA	TATATCGAAC	300
45	AGTCGACCGA	AGCCGAAATT	CTGGTCACGG	GCATCAAGGT	CGTCGACCTT	350
	CTGGCGCCTT	ACGCCAAGGG	CGGCAAGATC	GGCCTCTTCG	GCGGTGCAGG	400
	CGTCGGCAAG	ACCGTTCTCA	TCATGGAAC	CATCAACAAC	GTCGCCAAGG	450
	CGCACGGCGG	TTATTCCGTG	TTCGCAGGCG	TCGGTGAGCG	TACCCGTGAG	500
	GGCAACGACC	TTTACCACGA	AATGATCGAG	TCGGGCGTGA	ACAAGCTCGG	550
50	CGGCGGCGAA	GGCTCCAAGG	CAGCCCTCGT	TTACGGCCAG	ATGAACGAAC	600
	CCCCGGGTGC	CCGCGCCCGC	GTTGCCCTTT	CCGGTCTGAC	GCTTGCTGAA	650
	AACTTCCGTG	ACCAGGGCCA	GGACGTTCTG	TTCTTCGTGG	ACAACATCTT	700
	CCGCTTCACG	CAGGCAGGTT	CGGAAGTGTC	GGCTCTTCTC	GGCCGTATTC	750
	CTTCCGCTGT	GGGTTATCAG	CCGACGCTGG	CAACCGACAT	GGGCGCCATG	800
55	CAGGAACGCA	TCACCACGAC	GACCAAGGGT	TCGATCACCT	CG	842

2) INFORMATION FOR SEQ ID NO: 256

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

```

15  CGAGTTCCTT CAGGACGGCG TACCGCGCGT, TKATGATGCG CTTGAAGTAC      50
    AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
    GGTATCGTGC GTACCATCGC TATGGGTTCT TCCGACGGTC TCGTTCGTGG      150
    TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CGACCCTTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA      250
20  GGCGATATCG GCGAAGAAGA CCGTTGGGCT ATTACCGCGC CTGCACCTTC      300
    CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG      350
    TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC      400
    GGTGGTGCGG GCGTGGGTAA AACCCTAAAC ATGATGGAGC TTATCCGTAA      450
    CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTGCGGGC GTGGGTGAGC      500
25  GTAATCGTGA GGGTAACGAC TTCTATCACG AAATGACCGA CTCCAACGTT      550
    CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA      600
    CCGTCTGCGC GTAGCGCTGA CCGGTCTGAC CATCGCGGAG AAATTCCTGT      650
    ACGAAGGTCG TGACGTTCTG CTGTTCTGTTG ATAACATCTA CCGTTACACC      700
    CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTCTGATGC CTTCTGCGGT      750
30  AGGTTACCAG CCAACTCTGG CCGAAGAGAT GGGTGTCTTT CAGGAGCGTA      800
    TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                                833
  
```

2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```

50  TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
    TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
    TCGTACGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG      150
    GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC      200
55  TCTGGGTCTG ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG      250
    ACATCGGCGA AGAAGATCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAT      300
    GAAGAGCTGT CCAGCTCTCA GGAAGTCTG GAAACCGGCA TCAAAGTTAT      350
    CGACCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT      400
    GTGCGGGCGT AGGTAAACCC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
60  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC      500
  
```

	TCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTTGC	ACTGGTTTAC	GGCCAGATGA	ACGAGCCGCC	AGGTAACCGT	600
	CTGCGCGTAG	CGCTGACCGG	TCTGACCATC	GCGGAGAAAT	TCCGTGACGA	650
	AGGCCGTGAC	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	700
5	CCGGTACAGA	AGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	TGCGGTAGGT	750
	TATCAGCCTA	CTCTGGCAGA	AGAGATGGGT	GTTCTTCAGG	AGCGTATTAC	800
	CTCCACCAAG	ACCGGTTCCA	TCACTTCCG			829

10

2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
(B) STRAIN: ATCC 33855

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

	TCCCTCAGGA	CGGCGTACCG	CGCGTTTATG	ACGCGCTTGA	GGTACAGAAC	50
	AACAATGAGA	AGCTGGTGCT	GGAAGTTCAG	CAGCAGCTCG	GCGGCGGTAT	100
	CGTGCGTACC	ATCGCAATGG	GTTCTTCCGA	CGGTCTGCGT	CGTGGTCTGG	150
30	TAGTAACAGA	CCTCGAGCAC	CCGATCGAAG	TCCCGGTAGG	TAAAGCGACC	200
	CTTGGCCGTA	TCATGAACGT	GCTGGGTCAG	CCGATCGACA	TGAAAGGCCGA	250
	CATCGGCGAA	GAAGACCGTT	GGGCGATTCA	CCGCGCAGCA	CCTTCCTACG	300
	AAGAGCTGTC	CAGCTCTCAG	GAATTGCTGG	AAACCGGCAT	CAAAGTTATC	350
	GACCTGATTT	GTCCGTTTCG	TAAGGGCGGT	AAAGTAGGTC	TGTTCCGGTGG	400
35	TGCGGGCGTA	GGTAAAACCG	TAAACATGAT	GGAGCTGATC	CGTAACATTG	450
	CGATCGAGCA	CTCCGGTTAT	TCCGTGTTTG	CGGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACCGACTCCA	ACGTTCTGGA	550
	TAAAGTAGCA	CTGGTTTACG	GCCAGATGAA	CGAGCCACCA	GGTAACCGTC	600
	TGCGCGTAGC	GCTGACCGGT	CTGACCATCG	CGGAAAAATT	CCGTGACGAA	650
40	GGCCGCGACG	TTTTGCTGTT	CGTTGATAAC	ATCTACCGTT	ATACCTTGGC	700
	CGGTACCGAA	GTATCTGCAC	TGCTGGGTCG	TATGCCTTCT	GCGGTAGGTT	750
	ATCAGCCAAC	TCTGGCAGAA	GAGATGGGTG	TTCTTCAGGA	GCGTATTACC	800
	TCCACCAAGA	CCGGTTCTAT	CACCTCCGTA			830

45

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 931 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
(B) STRAIN: CDC B7681

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

	TTTCAGGAAG	TAGAGGAACT	ACCAAACATT	TATGACGCAC	TTGAAGTTGT	50
	CAGAGAAGGC	CAGAAAGGTC	TGATCTTAGA	AGTTGAACAA	CACATCGGTG	100
5	AGGATACAGT	GAGATGTATC	GCTATGGATG	CAACAGACGG	ACTTCAAAGA	150
	GGACAATCTG	TAATAGGACA	TGGAAGACAA	ATTACTATGC	CTATTGGTGA	200
	AGAAGTAAAT	GGTAGATTGT	TCAACGTGGT	AGGAGATGCT	ATCGACGGAC	250
	TTCAGGAATT	ATCTAAAGAC	AATGGTTTGC	CAATCCACAG	AGAAGCACCT	300
	AAATTTCGATC	AGTTATCAAC	TTCTGCTGAA	GTACTATATA	CAGGTATCAA	350
10	AGTAATCGAC	CTTATCGAGC	CTTATGCAAA	AGGTGGTAAA	ATTGGTTTGT	400
	TCGGTGGTGC	TGGTGTAGGT	AAAACAGTAT	TGATCCAGGA	ATTGATTAAT	450
	AACATTGCTA	AAGGACACGG	TGGTCTTTCT	GTATTCGCAG	GAGTAGGTGA	500
	GAGAACAAAG	GAAGGAAATG	ACCTTCTTCG	TGAGATGTTA	GAGTCTGGTA	550
	TTATTAAATA	TGGTGACGAA	TTCATGCATT	CTATGGAGAA	CGGTGGATGG	600
15	GATCTTTCTA	AAGTTGACAG	TGAGTTGATG	AAAGAGTCTA	AAGCTGCTTT	650
	CGTTTTTCGGA	CAGATGAACG	AGCCACCAGG	TGCAAGAGCA	CGTGTAGCCC	700
	TTTCTGGTAG	TACTTTAGCT	GAATACTACC	GTGATGGTGG	CGAAAGCGGA	750
	CAAGGTAGCT	ACGTTCTTTT	CTTCGTAGAC	AACATCTTCC	GTTTTACACA	800
	GGCTGGTTCT	GAGGTGTCTG	CACCTCTAGG	TCGTATGCCT	TCAGCGGTAG	850
20	GTTACCAACC	AACCTAGCT	TCTGAGATGG	GTGCAATGCA	GGAGAGAATT	900
	ACTTCAACTA	AAAACGGATC	TATTACATCT	G		931

25 2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

40	GTATCGTACG	TACCATCGCA	ATGGGTTCTT	CCGACGGTCT	GCGTCGTGGT	50
	CTGGAAGTCA	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	100
	AACCCTGGGT	CGTATCATGA	ACGTCTGGG	TCACCCGATC	GACATGAAAG	150
	GCGATATCGG	TGAAGAAGAG	CGTTGGGCTA	TCCACCGCGC	AGCACCGTCC	200
45	TATGAAGAGC	TGTCCAGCTC	TCAGGAAC TG	CTGGAAACCG	GTATCAAAGT	250
	TATCGACCTG	ATGTGTCCGT	TCGCGAASGG	CGGTAAAGTG	GGTCTGTTCTG	300
	GTGGTGCGGG	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	TATCCGTAAC	350
	ATCGCGATCG	AGCACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	400
	TACTCGTGAG	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTT	450
50	TGGATAAAGT	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCGGGAAAC	500
	CGTCTGCGCG	TTGCACTGAC	CGGTCTGACC	ATGGCAGAGA	AATTCCGTGA	550
	CGAAGGTCGT	GACGTACTGC	TGTTCTGTCG	TAACATCTAT	CGTTACACCC	600
	TGGCCGGTAC	GGAAGTTTCC	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	650
	GGTTACCAGC	CGACCCTGGC	GGAAGAGATG	GGTGTCTCTG	AGGAACGTAT	700
55	CACCTTCTACC	AAAACCGGTT	CTATCA			726

2) INFORMATION FOR SEQ ID NO: 261

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT      200
    CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
20  AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTATGA AGAGCTGTCC      300
    AGCTCTCAGG AACTGCTGGA AACC GGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
    TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTA CTC GTGAGGGTAA      500
25  CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC      550
    TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT      600
    CTGACCGGTC TGACCATGGC AGAGAAAGTTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTT GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG      700
    TATCCGCTCT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCGACC      750
30  CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAAC      800
    CGGTTCTATC AC                                     812
  
```

35 2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

50  GCGCGTGTAC GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC      50
    TGGAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG      100
    GGTTCCTCCG ACGGCCTGCG TCGTGGTCTG GATGTGAAAG ACCTTGAGCA      150
    CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG      200
55  TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT      250
    TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA      300
    GGAAGTCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTTCG      350
    CGAAGGGCGG TAAAGTGGGT CTGTTCCGGT GTGCGGGTGT AGGTAAAACC      400
    GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA      450
60  CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT      500
  
```

```

ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC CCTGGTTTAC 550
GGCCAGATGA ACAGAGCCGCC GGGAAACCGT CTGCGCGTTG CGCTGACCGG 600
CCTGACCATG GCGGAGAAAT TCCGTGACGA AGGTCGTGAC GTTCTGCTGT 650
TCGTCGACAA CATCTACCGT TACACCCTGG CCGGTACGGA AGTATCCGCA 700
5 CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TACCAGCCGA CCCTGGCGGA 750
AGAGATGGGT GTTTTGCAGG AACGTATCAC CTCCACCAA ACCGGTTCTA 800
TCACCTCCGT A 811

```

10

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

```

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTTATGA ATGGTAAAGA 50
GAGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT ATCGTACGTA 100
CCATCGCGAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
30 GACCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CTCTGGGTCTG 200
TATCATGAAC GTCCTGGGTC ACCCGATCGA CATGAAAGGC GATATCGGTG 250
AAGAAGAGCG TTGGGCTATC CACCGCGCAG CGCCATCCTA TGAAGAGCTG 300
TCCAGCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
35 TAGGTAAAAC CGTAAACATG ATGGAAGTCA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGATTC CAACGTTCTG GATAAAGTAT 550
CCCTGGTATA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
GCGCTGACCG GTCTGACCAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
40 CGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
AAGTATCCGC ACTGCTGGGC CGTATGCCAT CAGCGGTAGG CTACCAGCCA 750
ACCCTGGCGG AAGAGATGGG TGTTCGTCAG GAACGTATCA CTTCTACCAA 800
AACCGGTTCT ATTACC 816

```

45

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

```

5  AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA      50
   GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG      100
   TACCATCGCC ATGGGTTCCT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA      150
   AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT      200
   CGTATCATGA ACGTTCTGGG TCACCCGATC GACATGAAAG GCGATATCGG      250
   TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC      300
   TGTCAAGCTC TCAGGAACCTG CTGGAAACCG GTATCAAAGT TATCGACCTG      350
10 ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTTC GTGGTGCGGG      400
   TGTAGGTAAG ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG      450
   AACACTCCGG TTAATCCCGT TTTGCGGGCG TAGGTGAACG TACTCGTGAG      500
   GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT TGGACAAAGT      550
   ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCTGGAAAC CGTCTGCGTG      600
15 TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT      650
   GACGTTCTGC TGTTCTGTTG TAACATCTAT CGTTACACCC TGGCCGGTAC      700
   AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC      750
   CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC      800
   AAAACCGGTT CTATCACCT
20

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2) INFORMATION FOR SEQ ID NO: 265

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 822 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

30 (ii) MOLECULE TYPE: Genomic DNA

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```

    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Citrobacter koseri
35 (B) STRAIN: ATCC 27028

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

```

40 GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA      50
   ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGCGCGT ATCGTACGTA      100
   CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CGCTGGGTCTG      200
   TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG      250
   AAGAAGAGCG TTGGGCTATC CACCGTGCAG CACCGTCCTA CGAAGAGTTG      300
45 TCAAACCTCT AGGAAGTGTG GGAAGCCGGT ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTC GCGAAGGGCG GTAAAGTGGG TCTGTTCGGT GGTGCGGGTG      400
   TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA      450
   CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
50 CCTTGTTTAA CGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT      600
   GCGCTGACCG GCCTGACCAT GCGGAGAGAA TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACGG      700
   AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG      750
   ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA      800
55 AACCGGTTCT ATCACCTCCG TA
822

```

2) INFORMATION FOR SEQ ID NO: 266

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60

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

```

15  GATGCCGTAC  CGCGCGTGTA  CGACGCCCTT, GAGGTACAGA  ATGGTAATGA      50
    GCGTCTGGTG  CTGGAAGTTC  AGCAGCAGCT  CGGTGGCGGT  ATTGTACGTA      100
    CCATCGCCAT  GGGTTCTTCC  GACGGTCTGC  GTCGTGGTCT  GGAAGTAAAA      150
    GACCTTGAGC  ACCCGATCGA  AGTCCCGGTA  GGTAAAGCAA  CGCTGGGTCG      200
    TATCATGAAC  GTACTGGGCG  AACCAGTAGA  CATGAAAGGC  GACATCGGTG      250
20  AAGAAGAGCG  TTGGGCTATC  CACCGTGCCG  CGCCGTCCTA  TGAAGAGTTG      300
    TCTAACTCTC  AGGAACTGCT  GGAAACCGGC  ATCAAAGTTA  TCGACCTGAT      350
    GTGTCCGTTT  GCGAAGGGCG  GTAAAGTCGG  TCTGTTCCGT  GGTGCGGGCG      400
    TAGGTAAAAC  CGTAAACATG  ATGGAGCTGA  TCCGTAACAT  CGCGATCGAG      450
    CACTCCGGTT  ACTCTGTGTT  TGCGGGCGTG  GGTGAACGTA  CTCGTGAGGG      500
25  TAACGACTTC  TACCACGAAA  TGACCGACTC  CAACGTTATC  GACAAAGTAT      550
    CCCTGGTGTA  CGGCCAGATG  AACGAGCCGC  CTGGAAACCG  TCTGCGCGTC      600
    GCACTGACCG  GTCTGACCAT  GGCTGAGAAG  TTCCGTGACG  AAGGTCGTGA      650
    CGTTCTGCTG  TTCGTCGATA  ACATCTATCG  TTACACCCTG  GCCGGTACGG      700
    AAGTATCCGC  ACTGCTGGGT  CGTATGCCTT  CAGCGGTAGG  TTATCAGCCG      750
30  ACTCTGGCGG  AAGAGATGGG  TGTTCGTCAG  GAACGTATCA  CCTCAACCAA      800
    AACCGGTTCT  ATCACCTCCG
  
```

35 2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

```

50  GCCGTACCGC  GCGTGTACGA  TGCTCTTGAG  GTTATGAATG  GTAAAGAGAG      50
    CCTGGTGCTG  GAAGTTCAGC  AGCAGCTCGG  CGGCGGTATC  GTACGTACCA      100
    TCGCCATGGG  TTCTTCCGAC  GGTCTGCGTC  GTGGTCTGGA  AGTTAAAGAC      150
    CTTGAGCACC  CGATCGAAGT  CCCGGTAGGT  AAAGCAACCC  TGGGTCGTAT      200
55  CATGAACGTC  CTGGGTCATC  CGATCGACAT  GAAAGGCGAT  ATCGGTGAAG      250
    AAGAGCGTTG  GGCTATCCAC  CGCGCAGCAC  CTACCTATGA  AGAACTGTCC      300
    AGTTCTCAGG  AACTGCTGGA  AACCGGCATC  AAAGTTATCG  ACCTGATGTG      350
    TCCGTTCCGG  AAGGGCGGTA  AAGTTGGTCT  GTTCGGTGGT  GCGGGTGTAG      400
    GTAAACCGT  AAACATGATG  GAGCTGATCC  GTAACATCGC  GATCGAACAC      450
60  TCCGGTTACT  CAGTGTTTGC  GGGCGTTGGT  GAACGTACTC  GTGAGGGTAA      500
  
```

CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
 TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAAGTTC CGTGACGAAG GTCGTGACGT 650
 TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG 700
 5 TATCTGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACC 750
 CTGGCGGAAG AGATGGGTGT TCTGCAGGAA CGTATCACCT CTACCAAAC 800
 CGGTTC 806

10

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

GCCGTACCGC GCGTGACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG 50
 CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCCGTATC GTACGTACCA 100
 TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC 150
 30 CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
 CATGAACGTT CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGAGAAG 250
 AAGAGCGTTG GGCTATTAC CCGCAGCAC CTTCTATGA AGAGCTGTCC 300
 AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
 35 GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 TCCGGTTACT CTGTGTTTGC GGGTGATAGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGATTCCAA CGTTCTGGAT AAAGTATCCC 550
 TGGTTTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT 650
 40 ACTGCTGTTC GTCGATAACA TCTATCGTTA TACCCTGGCC GGTACGGAAG 700
 TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGTTA CCAGCCGACC 750
 CTGGCGGAAG AGATGGGTGT TCTGCAGGAA CGTATCACTT CTACCAAAC 800
 CGGTTCTATC 810

15

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
 (B) STRAIN: ATCC 14501

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5   TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
    AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA      100
    ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
    TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
    ATTCTGGGAA GAATGTTCAA TGTCCTCGGA CGTGAAATTG ATGGTCTGGG      250
    ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
    TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
10  ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG      400
    TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
    TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
    ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
    TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
15  GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
    CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC      700
    CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
    TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
    ATTACATCCA CGAAGGATGG TTCCATT                                827
20

```

2) INFORMATION FOR SEQ ID NO: 270

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40  GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
    CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
    TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
    GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
    ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
    AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT      300
15  GAAGAACAAT CAGTTGTTC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
    CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG      400
    GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
    GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
    AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
50  AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
    ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
    AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG      700
    CTGGATCAGA GGTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
    TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
55  ATCAACTACC CATGGATCAA TTACATCAG                                829

```

2) INFORMATION FOR SEQ ID NO: 271

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

10

TTGTCCACGT TGGATRTCTT CA

22

15 2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

30

CCCCGCTGGC	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTGAGGTCA	50
CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
GGCGACAACC	TCGTTTCGCGC	CGTGTCCATG	GCCCCCTACCG	ACGGCCTCGT	150
CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
35 GCGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
ACCACCATTC	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
CTGTTCCGTG	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
40 CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
GTGAGCGTAT	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
GGCGTTCTTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
45 CGTTTCAACC	AGGCCGGTTC	CGAGGTTTCG	ACCCCTTCTG	GTCGTATGCC	750
TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTTCTCC	800
AGGAGCGTAT	TACCTCTA				818

50

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

```

CGATGCCTGC TCTGTACAAC GCGCTGACTG TCGAGGTCAC CCTCGAGGCA      50
GTCGCCAAGA CCATCACGCT TGAGGTTGCA CAGCACCTCG GCGATAACCT      100
GATCCGGACC ATTGCGTTGG CACCTACGGA CGGTCTCGTC CGTGGCGCTG      150
10 AGGTTATCGA CACTGGTAAG CCAATTACTG TTCCCGTCGG CGATGCCGTC      200
AAAGGACACG TCTTCAATGC GCTCGGTGAG TGTTTGGACG AACCAGGATT      250
GGGCCGCGAC GGCGAACAGT GGGGAATCCA CCGCGATCCG CCACCATTCTG      300
ATGCGCTGGA GGGCAAAACC GAGATTCTGG AGACTGGAAT CAAGGTTATC      350
GACCTCCTTA CCCCTTACGT TAAGGGTGGC AAAATTGGTC TGTTCCGTGG      400
15 CGCCGGCGTC GGCAAGACCG TTCTTATCCA GGAAATGATC ACTCGTATCG      450
CTCGTAACTT CTCCGGTACT TCCGTGTTTC CCGGCGTCGG TGAGCGTACC      500
CGTGAGGGTA CTGACCTGTT CCTGGAAATG GAAGAGATGG GCGTGTTGCA      550
AGACCCGCC CTTGTCTTCG GTCAAATGGA CGAACCACCA GGGGTTTCGTA      600
TGC CGCTGGT CTTGTCTGGT CTAACCATGG CTGAATATTT CCGCGACGTT      650
20 CAAAACCAGG ACGTTTGTGTT GTTCATTGAC AACATCTTCC GTTTTACTCA      700
GGCAGGTTCC GAGGTTTCCA CGCTGTTGGG CCGTATGCCT TCCGCCGTGG      750
GTTATCAGCC AACATTGGCT GATGAGATGG GTGTTTTGCA GGAACGGATT      800
ACCTCTACAC GTGGTAAGTC AATTACTTCC CTG      833

```

25

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

```

CCGTGCTCAT CCAGGAGATG ATCACCCGTG TGGCCCGCAA CTTCGGCGGC      50
ACCTCTGTGT TCGCCGGCGT CGGCGAGCGC ACCCGTGAGG GCAACGACCT      100
15 CTGGGTCGAG ATGGACGAGG CCGACGTGCT CAAGGACACC GCCCTGGTGT      150
TCGGCCAGAT GGACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCCTGTCC      200
GCGCTGACCA TGGCGGAGTA CTTCCGCGAT GTGCAGAACC AGGACGTGCT      250
GCTGTTTCAT GACAACATCT TCCGCTTCTC CCAGGCCGGC TCCGAGGTCT      300
CCACCCTGCT GGGCCGCATG CCCTCCGCGG TGGGCTACCA GCCGAACCTG      350
50 GCGGACGAGA TGGGTGTGCT GCAGGAGCGC ATCACCTCGA CTCGCGGCCA      400
CTCCATCACC TCGATGC      417

```

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

164

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*

(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

10 GGGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA 50
 GGCAGTTGCG AAGACCATTA CCCTGGAGGT CGCACAGCAC CTGGGTGACA 100
 ACCTGGTGCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT 150
 GCAGAGGTCA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT 200
 15 TGTC AAGGGG CACGTCTTCA ACGCCCTGGG C GACTGCCTG GATGAGCCAG 250
 GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA 300
 TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT 350
 CATCGACCTG TGTACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG 400
 GTGGTGCAAG TGTGGGTAAG ACCGTCCTGA TTCAGGAGAT GATTACCCGT 450
 20 ATCGCCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG 500
 TACCCGTGAG GGTACGGACC TCTTCCCTCGA GATGGAGGAG ATGGGCGTGC 550
 TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC 600
 CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA 650
 TGTTCAAGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA 700
 25 CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA 750
 GTGGGTTACC AGCCGACCCT GGCTGACGAG ATGGGTGTTT TGCAGGAGCG 800
 CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC 835

30

2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCGTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT 50
 AATTTAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC 100
 AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA 150
 50 ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTTAGGTCGT 200
 ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC 250
 AAAAGAAAAA CTCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT 300
 CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT 350
 TGCCCCCTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT 400
 55 TGGAAAAACG GTTAATATGA TGGAATTAAT CCGTAATATC GCCATTGAAC 450
 ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC 500
 AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC 550
 GTTGGTGTAC GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG 600
 GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC 650
 60 GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTTGA 700

AGTCTCTGCC	CTCCTCGGTC	GGATGCCATC	GGCTGTGGGT	TATCAGCCGA	750
CGTTGGCCGA	AGAGATGGGG	GCCCTGCAAG	AACGCATTAC	TTCCACTAAA	800
AAAGGGTCCA	TTACGTCG				818

5

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA,

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG	ACGCCGTGCC	GAAGGTGTAT	AACGCACTGG	AAGTAAAAGG	50
CGGTGCCACG	AAACTGGTAC	TGGAAGTGCA	GCAGCAGCTG	GGTGGCGGCG	100
25 TAGTTCGCTG	CATCGCGATG	GGCTCTTCCG	ACGGTCTGCG	CCGTGGGCTA	150
GAGGTTGAAG	ACCAAGACCA	TCCGATCGAG	GTTCTGTGTTG	GCAAGGCGAC	200
TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	TCCGGTCGAC	ATGAAGGGCG	250
AGATCGGTGA	AGAAGAGCGT	TGGGCTATCC	ATCGTGCTGC	ACCGAGCTAT	300
GAAGATCTGT	CTAACTCTCA	GGAAGTGTG	GAGACCGGCA	TTAAGGTTAT	350
30 CGACCTGATT	TGCCCCGTTCG	CTAAAGGCGG	TAAAGTGGGC	CTGTTCGGTG	400
GGGCCGGTGT	GGGTAAGACC	GTTAACATGA	TGGAGCTTAT	CCGTAACATC	450
GCTATCGAGC	ACTCCGGTTA	CTCAGTCTTC	GCCGGTGTGG	GTGAGCGTAC	500
CCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGATTCC	AACGTATTGG	550
ATAAAGTTTC	TCTGGTGTAT	GGTCAGATGA	ACGAGCCACC	GGGAAACCGT	600
35 CTGCGCGTGG	CGCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGATGA	650
AGGTCGTGAT	GTACTGTTGT	TCATCGATAA	CATCTACCGT	TATACCTTGG	700
CCGGTACTGA	AGTCTCCGCT	CTGCTGGGCC	GTATGCCGTC	GGCGGTAGGT	750
TATCAGCCGA	CTCTGGCGGA	GGAAATGGGG	GTGCTGCAAG	AGCGTATTAC	800
CTCCACTAAG	ACCGGGTCCA	TCACCTCTG			829

40

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA	AGGTGTATAA	CGCACTGGAA	GTAAAAGGCG	GTGCCACGAA	50
50 ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTCTGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGCTCGGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTCGACAT	GAAGGGCGAG	ATCGGCCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTCCGC	AAAGGCGGTA	AAGTTGGCCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCCG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTC	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

2) INFORMATION FOR SEQ ID NO: 279

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAGT	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTTCATCAAT	TTGCACCTAA	GTTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCCGT	ATTGCCCGGT	GTGGGTGAGC	GTACTCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AAACTGGTTC	CATTACCTCT		840

55 2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*

(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

10 GCGGTACCAC GAGTGTACGA TGCACCTGAG GTAAAGAATG GTGAAGAGCG 50
 TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CCGTGGCGTT GTACGTACCA 100
 TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150
 CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
 15 CATGAACGTA CTGGGCGAAC CAGTAGACAT, GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GCGGATCCAC CGTGCAGCAC CGTCCTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAACCCTG AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 20 TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTAATC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
 TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAAGTTC CGTGACGAAG GTCGTGACGT 650
 ACTGTTGTTC GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 25 TATCCGCACT GCTGGGCCGT ATGCCTTCTG CCGTAGGTTA TCAGCCGACG 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
 CGG 803

30

2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*

(B) STRAIN: ATCC 33072

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50
 AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100
 GGTATCGTAC GTACTATCGC CATGGGTTCT TCCGACGGTC TGCGTCGTGG 150
 50 TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG 200
 CAACACTGGG TCGTATCATG AACGTTTGG GTCAACCAAT CGACATGAAA 250
 GGCACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300
 CTATGAAGAG CTGTCTAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG 350
 TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400
 55 GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450
 CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550
 CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600
 CCGTCTGCGC GTTGCCTGTA CCGGTCTGAC TATGGCTGAG AAGTTCCTGTG 650
 50 ACGAAGGTCG TGACGTACTG CTGTTCTGTA ATAACATCTA CCGTTACACC 700

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

5

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
25 TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
30 TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTTG	400
GTAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
35 CTGACCGGTC	TGACGATGGC	TGAGAAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
CGGTTCTATC					810

40

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 55 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
60 CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTAAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGTTTATT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CAACCAAAAC	800
15	CGGTTCTATC	A				811

2) INFORMATION FOR SEQ ID NO: 284

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

35	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
10	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTTCG	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGTTTACT	CCGTATTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
15	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACTGGTC	TGACGATGGC	TGAGAAAGTTC	CGTGACGAAG	GCCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
50	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTCTATC	ACTTCCG				817

55 2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

170

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

10 AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT 50
 GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG 100
 TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC 150
 GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT 200
 15 CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG 250
 AGCTCTCCAG CTCTCAGGAA CTGCTGGA AAA CCGGTATCAA GGTAATGGAC 300
 CTGATTTGCC CGTTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC 350
 GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA 400
 TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGCGTGA ACGTACTCGT 450
 20 GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA 500
 AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGA AACCGTCTGC 550
 GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT 600
 CGTGACGTTT TGCTGTTCGT CGATAACATC TACCGCTATA CCCTCGCCGG 650
 TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTTACC 700
 25 AGCCGACGCT GGC GGAAGAG ATGGGTGTTT TGCAGGAACG TATCACCTCC 750
 ACCAAAACCG GTTCTA 766

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

45 GCCGTACCAC GCGTGACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
 CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
 TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC 150
 CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
 50 CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTTACGA AGAGCTGTCC 300
 AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 55 TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
 TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
 TCTGCTGTTC GTCGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 50 TATCTGCACT GCTGGGTCGT ATGCCTTACG CGGTAGGTTA TCAGCCAACG 750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800
CGGTT 805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasaki*
(B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50
CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100
CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150
25 GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200
TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250
TTCATCGCGC GCGCCCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAACTG 300
CTGGAAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350
CGGTAAAGTC GGTCTGTTCG GTGGTGCAGG TGTAAGTAAA ACCGTAAACA 400
30 TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTA CTCCGTG 450
TTTGCGGGCG TGGGCGAACG TACCCGTGAA GGTAACGACT TCTACCACGA 500
AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550
TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600
ATGGCTGAGA AATTCCGTGA CGAAGGTCGT GACGTTCTGC TGTTTCGTGA 650
35 CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700
GCCGTATGCC TTCAGCGGTA GGTATCAGC CGACCCTGGC GGAAGAGATG 750
GGTGTCTGC AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50
AAAAAAGATA AAACAAAAGT TGTTCCTTGAA GTTGCTTTGG AACTTGGTGA 100
TGGTGTATC CGCACAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150
50 GAATGGAAGT TGTCGATACT GGCAATCAA TCTCCGTTCC TGTAAGTAAA 200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGA	AACAGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCCGTGGT	GCCGGTGTG	GTAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAG	AAAACAGCCA	TGGTGTTCGG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	GCGTGTGTC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTTC	ATCACTTCA		839

15

2) INFORMATION FOR SEQ ID NO: 289

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 847 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: ATCC 25788

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCCT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTTGGTA	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCA	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGACAA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTA CTTCGGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTTCTGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
50	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

2) INFORMATION FOR SEQ ID NO: 290

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 845 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 5 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

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10 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCTTT AGTTGTTTAT 50
    AAAAATGATG AGAAGAAATC GAAAGTTGTT CTTGAAACAG CGCTAGAATT 100
    AGGTGACGGT GTCATCCGTA CAATCGCGAT GGAATCAACA GATGGTTTAC 150
    AACGCGGAAT GGAAGTCATT GATACAGAAA AAGCAATTTT TGTACCAGTG 200
    GGTAAAGAAA CGTTAGGTCG TGTATTCAAT GTATTAGGAG ATACGATCGA 250
    TTTATCTGCA CCTTTCCCAG AAGATGCAAA ACGTAGCGAA ATCCATAAAA 300
15 AAGCACCAAA CTTTGATGAG TTAAGTACAA GTACTGAGAT CCTTGAAACT 350
    GGGATCAAAG TTATTGACTT GCTTGCTCCT TACTTAAAAG GTGGGAAAGT 400
    TGGATTATTC GGTGGTGCCG GTGTAGGTAA AACTGTATTG ATCCAAGAAT 450
    TGATCCATAA TATCGCTCAA GAACACGGTG GTATTTCTGT ATTTACTGGT 500
    GTTGGTGAAC GTACACGTGA AGGTAATGAC CTTTATTATG AAATGAAAGA 550
20 TTCAGGAGTT ATTGAAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC 600
    CACCAGGTGC ACGTATGCGT GTTGCCTTGA CTGGTTTGAC GATTGCTGAA 650
    TACTTCCGTG ATGTTGAAGG GCAAGACGTG CTATTGTTTA TTGATAATAT 700
    TTTCCGTTTC ACTCAAGCCG GTTCAGAAGT TTCTGCCCTA TTAGGTCGTA 750
    TGCCTTCTGC CGTTGGGTAC CAACCAACGC TAGCAACAGA AATGGGTCAA 800
25 TTACAAGAAC GGATCACTTC AACGAAAAAA GGTTCAATCA CTTC      845
  
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2) INFORMATION FOR SEQ ID NO: 291

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

```

15 TTAGATCAAT CCTTACCCGA TATTAACAAC GCTTTAGTCG TTTATAAAAA 50
    TGGCGAAGCA AAACAAAAG TAGTACTTGA AGTCGCTTTA GAACTAGGTG 100
    ATGGAGTGAT TCGTTCTATC GCCATGGAAT CGACAGATGG TTTACAACGT 150
    GGAATGGAAG TTATCGATAC AGGAAAATCA ATTCAGTTC CTGTTGGTAA 200
    AGATACATTA GGTCGTGTGT TTAACGTTTT AGGAGACACA ATTGACTTAG 250
50 AAGCGCCATT CCCTGCAGAT GCTGAACGTA GTGGGATTCA TAAAAAGCG 300
    CCAGCATTTG ATGAATTAAG TACCAGTAAT GAAATTTTAG AAACAGGGAT 350
    TAAAGTTATT GACTTATTAG CACCTTATCT AAAAGGTGGT AAAGTCGGAC 400
    TTTTCGGTGG TGCCGGTGTT GGTAAAACCG TCTTAATTCA AGAATTAATT 450
    CATAATATTG CCAAGAACA TGGAGGGATT TCCGTCTTTA CTGGTGTTGG 500
55 TGAACGGACA CGTGAAGGGA ACGATCTGTA CTATGAAATG AAAGATTCAG 550
    GCGTTATTGA AAAACAGCC ATGGTTTTTG GTCAAATGAA CGAACCGCCA 600
    GGTGCACGGA TGCGTGTGGC CTTAACTGGG TTAACGATTG CTGAATATTT 650
    CCGTGATGTG GAAGGACAAG ACGTGCTATT ATTTATTGAT AACATTTTCC 700
    GTTTCACCCA AGCCGGTTCA GAAGTTTCTG CCCTTTTAGG TCGGATGCCG 750
60 TCAGCCGTTG GTTACCAACC AACCTTAGCG ACTGAAATGG GACAATTACA 800
  
```

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

5 2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTCCTGTGA 200
25 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
TTTAGAAACA CCTTTCCCGA AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
TGCCTTCTGC GGTTGGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

40

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
60 TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

175

	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTCGGTGG	400
5	TGCCGGTGTT	GGTAAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTTGG	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
	TGCGGGTTGC	TTTGA CTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
10	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

2) INFORMATION FOR SEQ ID NO: 294

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTGGTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTT	TGTTCTGTGT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAT	GTTTTAGGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCATAAAA	300
	AGGCACCTGA	TTTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCACT	ATTTGCGGGT	500
	GTTGGTGAGC	GTA CTCTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTGGACAA	ATGAACGAAC	600
15	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTTTCAAGAGT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
50	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

2) INFORMATION FOR SEQ ID NO: 295

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia fergusonii*
 5 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

```

10  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTGCAAAATG GTAATGAGCG      50
    TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CCGGTGGTATC GTGCGTACCA      100
    TCGCAATGGG GTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAAAGAC      150
    CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT      200
    CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG      250
    AAGAGCGTTG GGCATTAC CCGCAGCAC CTTCTACGA AGAGCTGTCA      300
15  AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAACTGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC      450
    TCCGGTTCT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAAATGA CTGACTCCAA CGTTATCGAC AAAGTATCCC      550
20  TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA      600
    CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTC GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
    TATCCGCACT GCTGGGCCGT ATGCCTTCAG CGGTAGGTTA TCAGCCGACT      750
    CTGGCGGAAG AGATGGGCGT TCTTCAGGAA CGTATCACCT CCACCAAAC      800
25  TGG                                     803
  
```

2) INFORMATION FOR SEQ ID NO: 296

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

```

45  GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA ATGGTGATGA      50
    GCGTCTGGTG CTGGAAGTGC AGCAGCAGCT CGGCGGCGGT ATCGTGCGTA      100
    CCATCGCAAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GACTGTCGTC      150
    GACCTCGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCGA CCCTGGGCCG      200
    TATCATGAAC GTGCTGGGTC AGCCGATCGA CATGAAAGGC GATATCGGTG      250
50  AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCGTCCTA TGAAGAGCTG      300
    TCCAGCTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
    GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGT GGTGCGGGCG      400
    TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
    CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
55  TAACGACTTC TACCATGAAA TGACCGACTC CAACGTTCTG GACAAAAGTAT      550
    CCCTGGTTTA CGGCCAGATG AACGAACCGC CGGGAAACCG TCTGCGCGTT      600
    GCACTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA      650
    CGTTCTGTTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACTG      700
    AAGTATCCGC ACTGCTGGGC CGTATGCCTT CTGCGGTAGG TTACCAGCCG      750
60  ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAGCGTATCA CCTCCACCAA      800
  
```

5 2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150
CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200
25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
CAGGAACTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
CGCCAAGGGC GGTAAAGTCG GCCTGTTCGG CGGCGCGGGC GTGGGTAAAA 400
CCGTAAACAT GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT 450
30 TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500
CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
ACGGCCAGAT GAACGAGCCG CCGGGAAACC GTCTGCGCGT GGCAC TGACC 600
GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
GTTTCGTTGAC AACATCTATC GTTACACCCT GGCCGGTACG GAAGTATCTG 700
35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTC 800
TATCACCT 808

40 2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GGCGATTTAC AACGCGCTGA CGGTTGATGC 50
CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
TGCCGGGCAA CCTTGTCGCG TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
50 GTCCGCGGCC TCGAGGTCGT CGACACGGG AACC CGATCA TGATGCCCCG 200

	GGGTCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCGTGG	250
	ACGAGAAGCC	GATGCCCGAG	GTGAAGGGCT	ACATGCCCAT	CCACCGTCCG	300
	GCTCCGGA	CTACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
5	GTCTGTTTCG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
10	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTTCGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGGCA	ACCGAGATGG	GCGACCTGCA	800
	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

15

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*

(B) STRAIN: ATCC 33852

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
	GGTGCCTCCA	AACTGGTTCT	GGAAGTTCAG	CAACAGTTAG	GCGGCGGCGT	100
35	TGTTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTCGTA	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
	AAGAGCTGGC	TAACTCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
40	GACCTGATGT	GTCCGTTTCG	TAAGGCGCGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTT	GGTAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTTTG	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
45	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCCCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
50	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

50

2) INFORMATION FOR SEQ ID NO: 300

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
 5 (B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

```

AACACGCCTA AAGTATATGA TGCTTTAAAT GTAGTAGAAG CTGGTTTAGT      50
10 ATTAGAAGTT CAGCAACAAA TTGGTGATGG CGTAGTTCGT ACAATTGCTA      100
   TGGGATCTAG TGATGGTCTT AGACGTGGTA TGGAAGTTAA GAACACAAAT      150
   GCGCCTATTT CTGTTCCAGT TGGACATGGC ACACTTGGAC GTATCATGAA      200
   TGTTTTAGGT GAACCAATTG ATGAAGCTGG TCCAATTGAA TATACTGAGA      250
   AAAGATCTAT CCATCAAGCT CCTCCTGCAT ATGATGAGTT AGCATTAAGT      300
15 ACAGAAATAT TAGAAACAGG TATCAAAGTA GTTGACCTTA TTTGTCCATT      350
   TGCTAAGGGC GGTAAAGTTG GTTTATTTGG CGGTGCAGGT GTTGGTAAAA      400
   CTGTAACGAT GATGGAACCT ATCAACAATA TTGCAAAAGA ACATAGTGGC      450
   TACTCTGTAT TTTCCGGTGT TGGTGAAAGA ACTCGTGAAG GTAATGACTT      500
   CTACTATGAG ATGAAATATT CTAATGTATT GGATAAAGTA TCATTAGTAT      550
20 ATGGTCAGAT GAATGAGCCG CCTGGAAACA GATTAAAGAGT AGCTCTTAGT      600
   GGCTTAACAA TAGCAGAAGG ATTCCGTGAT GAAAAGCGTG ATGTTTTGAT      650
   GTTTATCGAT AACATCTATC GTTATACATT AGCAGGTACA GAGGTATCGG      700
   CGCTACTTGG TCGTATGCCA TCTGCTGTGG GTTATCAGCC AACGCTTGCA      750
   GCTGAGATGG GTGCTTTACA GGAGCGTATT ACATCTACTA AGACAGGATC      800
25 TATTA                                         805

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2) INFORMATION FOR SEQ ID NO: 301

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Fusobacterium gonidiaformans*
 (B) STRAIN: ATCC 25563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

```

45 GACGAATTGC CAAAATATA CAATGCATTA AAGGTGCAAG TTGGAGAAAA      50
   AGAAGTTGTA TTGGAAGTGC AACAAATTT GGGAAATAAT GTTGTGAGAA      100
   CAGTAGCGAT GGAATCAACA GATGGATTGC TTCGAGGAAT GGAAGTAATG      150
   GATACCGGAG CACCGATTAC TGTTCCAGTA GGAAGGCGG TTTTAGGAAG      200
   AATATTGAAT GTTTTGGGAG AGCCTGTGGA TCAAAAAGGG CCTGTGGAAA      250
50 CAGAAGAATA TTTACCTATC CATAGAGAAG CACCAAAATT TGAAGAACAA      300
   GAAACAGTAA CAGAAATTTT TGAAACAGGA ATTAAAGTCA TAGATTTGTT      350
   AGCCCCTTAT ATCAAAGGAG GAAAGACAGG TCTATTCGGT GGAGCCGGAG      400
   TAGGGAAAAC AGTTTTAATT ATGGAATTAA TTAATAACAT TGCAAAGGGC      450
   CACGGAGGAA TTTCTGTGTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG      500
55 AAGAGATTTA TACAACGAAA TGACAGAGTC CGGAGTTTGT AATAAGACCT      550
   CGTTGGTGTA TGGTCAAATG AATGAGCCGC CCGGAGCAAG ACTTCGTGTG      600
   GCGTTGACAG GATTAACGCT TGCTGAAAAC TTTAGAGATA AAGAAGGGCA      650
   AGATGTATTG TTGTTTATCG ACAATATCTT CCGTTTCACA CAAGCAGGAT      700
   CAGAAGTATC GGCTCTATTG GGAAGAATTC CATCGGCAGT AGGATATCAA      750
60 CCGAACTTAG CGACAGAAAT GGGAACTTTA CAAGAAAGAA TTACTTCTAC      800

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AAAATCAGGA TCTATCACTT CGGTA

5 2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium necrophorum* subsp.
necrophorum
 (B) STRAIN: ATCC 25286

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT AAAGGTACAG GTGGGAGAAA GGGAACTTGT GTTGGAAGTG 50
 CAGCAACATT TAGGAAATAA TGTTGTCAGA ACAGTAGCAA TGGATTCAAC 100
 AGACGGATTA CTTCGGGGAA TGGAAGTGAG AGATACAGGA GTTCCCATTA 150
 25 CTGTTCCGCT AGGAAAGGCG GTTTTGGGAA GAATATTAAA TGTCTTAGGG 200
 GAGCCTGTGG ACGAAAAAGG TCCGATAGAG ACAGAAGAAT ATTTACCAAT 250
 ACATAGAGAA GCACCGAAAT TTGAAGAACA GGAAACGGTG ACAGAAATTT 300
 TTGAAACAGG AATTAAAGTC ATTGATTTGT TAGCTCCTTA TATTAAAGGA 350
 GGAAAAACAG GCCTATTCGG AGGAGCCGGA GTAGGAAAAA CCGTTTTGAT 400
 30 TATGGAACGT ATCAATAATA TTGCAAAAGG TCATGGAGGA ATTTCTGTTT 450
 TTGCAGGAGT TGGAGAAAGA ACGAGAGAGG GAAGAGATCT ATACAACGAA 500
 ATGACAGAGT CCGGAGTTT GAATAAACT TCTTTGGTAT ATGGGCAAAT 550
 GAATGAGCCG CCCGGAGCAA GACTTCGAGT GGCTTTAACC GGACTTACTG 600
 TTGCCGAAAA TTTCAGAGAT AAAGAGGGAC AGGATGTCTT ATTGTTTATT 650
 35 GACAATATTT TCCGTTTCAC ACAAGCAGGT TCGGAAGTAT CGGCACTTTT 700
 GGGGAGAATT CCTTCTGCAG TGGGATATCA ACCGAAGTTG GCGACAGAAA 750
 TGGGAAGCTT ACAAGAAAGA ATTACTTCTA CAAAATCCGG TTCTATCACT 800
 TCCGTG 806

40

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC CTGCAATATA TAATGCTTTA AAAGTAAAAT TAGAAGATAA 50
 GGAAGTTGTT CTAGAAGTTG AACCAATCTT TGGTAACAAT GTTGTAAGAA 100
 50 CTGTTGCTAT GGATTCAACT GATGGATTAA AAAGAGGAAT GGAAGTTATA 150

	GATACAGGTA	AACCAATTAC	AGTACCAGTT	GGTAAAGCTG	TTCTTGGTAG	200
	AATATTAAAT	GTTTTAGGAG	AACCTGTTGA	TAATCAAGGT	CCTATAAATG	250
	CTGAAACATT	TTTACCTATT	CATAGAGAAG	CACCAGAATT	TGATGACTTA	300
	GAAACTGAAA	CTGAAATATT	TGAAACAGGA	ATAAAAGTTA	TAGACTTATT	350
5	AGCACCATAT	ATTAAAGGTG	GAAAAATAGG	ATTATTTGGT	GGAGCTGGAG	400
	TAGGAAAAAC	AGTTTTAATA	ATGGAACCTA	TCAACAACAT	TGCAAAAGGA	450
	CATGGAGGAA	TTTCAGTTTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
	TAGAGACTTA	TATGGTGAAA	TGACTGAATC	AGGAGTTATC	ACAAAAACAG	550
	CTCTTGTTTA	TGGACAAATG	AATGAGCCAC	CTGGAGCAAG	ACTTAGAGTT	600
10	GCATTAACAG	GGCTTACTGT	TGCAGAAAAC	TTTAGAGATA	AAGATGGGCA	650
	AGATGTTCTT	CTATTTATAG	ATAATATATT	TAGATTTACA	CAAGCAGGTT	700
	CAGAAGTTTC	AGCTTTACTT	GGAAGAATAC	CATCAGCTGT	TGGATATCAA	750
	CCAAACCTAG	CAACTGAAAT	GGGTGCTTTA	CAAGAAAGAA	TAACATCTAC	800
	AAAATCTGGT	TCAATTACAT	C			821

2) INFORMATION FOR SEQ ID NO: 304

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
 (B) STRAIN: ATCC 49145

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

	TTCCCAGTTG	GCTATCTTCC	AGATATTTAT	AATGCTCTCA	AGGTTGATAT	50
35	CAACACCGTT	GGAAACACGG	AGGGAGATAC	CGTCCACGAG	ATTACATTGG	100
	AAGTTGAGCA	GCACCTTGGT	GATTCAACTG	TGCGAGCAGT	GGCACTTAAG	150
	CCTACGGACG	GCTTGGTCCG	TGGTGCTTTA	GTGCGAGATA	CTGGTGGCCC	200
	AATTTCTGTG	CCTGTTGGAG	ATGTTACAAA	AGGTCACGTT	TTTGACGTAA	250
	CTGGTAACAT	TTTAAACGCT	AAACCAGGCG	AAAACATTGA	GGTGACCGAG	300
40	CGCTGGCCAA	TCCACCGCAA	CCCACCTGCT	TTCGATCAGC	TTGAGTCTAA	350
	GACTCAAATG	TTTGAAACAG	GCATTAAGGT	TATCGATTTG	CTTACGCCTT	400
	ACGTTACAGG	CGGAAAGATT	GGTCTGTTTC	GTGGTGCAGG	CGTTGGTAAA	450
	ACTGTGTTGA	TTCAGGAGAT	GATTCAGCGC	GTTGCACAGA	ACCACGGCGG	500
	TGTGTCTGTG	TTTGCTGGCG	TTGGCGAACG	TACTCGTGAG	GGTAACGATT	550
45	TGATTGGCGA	AATGGCTGAG	GCTGGCGTTT	TGGAGAAAAC	AGCGCTTGTC	600
	TTTGGTCAGA	TGGATGAGCC	TCCTGGGACT	CGTCTTCGTG	TGCCTCTTAC	650
	TGCTTTGACT	ATGGCTGAGT	ATTTCCGTGA	TGTTTACAAT	CAGGATGTGT	700
	TGCTGTTTAT	CGACAACATC	TTCCGCTTTA	CTCAGGCAGG	TTCTGAGGTT	750
	TCCACGTTGC	TTGGTCGTAT	GCCTTCTGCA	GTTGGTTATC	AGCCAAACTT	800
50	GGCGGATGAA	ATGGGTGCGT	TGCAGGAGCG	CATTACTTCT	ACGCGCGGTC	850
	ATTCTATTAC	GTCG				864

55 2) INFORMATION FOR SEQ ID NO: 305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

10 TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA 50
 GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATTGGTGAT AACGTAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT 150
 TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT 200
 15 GTAGGTAAGT ACACATTAGG TCGTGTGTTC AACGTATTAG GTGAAGCAGT 250
 TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA 300
 AAGAAGCTCC AACATTTCGAT GAATTATCAA CTCACGTTGA GGTTCCTGAA 350
 ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA 400
 AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAAACGGTT CTTATCCAAG 450
 20 AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA 500
 GGTGTAGGTG AGCGTACTCG TGAAGGAAAT GACTTATACT ATGAAATGAA 550
 AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTCGGA CAAATGAACG 600
 AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAATGGCG 650
 GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA 700
 25 CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTCCTGCG TTATTAGGAC 750
 GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA 800
 CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT 848

30

2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA 50
 GAAAAAGGCG ATGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100
 AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT 150
 50 TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA 200
 GTAGGTAAGT ATACATTAGG ACGTGTGTTC AACGTATTAG GTGAAGCAGT 250
 TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTCATA 300
 AAGAAGCTCC AACTTTCGAA GAATTATCAA CACATGTTGA GGTATTAGAA 350
 ACAGGTATTA AAGTTATCGA CCTTCTTGCA CCATATATTA AAGGTGGTAA 400
 55 GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG 450
 AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT 500
 GGGGTAGGTG AACGTACTCG TGAGGGTAAC GACTTGTAAT ATGAAATGAA 550
 AGACTCTGGA GTTATTAATA AAACAGCCAT GGTATTTGGT CAAATGAATG 600
 AGCCACCAGG TGCACGTATG CGTGTGTCCT TAACAGGATT AACAATGGCA 650
 60 GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA 700

TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750
GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

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2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
25 TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
AACCCTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAGG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
30 TGCAAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAACC	GCCTACGTGT	TGCGTTAACA	600
35 GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
AATCACGGCA	GTA				813

40

2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 55 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
50 AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100

	CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150
	AGAAAACACG	AATGATCCGA	TTCAAGTACC	GGTAGGCACA	AAAACCCTTG	200
	GTCGTATCAT	GAATGTATTG	GGTGAACCAA	TTGACGAACA	AGGTCCAATC	250
	GGTGAAGAAG	AGCGTTGGGC	TATCCATCGT	TCTGCACCAA	GCTATGAAGA	300
5	ACAATCAAAC	AGTACGGAAT	TATTAGAGAC	TGGTATCAAA	GTTATCGACT	350
	TAATTTGTCC	ATTTCGAAAA	GGTGGTAAAG	TTGGTCTATT	CGGTGGTGCG	400
	GGTGTAGGTA	AAACCGTTAA	CATGATGGAA	TTAATCCGTA	ACATCGCGAT	450
	CGAGCACTCA	GGTTACTCCG	TATTTGCGGG	TGTAGGTGAA	CGTACTCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGAAAG	ATTCTAACGT	ATTAGATAAA	550
10	GTATCTTTTG	TTTATGGTCA	GATGAATGAG	CCACCAGGTA	ACCGTTTACG	600
	TGTTGCGTTA	ACTGGTTTAA	CCATGGCAGA	AAAATTCCGC	GATGAAGGTC	650
	GTGATGTATT	ATTCTTCGTG	GATAATATCT	ATCGTTATAC	CCTTGCTGGT	700
	ACGGAAGTAT	CTGCGTTATT	AGGTCGTATG	CCATCTGCGG	TAGGTTACCA	750
	ACCAACTCTT	GCTGAAGAAA	TGGGTGTGTT	ACAAGAACGT	ATCACTTCAA	800
15	CCAAAACAGG	TTCTATTACA	TCTGTA			826

2) INFORMATION FOR SEQ ID NO: 309

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

35	GATGCAGTAC	CAAAAGTATA	TGATGCGTTA	AAAGTTGAAT	CAGGTTTAAAC	50
	GCTTGAAGTT	CAACAACAAT	TAGGCGGTGG	CTTAGTGCGC	TGTATCGCAT	100
	TAGGTACGTC	TGATGGTTTA	AAACGTGGCT	TAAAAGTAGA	AAATACAGGC	150
	AACCCAATTG	AAGTGCCAGT	GGGCACTAAA	ACCCTTGGTC	GTATTATGAA	200
	CGTATTGGGT	GAGCCGATTG	ACGAAAAAGG	TCCTATCGGT	GAAGAAGCAC	250
40	GCTGGGCAAT	CCACCGTGCA	GCACCAAGCT	ACGAAGAGCA	ATCAAATAGC	300
	ACGGAATTAC	TCGAAACAGG	TATCAAAGTT	ATCGACTTAA	TCTGCCCAT	350
	CGCAAAAGGG	GGTAAAGTTG	GTTTATTTGG	TGGTGCAGGT	GTAGGTAAAA	400
	CCGTAAATAT	GATGGAGTTA	ATCCGTAACA	TCGCGATCGA	ACACTCTGGT	450
	TACTCTGTAT	TTGCAGGGGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGACTT	500
45	CTACCACGAA	ATGACAGACT	CTAACGTATT	AGATAAAGTA	TCGTTAGTGT	550
	ATGGTCAAAT	GAACGAACCA	CCAGGTAACC	GTTTACGCGT	AGCTTTAACA	600
	GGCTTAACCA	TGGCGGAAAA	ATTCCGCGAT	GAAGGTCGTG	ACGTATTATT	650
	CTTCGTCGAT	AACATCTACC	GTTATACCCT	AGCAGGTACG	GAAGTGTCAG	700
	CACTTCTCGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAGCC	AACCTTAGCA	750
50	GAAGAAATGG	GTGTATTACA	AGAGCGTATC	ACTTCAACCA	AAACTGGTTC	800
	TATCACCTC					809

55 2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

185

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

10 CGAATTTCCA CAAGATGCAG TACCAAAAAGT TTATGATGCA TTAAAAGTTG 50
 AATCGGGTTT AACCCCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA 100
 CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT 150
 TGAAAATACC AATAAACCAA TTTCAGTACC GGTTGGTGTA AAAACTCTCG 200
 15 GTCGTATTAT GAACGTATTG GGC GAACCGA TTGATGAAAG AGGTCCTATC 250
 GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA 300
 ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT 350
 TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG 400
 TGAGCACTCA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT 450
 20 TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG 500
 AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA 550
 GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG 600
 TGTTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC 650
 GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG 700
 25 ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA 750
 GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA 800
 CCAAACAGG TTCTATTACT TCTG 824

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2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

GCCGTGCCTA AAGTGATATA CGCACTTGAG GTGAAAGGCG GTGCCACTAA 50
 ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA 100
 TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC 150
 50 CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT 200
 TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG 250
 AAGATCGCTG GGCTATTCAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT 300
 AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG 350
 TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTG 400
 55 GTAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC 550
 TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGAATATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 60 ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGCC GGTACCGAAG 700

TATCTGCACT GTTGGGTCGT ATGCCTTCTG CGGTAGGTTA TCAGCCAACG 750
 CTGGCGGAAG AGATGGGTGT TCTGCAAGAA CGTATCACCT CGACCAAAAC 800
 GGGTTCAATC A 811

5

2) INFORMATION FOR SEQ ID NO: 312

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GCGATGCTAT TCCACGCGTT TACGATGCGT TGAAACTGGT TGATGTGGAC 50
 TTGACATTAG AAGTGCAACA ACAACTGGGC GATGGCGTAG TCGTACCAT 100
 25 TGCGATGGGT AGTACCGATG GTTTGAAACG CGGCTTAGCC GTGAACAACA 150
 CAGGCGCACC TATTACAGTG CCTGTTGGTA AAGCAACATT GGGTCGTATT 200
 ATGGACGTAT TGGGTAATCC TGTTGATGAA GCAGGTCCAA TTGGTTCTGA 250
 CCAAACGCGT GCTATTCACC AACCAGCTCC TAAATTTGAT GAACTGTCTA 300
 GCGCAACCGA ATTGCTGGAA ACAGGCATCA AAGTGATTGA CTTGCTTTGC 350
 30 CCATTTGCAA AAGGTGGTAA AGTAGGTTTG TTTGGTGGTG CAGGTGTGGG 400
 CAAACTGTG AACATGATGG AGTTGATTAA CAACATTGCC AAAGCGCACA 450
 GTGGTTTGTG TGTATTTGCA GCGGTGGGTG AACGTACTCG CGAAGGTAAT 500
 GACTTCTATC ACGAGATGAA AGATTCTAAC GTGTTGGATA AAGTTGCCAT 550
 GGTGTATGGT CAAATGAATG AACCTCCTGG CAACCGTTTG CGCGTTGCAT 600
 35 TGACTGGTTT GTCTATGGCA GAACACTTCC GTGATGAAAA AGACGAAAAAT 650
 GGCAAGGTC GCGATGTATT GTTCTTTGTG GACAACTCT ATCGCTACAC 700
 ATTGGCAGGT ACAGAAAGTAT CGGCATTGCT GGGTCGTATG CCCTCTGCGG 750
 TAGGTTATCA ACCAACATTG GCAGAAAGAA TGGGTCGTTT GCAAGAGCGT 800
 ATTACTTCAA CGCAAACAGG TTCGATTACT T 831

40

2) INFORMATION FOR SEQ ID NO: 313

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 55 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC ACGCGTGTAC GAAGCCCTTG AGGTACAGAA TGGTAATGAA 50
 50 GTTCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGTA TCGTACGTAC 100

	CATCGCCATG	GGTTCTTCTG	ATGGTCTGCG	CCGCGGTCTG	GATGTAAAG	150
	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTCA	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCGA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
5	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CCAAGGGCGG	TAAAGTTGGT	CTGTTTCGGCG	GTGCGGGTGT	400
	AGGTAAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
10	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTAATGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
15	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 314

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Klebsiella ornithinolytica*
- (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

35	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCGATCGAA	GTCCCGGTTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAATCGAT	ATGAAAGGCG	ACATCGGCGA	250
40	AGAAGAGCGT	TGGGCTATTC	ACCGTGCAGC	TCCGTCCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTTCGGTG	GTGCGGGTGT	400
	AGGTAAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
45	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
	CCTGGTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

55 2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

10 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT 50
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CCGTATTGTT CGTACCATCG 100
 CCATGGGTTC TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC 150
 GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT 200
 15 GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG 250
 AGCGTTGGGC GATTACCCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC 300
 TCTCAGGAAC TGCTGGAAC CCGCATCAAA GTTATCGACC TGATGTGTCC 350
 GTTTGCGAAG GCGGTAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 20 GGTTACTCCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG 550
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG 600
 ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT 650
 GCTGTTCTGC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT 700
 25 CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG 750
 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAACGGG 800
 TTCTATCACT TCC 813

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2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA 50
 GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG 100
 CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA 150
 50 GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCTG 200
 TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG 250
 AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG 300
 TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTCCGT GGTGCGGGCG 400
 55 TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA 650
 60 CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG 700

AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGGTTCT	ATCACTTCCG	TA			822

5

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GCGGGTGCGG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTA CTCTGTA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCG	TGACGTACTG	CTGTTGCTCG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAAACCGGT	TCTATCACCT	CCGTA		785

40

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTTAAAGATC	100
50 TCGAGCACCC	AATCGAAGTT	CCGGTMGGTA	AAGCAACMCT	GGGTCGTATC	150

	ATGAACGTAC	TGGGTCAKCC	AGTMGACATG	AAAGGCGACA	TCGGTGAAGA	200
	AGAGCGTTGG	GCTATCCACC	GCGCTGCACC	TTCCTACGAA	GAGCTGTCTA	250
	GCTCTCAGGA	ATTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	300
	CCGTTTCGTA	AGGGCGGTAA	AGTCGGTCTG	TTCGGTGGTG	CSGGTGTTGG	350
5	TAAAACCGTA	AACATGATGG	AGCTGATCCG	TAACATCGCG	ATCGAGCACT	400
	CCGGTTACTC	CGTGTTTGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGTAAC	450
	GACTTCTACC	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	500
	GGTATATGGC	CAGATGAACG	AGCCACCGGG	AAACCGTCTG	CGCGTTGCTC	550
	TGACCGGTCT	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTA	600
10	CTGCTGTTTC	TCGATAACAT	CTATCGTTAC	ACCCTGGCCG	GTAAGTGAAGT	650
	ATCTGCWCTG	CTGGGTCGTA	TGCCTTCAGC	GGTAGGTTAC	CAGCCGACCC	700
	TGGCGGAAGA	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAGACC	750
	GGTTCTATC					759

15

2) INFORMATION FOR SEQ ID NO: 319

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*

(B) STRAIN: ATCC 33435

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

	TTCCCTCAGG	ATGCCGTACC	GCGTGTGTAC	GAAGCCCTTG	AGGTTGAGAA	50
	TGGTAATGAA	GTGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
35	TCGTACGTAC	CATCGCTATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	ACTGGGTCGT	ATCATGAACG	TACTGGGCCA	ACCGGTAGAC	ATGAAAGGCG	250
	ACATCGGTGA	AGAAGAACGT	TGGGCTATCC	ACCGTGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
40	CGACCTGATG	TGTCCGTTTG	CGAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	450
	GCGATTGAGC	ACTCCGGTTA	TTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTTTC	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	AGGAAAACCGT	600
45	CTGCGCGTTG	CGCTGACTGG	TCTGACTATG	GCTGAGAAAGT	TCCGTGACGA	650
	AGGTCGCGAC	GTAAGTCTGT	TCGTGATAAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACAGA	AGTATCTGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
50	CTCCACCAA	ACCGTTCTA	TCACCTCCGT	A		831

50

2) INFORMATION FOR SEQ ID NO: 320

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
 5 (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

```

10  GCCGTACCGC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT      50
    GCTGGTGTCTG GAAGTTCAGC AGCAGCTCGG TGGCGGTATC GTGCGTACCA      100
    TCGCCATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT TCCGGTAGGT AAAGCAACAC TGGGTCGTAT      200
    CATGAACGTA CTGGGTCACC CGGTAGACAT GAAAGGCGAC ATCGGTGAAG      250
    AAGAGCGTTG GGCTATCCAC CGCGCTGCGC CTTCTACGA AGAGCTGTCC      300
15  AGCTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGCGGT GCGGGTGTG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
    TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC      550
20  TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG      600
    CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
    ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG      700
    TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA CCAGCCGACT      750
    CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC      800
25  CGGTTCTATC                                     810
  
```

2) INFORMATION FOR SEQ ID NO: 321

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Lactobacillus acidophilus*
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

```

45  TCGATAAGAA TTTACCTGAT ATTAACAACG CCTTACGTGT AATCAAGTCC      50
    GAAGATGAAA GCATCGTTCT TGAAGTTACA CTTGAACTCG GTGATGGTGT      100
    TTTAAGAACA ATCGCCATGG AATCTACCGA TGGTCTTCGT CGTGGTATGA      150
    AAGTCGAAGA TACTGGCGCT CCAATTCAG TTCCAGTTGG AGAAGACACT      200
    TTAGGTCGTG TGTTTAACGT TTTAGGACAG CCTATTGATG GTGGTCCAGC      250
50  CTTTCCAAAG GATCACCAC GTGAGGGTAT CCACAAGGAA GCACCTAAAT      300
    ATGAAGATTT AACTACTAGT CGTGAAATTC TTGAAACTGG TATCAAGGTT      350
    ATCGACCTTC TTGAACCATA TGTTCTGGT GGTAAAGTTG GTTTGTTTGG      400
    TGGTGCCGGT GTTGGTAAAA CTACTATTAT TCAAGAATTA ATTCACAACA      450
    TCGCTCAAGA ACACGGTGGT ATTTCCGTAT TTAGTGGTGT TGGTGAAAGA      500
55  ACTCGTGAAG GTAATGACCT TTAGTTGAA ATGAAAGCTT CAGGCGTTTT      550
    AAGTAAGACT GCCATGGTAT TTGGTCAGAT GAACGAGCCG CCTGGTGCCA      600
    GAATGCGTGT TGCATTAACC GGTGTTGACAC TTGCTGAATA CTTTAGAGAT      650
    GTTGAAGGTC AAGACGTATT GCTCTTTATT GACAATATCT TTAGATTTAC      700
    TCAGGCTGGT TCAGAGGTAT CTGCTTTGCT TGGTCGTATG CCAAGTGCCG      750
60  TAGGTTATCA GCCAACCTTG GCAACAGAAA TGGGTCAATT GCAGGAAAGA      800
  
```

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

5 2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT 50
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG 150
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200
 25 CGCATTATGG ATGTTCTTGG GCGTCTGTGA GATGATGCTG GGCCTATCGA 250
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300
 AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTTG 350
 CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCG GTGGTGCCGG 400
 TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450
 30 AGCATAGCGG TTATTCAAGT TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600
 TTGCTCTAAC CGGTTTGAAT ATGGCTGAAA AATTCCGGGA TGAAGGGCGA 650
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700
 35 TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800
 AAAACAGGTT CTATTACTTC CATA 824

40

2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimonitii*
 (B) STRAIN: ATCC 33999

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150
 60 CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT 200

	CATGAACGTG	CTTGGTCACC	CTATCGACAT	GAAGGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCTG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTCGGCCT	GTTTCGGCGGC	GCCGGCGTAG	400
5	GTAAACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTCTGC	550
	TGGTATACGG	TCAGATGAAC	GAGCCGCCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAAGTTC	CGTGATGAAG	GCCGTGACGT	650
10	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

15

2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

	GTGGAAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACCT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
35	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
	GTAGGTACAG	TAACCTCTGG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCACC	300
	GCGAAGCTCC	AACTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCCTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
40	AATCGGATTG	TTCGGTGGTG	CCGGTGTGTT	TAAAACCGTT	CTAATTCAAG	450
	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTT	TGTGTTTCGCT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTACAGC	GTTATTGAAA	AAACAGCGAT	GGTATTCGGT	CAAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTGCCT	TAACCTGGTCT	AACAATTGCT	650
45	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
	CATTTTCCGT	TTCACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus lylae*
 (B) STRAIN: ATCC 27566

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

```

10  CCCGCGTGGC GAGTTGCCGG CACTGTTCAA CGCGCTGACT GTCGAGGTCA      50
    CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC      100
    GGCACAACT  TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT      150
    CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG      200
    GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT      250
    GAGCCAGGTC TTGGCCGTGA CGGTGAGCAG TGGGGCATCC ACCGCGATCC      300
    GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA      350
15  TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC      400
    CTGTTCCGTG GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT      450
    CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG      500
    GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTGGAAT GGAAGAGATG      550
    GCGTTCTCC  AGGACACCGC TCTTGTGTTT GGCCAGATGG ACGAGCCTCC      600
20  AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT      650
    TCCGCGATGT GCAGCAGCAG GACGTGCTTC TGTTTCATCGA CAACATCTTC      700
    CGTTTACCCC AGGCAGGTTT CGAGGTTTCC ACCCTCCTAG GCCGCATGCC      750
    TTCTGCCGTG GGTTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC      800
    AGGAGCGTAT TACCTCCACA AAGGGTAA                                828
25

```

2) INFORMATION FOR SEQ ID NO: 326

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

```

15  GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA      50
    AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTCGTT      100
    GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA      150
    AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGGCCG      200
    TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG      250
    AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG      300
50  GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT      350
    TTGCCCATTC GCTAAAGGGG GTAAAGTGGG TCTGTTCGGT GGTGCGGGTG      400
    TCGGTAAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG      450
    CACTCAGGTT ATTCTGTATT CGCGGGTGTT GGTGAACGTA CTCGTGAAGG      500
    TAACGATTTT TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT      550
55  CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT      600
    GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA      650
    CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG      700
    AAGTATCTGC ACTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA      750
    ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCGACTAA      800
60  GACCGGCTCT ATCACTCCG TA                                822

```

2) INFORMATION FOR SEQ ID NO: 327

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

20 CCGTGGCGAT GTCCCCCAA TCTTTGATGC ACTTCATGTT GATGGTACTG 50
 AAACCACCCT TGAAGTCCAA CAACAGTTAG GTGATGGTGT GGTGCGTACC 100
 ATTGCCATGG GTTCTACCGA AGGCTTAAAG CGTGGCTTGC CTGTCTCTAA 150
 TTCAGGTGCA CCCATTTCGG TACCAGTCGG TCAAGCAACA CTGGGTGCGA 200
 TTATGGATGT CCTAGGTCGC CCAATCGATG AAGCAGGTCC GTTAAATGCT 250
 25 GAACAAAAAT GGTCCATTCA TCGTGAAGCA CCAAGTTATG ATGAACAGTC 300
 AAATAGTACA GAACTTTTAG AAACAGGCAT CAAAGTGATT GATTTGCTTT 350
 GTCCATTTGC CAAAGGTGGT AAAGTCGGTC TGTTCGGTGG TGCTGGTGTG 400
 GGTAAGACCG TTAACATGAT GGAGCTTATC AATAATATCG CCCTAAAACA 450
 CTCAGGTCTG TCGGTTTTTG CTGGTGTGGG TGAGCGTACT CGTGAGGGTA 500
 30 ATGACTTCTA CCATGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAT 550
 TTTACTCAGT CAAAAGTTGC CATGGTTTAT GGTGAGATGA ATGAGCCACC 600
 AGGAAACCGT CTGCGTGTG CCTTAAGTGG TTTGACCATG GCAGAGTATT 650
 TCCGTGATGA AAAAGACGAA GCAACGGGCA AAGGCCGTGA TGTTCTGCTG 700
 TTCGTTGATA ATATTTATCG TTACACATTG GCAGGTACTG AGGTATCAGC 750
 35 ACTTTTAGGT CGTATGCCAT CTGCGGTAGG TTATCAGCCG ACTTTGGCCG 800
 AAGAGATGGG CTTGCTACAA GAGCGTATCA CCTCCACCCA ATCAGGCTCA 850
 ATTA 854

40

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

CCGTCAAAGC GTACCAAGAA TTTATGATGC CTTAAAAGTT GAAGGCACAG 50
 AAACATACATT AGAAGTACAA CAACAATTGG GTGATGGTAT CGTACGTACT 100
 ATTGCCATGG GTTCTACTGA AGGTCTAAAA CGTGGTCTAC CAGTTAGCAA 150
 50 CACTGGCGCA CCAATCTCTG TACCTGTGGG TAAAGGTACA CTAGGTCTGA 200

	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGT A G A G C A T	250
	AGTAACACTT	GGGCGATTCA	CCGTGAAGCG	CCAAGCTATG	ATGAACAATC	300
	AAACTCTACT	GAACCTTTAG	AAACCGGTAT	TAAAGTAATT	GACTTACTAT	350
	GCCCATTTCG	TAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTGG	CGCGGGTGTG	400
5	GGTAAAACCG	TTAACATGAT	GGAACCTATC	AATAACATCG	CAAAAGCACA	450
	CTCAGGTTTA	TCGGTATTTG	CTGGTGTAGG	TGAGCGTACT	CGTGAAGGTA	500
	ATGACTTCTA	CCACGAGATG	AAAGACTCAA	ACGTACTTGA	TAAAGTTGCG	550
	ATGGTGTATG	GTCAGATGAA	TGAGCCACCA	GGAAACCGTT	TACGTGTTGC	600
	CCTGACAGGT	TTAACCATGG	CAGAATACTT	CCGTGACGAA	AAAGATGAAA	650
10	ACGGTAAAGG	TCGTGACGTA	TTATTGTTTCG	TTGACAATAT	TTATCGTTAC	700
	ACGCTAGCGG	GTACCGAAGT	ATCAGCATTG	TTAGGTCGTA	TGCCATCTGC	750
	AGTAGGGTAT	CAGCCAACGC	TTGCAGAAGA	GATGGGTGTA	CTACAAGAAC	800
	GTATTACTTC	AACCCAATCA	GGCTCTATTA	C		831

15

2) INFORMATION FOR SEQ ID NO: 329

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

	CGAATTTTCCT	CAGGATGCAG	TACCGAAAGT	GTACGATGCG	CTTGAGGTAA	50
	CAAATGGTAA	AGAAAACTG	GTGCTGGAAG	TTCAGCAGCA	GTTAGGCGGC	100
35	GGGGTTGTCC	GTTGTATCGC	TATGGGTACA	TCTGATGGTC	TGAGCCGTAA	150
	TCTGGAAGTA	ACCGATTTAG	GCCACCCGAT	CGAAGTCCCT	GTCGGCGTGA	200
	AAACCTTAGG	ACGTATCATG	AACGTTCTGG	GTGATCCGAT	CGATATGAAA	250
	GGTGACATCG	GCGCAGAAGA	AAAATGGTCT	ATTACCCGTG	CTGCACCAAC	300
	ATACGAAGAA	CTGTCTAACT	CCCAGGAAC	GCTGGAAACA	GGTATCAAAG	350
40	TAATGGACCT	GATCTGCCCC	TTCCGGAAGG	GTGGTAAAGT	CGGTCTGTTC	400
	GGTGTGCGCG	GTGTGGGTAA	AACCGTAAAC	ATGATGGAAC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCTGT	ATTGCGAGGG	GTCGGTGAGC	500
	GTACCCGTGA	AGGTAACGAC	TTCTATCATG	AAATGACAGA	CTCCAACGTT	550
	CTGGACAAAG	TATCACTCGT	GTACGGCCAG	ATGAACGAGC	CACCGGGAAA	600
45	CCGTCTGCGC	GTTGCTCTGA	CCGGTCTGAC	CATGGCGGAA	AAATTCCGTG	650
	ATGAAGGCCG	CGATGTACTG	CTGTTTCGTT	ATAACATCTA	CCGTTATACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGTTA	GGCCGTATGC	CTTCAGCGGT	750
	AGGTTACCAG	CCGACACTGG	CGGAAGAAAT	GGGTGTGCTT	CAGGAACGTA	800
50	TCACATCGAC	CAAAACAGGC	TCTATCACGT	CTGTA		835

2) INFORMATION FOR SEQ ID NO: 330

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 5 (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

	GACGCGGTAC	CGCAAGTGTA	CAGCGCCCTC	GAGGTTATGA	ATGGTGATGC	50
10	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGC	GTAGTACGTA	100
	CCATCGCAAT	GGGTACGTCT	GACGGCCTGA	AGCGTGGTCT	GAGCGTCAAC	150
	GACCTGCAGA	AACCGATTCA	GGTACCCGTC	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTTCTCGGCG	AGCCAATCGA	TATGAAAGGC	GAGCTGAAAG	250
	AAGAAGATGG	CAGCGCAGTA	GAGATCGCCT	CTATTCACCG	CGCAGCCCCT	300
15	TCTTATGAAG	ATCAGTCTAA	CTCGCAGGAA	CTGCTGGAAA	CCGGCATCAA	350
	GGTTATCGAC	CTGATGTGTC	CGTTTGCTAA	AGGCGGTAAA	GTCGGTCTGT	400
	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTCA	ACATGATGGA	ACTGATCCGT	450
	AACATCGCGG	CTGAACACTC	AGGTTACTCA	GTGTTTGCCG	GTGTGGGTGA	500
	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	CGAAATGACT	GACTCTAACG	550
20	TTATCGATAA	AGTTGCACTG	GTCTATGGCC	AGATGAACGA	GCCGCCGGGT	600
	AACCGTCTGC	GCGTAGCACT	GACCGGTCTG	ACCATGGCGG	AAAAATTCCG	650
	TGATGAAGGT	CGCGACGTTC	TGCTGTTCAT	CGATAACATC	TACCGTTATA	700
	CCCTGGCCGG	TACAGAAGTT	TCTGCACTGC	TGGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AGCCAACGCT	GGCAGAAGAG	ATGGGTGTGT	TGCAGGAGCG	800
25	TATTACCTCC	ACCAAGACCG	GTTC			824

2) INFORMATION FOR SEQ ID NO: 331

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

45	TATACAGCGC	TCTCGAGGTA	AAAAATGGTG	ATGCTCGTCT	GGTGCTGGAA	50
	GTACAGCAGC	AGCTGGGCGG	TGGCGTGGTG	CGTACCATCG	CCATGGGTTC	100
	TTCTGACGGC	CTGAAGCGCG	GTCTGGAAGT	CACCGACCTG	AAAAAACCTA	150
	TCCAGGTTCC	GGTTGGTAAA	GCAACACTCG	GCCGTATCAT	GAACGTGCTG	200
	GGTGAGCCAA	TCGACATGAA	AGGCGACCTG	AAAGAAGAAG	ACGGCAGCGC	250
50	TGTAGAGGTT	TCCTCTATTC	ATCGCGCAGC	GCCTTCTTAT	GAAGATCAGT	300
	CAAACCTCGA	GGAACCTGCTG	GAAACCGGCA	TCAAGGTTAT	CGACCTGATG	350
	TGTCCGTTCC	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGGCTGAGC	450
	ACTCAGGTTA	TTCGGTCTTT	GCCGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
55	AACGACTTCT	ACCACGAAAT	GACGGACTCC	AACGTTATCG	ATAAAGTAGC	550
	GCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGTAACCGT	CTGCGCGTAG	600
	CACTGACCGG	TCTGACCATG	GCGGAAAAAT	TCCGTGATGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCATCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACAGA	700
	GGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	GGCGGTAGGT	TATCAGCCAA	750
60	CGCTGGCTGA	AGAGATGGGT	GTGCTGCAGG	AGCGTATTAC	CTCCACCAAG	800

5 2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
(B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20 GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50
ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAGTTCGC TGTATCGCAA 100
TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150
AACCCAATTT CTGTTCCAGT GGGAACGAAA ACATTGGGTC GTATCATGAA 200
25 CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250
ATTGGTCTAT TCACCGTGCG CCACCAAGTT ATGAAGAACA ATCTAACAGT 300
ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350
TGCGAAAGGG GGTAAAGTAG GTTTATTCGG TGGTGCGGGT GTCGGTAAAA 400
CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450
30 TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500
CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGTTT 550
ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600
GGCTTAACTA TGGCGGAAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650
CTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700
35 CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCCTTGCA 750
GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AAACAGGTTC 800
TATTA 805

10 2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50
CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTCTG 100
TTCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150
50 GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200

	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250
	TTGGTGAAGA	AGAGCGTTGG	GCTATTCACC	GTGAAGCACC	AAGTTATGAA	300
	GATTTATCTG	GCGCCAATGA	ACTGCTGGAA	ACGGGTATCA	AGGTTATCGA	350
	CCTGATTTGT	CCGTTTGCTA	AAGGTGGTAA	AGTTGGTCTG	TTTGGTGGTG	400
5	CGGGTGTAGG	TAAAACCGTA	AACATGATGG	AGCTGATTCG	TAACATTGCG	450
	ACTGAGCACT	CAGGTTACTC	CGTATTCGCC	GGTGTAGGGG	AACGTACCCG	500
	TGAAGGTAAT	GACTTCTACC	ACGAAATGAC	CGAATCAAAC	GTAAGGATA	550
	AAGTATCTCT	GGTTTATGGC	CAGATGAACG	AGCCACCAGG	AAACCGTCTG	600
	CGCGTGGCGT	TAACGGGTTT	GACCATGGCT	GAAAAATTCC	GTGATGAAGG	650
10	TCGTGACGTT	CTGTTATTTA	TCGATAACAT	TTATCGCTAT	ACCTTAGCCG	700
	GTACCGAAGT	ATCAGCACTG	TTGGGGCGTA	TGCCATCAGC	GGTAGGTTAT	750
	CAGCCAACGT	TAGCAGAAGA	GATGGGTGTG	TTGCAGGAAC	GTATTACTTC	800
	AACCAAAACC	GGTTCAATCA	CTTCTGTA			828

15

2) INFORMATION FOR SEQ ID NO: 334

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

	GTCCCTAAAG	TATACGACGC	TCTTGAGGTT	ATGAATGGTA	AAGAAAAACT	50
	GGTGCTGGAA	GTTCAAGCAAC	AGTTAGGCGG	TGGTATCGTT	CGTTGTATCG	100
35	CAATGGGTAC	ATCAGACGGT	TTAAGCCGTG	GCTTAAAGGT	TGAAGATTTA	150
	GGCCACCCAA	TTGAAGTACC	AGTAGGTAAA	GCGACTTTAG	GACGTATCAT	200
	GAACGTTCTG	GGTACACCTA	TTGATATGAA	AGGTGAGATT	GAAACCGAAG	250
	AGCGTTGGTC	AATCCACCGT	GAAGCACCAA	CTTACGAAGA	GTTATCAAAC	300
	TCTCAAGAAC	TGCTTGAAAC	CGGTATCAAA	GTTATGGACT	TAATCTGTCC	350
40	ATTTGCTAAA	GGTGGTAAAG	TCGGTCTGTT	CGGTGGTGCG	GGTGTTGGTA	400
	AAACAGTTAA	CATGATGGAA	TTGATCCGTA	ATATCGCGAT	CGAGCACTCA	450
	GTTTACTCTG	TATTTGCTGG	TGTTGGTGAG	CGTACTCGTG	AGGGTAACGA	500
	CTTCTATCAT	GAAATGACAG	ATTCTAACGT	TCTTGACAAA	GTATCGTTAG	550
	TTTACGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTGCG	TGTTGCACTG	600
45	ACTGGTCTGA	CTATGGCTGA	GAAATTCCGT	GATGAAGGCC	GTGACGTACT	650
	GTTATTCGTC	GATAACATCT	ATCGTTACAC	CTTAGCCGGT	ACAGAAGTAT	700
	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	ACCAACATTG	750
	GCTGAAGAGA	TGGGTGTTCT	GCAAGAGCGT	ATCACTTCAA	CCAAAACAGG	800
	TTCTATC					807

50

2) INFORMATION FOR SEQ ID NO: 335

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 811 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 5 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

```

10 CCCTAAAGTA TACGACGCTC TTGAGGTTAT GAATGGTAAA GAGAAACTGG      50
   TGCTAGAAGT TCAGCAACAG TTAGGCGGTG GTATCGTTTCG TTGTATCGCA      100
   ATGGGTACAT CAGACGGTTT AAGCCGTGGC TTAAGAGTTG AAAACTTAGG      150
   CCACCCAATT GAAGTACCAG TAGGTAAAGC AACACTGGGA CGTATCATGA      200
   ACGTTCTGGG TACACCTATC GATATGAAAG GTGATATTGC AACTGAAGAA      250
   CGTTGGTCTA TTCACCGCGA AGCGCCAACC TATGAAGAGT TATCAAGCTC      300
15 TCAAGAACTA CTAGAAACCG GTATCAAAGT AATGGACTTA ATCTGTCCGT      350
   TTGCTAAAGG TGGTAAAGTA GGTCTCTTCG GTGGTGCGGG TGTGGTAAA      400
   ACAGTTAACA TGATGGAATT GATCCGTAAC ATCGCGATTG AGCACTCAGG      450
   TTATTCTGTA TTTGCAGGTG TTGGTGAGCG TACTCGTGAG GGTAACGACT      500
   TCTATCATGA AATGACAGAT TCTAACGTTT TTAGCAAAGT ATCGTTAGTT      550
20 TATGGTCAGA TGAATGAGCC ACCAGGAAAC CGTCTACGTG TAGCACTGAC      600
   GGGTTTAACC ATGGCGGAAA AATTCCGTGA TGAAGGCCGT GACGTAAGT      650
   TATTCGTCGA TAACATCTAT CGTTACACCT TAGCCGGTAC CGAAGTATCA      700
   GCACTGTTAG GCCGTATGCC ATCAGCAGTA GGTACCAAC CAACATTGGC      750
   TGAAGAGATG GGTGTTCTGC AAGAACGTAT CACTTCAACC AAAACAGGTT      800
25 CAATCACCTC T                                     811

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2) INFORMATION FOR SEQ ID NO: 336

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

```

45 TCAAGATAAC GTACCAAAAG TGTACGATGC TCTTGAGGTT ATTAACGGTA      50
   AAGAAAAACT GGTGTTGGAA GTTCAACAAC AGTTAGGTGG TGGTGTGTC      100
   CGTTGTATCG CAATGGGTAC ATCAGATGGT CTGAGCCGTG GTTTAGAAGT      150
   TGTAACCTTA GAGCACCCAA TCGAAGTACC AGTCGGTAAA GCAACTCTGG      200
   GACGTATCAT GAACGTTCTG GGTGAACCAA TCGACATGAA AGGTGATATC      250
50 GGCGAAGAAG AGCGCTGGTC TATTCACCGT GCTGCACCAA GCTACGAAGA      300
   ATTAGCTAAC TCAACTGAAC TGCTGGAAAC CGGTATCAAA GTAATGGACT      350
   TAATCTGTCC ATTCGCGAAA GGTGGTAAAG TAGGTCTGTT CGGTGGTGCG      400
   GGTGTTGGTA AAACCGTAAA CATGATGGAAC CTGATCCGTA ACATCGCGAT      450
   TGAGCACTCA GGTACTCAG TGTTTCGCTGG TGTTGGTGAG CGTACCCGTG      500
55 AAGGTAACGA CTTCTATCAT GAAATGACAG ACTCAAACGT TCTGGATAAA      550
   GTATCACTGG TTTATGGCCA GATGAACGAG CCACCAGGAA ACCGTCTGCG      600
   TGTTCGCTG ACTGGTCTGA CTATGGCTGA AAAATTCCGT GACGAAGGTC      650
   GTGACGTAAT GCTGTTCTGT GACAACATTT ATCGTTATAC ACTGGCAGGT      700
   ACTGAAGTAT CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA      750
60 ACCAACGCTG GCGGAAGAGA TGGGTGTTCT TCAAGAACGT ATTACCTCAA      800

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5 2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
(B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50
CGGTAAAGAA ACACTGGTGC TGGAAGTTCA GCAACAGTTA GGCGGTGGTG 100
TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200
25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
GGACTTAATC TGTCCATTCT CGAAAGGTGG TAAAGTTGGT CTGTTTCGGTG 400
GTGCGGGTGT TGGTAAACA GTAAACATGA TGGAAGTATG CCGTAACATC 450
30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTG GTGAGCGTAC 500
TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTACTGG 700
35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

10 2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
ACTGGTGTTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTT GTCCGTTGTA 100
TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
50 TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTGCGG	AAAGGTGCTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTTG	400
5	GTAACACAGT	AAACATGATG	GAAGTATGAT	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTGTTG	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTTGCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTT	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTAAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTTTCAGCAAC	AGTTAGGCGG	TGGTGTGTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
40	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTGTTGA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGCAGC	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
15	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
50	CTAAGACAGG	TTCTATCAC				819

2) INFORMATION FOR SEQ ID NO: 340

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 5 (B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

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10 AACCGCACTG ACGTGCCTCA AATTTATGAC GCGTTAGTTG TAGATGGTAC      50
   CGAAACCACC CTAGAAGTTC AGCAGCAGCT GGGCGATGGT GTGGTACGTA      100
   CTATTGCAAT GGGATCTACT GAAGGTCTTA AGCGTGGTTT ACCAGTAACA      150
   AACACTGGTG CCCCAATTAC AGTTCCAGTA GGTGATGCGA CTTTAGGTCG      200
   TATTATGGAC GTTTTAGGTC GTCCAATTGA CGAACAAGGT CCAGTTAATT      250
   CTGAAGACCA TTGGTCAATC CACCGTCAAG CGCCATCATA TGATGAGCAA      300
15 GCTAACAGTA CTGACCTATT AGAGACAGGT ATTAAAGTAA TTGACTTACT      350
   TTGTCCGTTT GCTAAAGGGG GTAAAGTTGG TCTGTTCGGT GGTGCCGGTG      400
   TTGGTAAAAC CGTAAACATG ATGGAATTGA TTAATAACAT CGCTCTTAAG      450
   CACTCAGGTT TATCAGTATT TCGTGGTGTG GGTGAGCGTA CTCGTGAAGG      500
   TAACGAGTTC TACCACGAGA TGCAAGAAGC GGGTGTGTGT GACGTTGAAA      550
20 ACTTCACCAA CTCAAAAGTT GCGATGGTTT ATGGTCAGAT GAATGAGCCA      600
   CCAGGTAACC GTTTACGTGT TGC GTTAACC GGTCTGACTA TGGCTGAGTA      650
   CTTCCGTGAT CAAAAAGATG AAAACGGTAA AGGTAAAGAC GTTCTATTAT      700
   TCGTTGATAA CATCTACCGC TACACGCTAG CCGGTACTGA AGTATCAGCA      750
   CTTCTAGGTC GTATGCCATC AGCAGTAGGT TATCAGCCAA CACTAGCGGA      800
25 AGAGATGGGT GTACTACAAG AGCGTATTAC TTCAACTCAG ACTGGTTCTA      850
   TTA CTTC      907

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30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

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45 GTTCCCTCAG GATGCAGTAC CGAACGTGTA CAATGCTCTT GAGGTAGAAA      50
   ACGGTACCTC CAAACTGGTG CTGGAAGTTC AGCAACAGTT AGGCGGCGGC      100
   GTTGTTTCGT GTATCGCAAT GGGTACCTCA GACGGCCTGC GTCGCGGTCT      150
   GAAAGTGAAC AACCTGGAAC ACCCAATTGA AGTACCGGTA GGTAAAGCGA      200
50 CTCTGGGTCG TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAAGGT      250
   GAAATCGGCG AAGAAGAACG TCGTGCTATT CACCGTGCTG CGCCTTCTTA      300
   TGAAGAGCTG GCAAACCTCC AGGAATTGCT GGAAACCGGT ATCAAAGTTA      350
   TGGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCGGT      400
   GGTGCGGGTG TAGGTAAAAC TGTGAACATG ATGGAGCTGA TCCGTAACAT      450
55 TGCGATCGAG CACTCCGGTT ATTCTGTGTT TGCAGGCGTG GGTGAACGTA      500
   CTCGTGAGGG TAACGACTTC TACCACGAAA TGA CTGATTTC CAACGTTATC      550
   GACAAAGTTT CCCTGGTGTA TGGCCAGATG AATGAGCCAC CAGGTAACCG      600
   TCTGCGCGTT GCACTGACCG GCCTGACCAT GGCGGAAAAA TTCCGTGATG      650
   AAGGTCGTGA CGTACTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG      700
60 GCCGGTACCG AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG      750

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TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA' 800
 CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGATG GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGC GGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
 25 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTCTG GAAACCGGTA TAAAAGTTAT 350
 CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTTCGGTG 400
 30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TAYCASC CGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCACCAAAA ACCGGTTCTA TCAC 824

40

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 55 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
 60 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

	CCATCGCGAT	GGGGTCTTCT	GACGGTCTGC	GTCGCGGTCT	GGATGTAAAA	150
	GATCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCCA	CGCTGGGTCTG	200
	TATCATGAAC	GTCCTGGGCG	AACCGGTCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	CGAAGAGTTG	300
5	TCAAACCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTTA	TTCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCGGGCGTA	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GATAAAGTAT	550
10	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	TGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CCGCAGTAGG	TTACCAGCCG	750
	ACTCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
15	AACCGGTTCT	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 344

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

35	TTCCCTCAGG	ATGCCGTACC	ACGCGTGATC	GATGCTCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTT	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGTGA	ACCGGTCGAT	ATGAAAGGCG	250
40	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCGGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAAGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTC	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
45	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCT	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCACC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTCGACAA	CATCTACCGT	TATACCCTCG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
50	TATCAGCCGA	CTCTGGCTGA	AGAAATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55 2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

10 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCCGTA 100
 TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG 150
 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC 200
 15 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCCA AGAAGAGCGT TGGGCGATTC ACCGCGCTGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTCTG CGAAGGCGCG TAAAGTCGGT CTGTTCGGTG 400
 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 20 GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGTCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA 650
 AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
 25 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAG ACCGGTTCTA TCACCTCCGT A 831

30

2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*

(B) STRAIN: ATCC 43974

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCCGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG 150
 50 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCCA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCGTCCTAT 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTCTG CGAAGGCGCG TAAAGTCGGT CTGTTCGGTG 400
 55 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAAGT TCCGTGACGA 650
 60 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700

CCGGTACGGA	AGTTTCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
TATCAGCCAA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
CTCCACCAAA	ACCGGTTCTA	TCACCTCCG			829

5

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

25	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCTACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTCAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
30	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGC	AAGGGCGGTA	AAGTCGGTCT	GTTCCGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGTTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CATGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
35	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCTTCCG	CGGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
40	CGGTTCTATC	ACCTCCG				817

2) INFORMATION FOR SEQ ID NO: 348

45

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATT	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAGAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTCAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
	GTAAACCCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTAATC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTTC					806

20

2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
 (B) STRAIN: ATCC 43972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCCGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGKGGTCTG	150
40	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATTGGTGA	AGAAGAGCGT	TGGGCTATTC	ACCGTGCTGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGCGCG	TAAAGTCGGT	CTGTTCCGGTG	400
45	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGACGA	650
50	AGGTCGTGAC	GTAATGCTGT	TCGTGATAA	CATCTATCGT	TATACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TATCAGCCGA	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACTAAA	ACCGTTCTA	TCACCTCCGT	A		831

55

2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases

60

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhi
 10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
15	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
20	GAAGAGTTAT	CAAACTCTCA	GGAAGTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
25	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTAAGTGTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
30	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
55	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACTCTCA	GGAAGTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
60	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTT	GCGGGCGTAG	GGGAACGTAC	500

	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	561
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCCGCTTG	CATTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	700
5	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	CGCAGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

10

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGTCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
30	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
35	TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTCTCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
40	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
45	CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia ficaria*
 (B) STRAIN: ATCC 33105

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCCTG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAACCTCCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTTC	GCCAAGGGCG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCCG	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 354

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia fonticola*
 (B) STRAIN: ATCC 29844

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACC GA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAAAC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCCCTTC	GCCAAGGGTG	GTAAAGTTGG	TCTGTTCGGT	GGTGCTGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTC	CAACGTACTG	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTCGTCGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

60 2) INFORMATION FOR SEQ ID NO: 355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

15 GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA 50
 TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT 100
 GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA 150
 GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAGCTA CTCTGGGCCG 200
 20 TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG 250
 AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTTG 300
 GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
 CTGCCCCGTT GCCAAGGGTG GTAAAGTCGG TCTGTTCCGGT GGTGCGGGTG 400
 TTGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 25 CACTCCGGTT ATTCTGTGTT TGCGGGCGTG GGTGAGCGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGAACGACTC CAACGTA CTG GACAAAGTAT 550
 CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
 GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
 30 AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
 ACGCTGGCGG AAGAGATGGG TGTCTGCAA GAACGTATCA CCTCTACCAA 800
 GACTGGTTCA ATCACCTCCG TA 822

35

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

ATGCCGTACC AAAAGTGTA AATGCTCTTG AGGTAGAAAA CCGTACCGAG 50
 AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GGCAGGTGGCG TAGTTCGCTG 100
 TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG 150
 55 ATCTGGAACA CCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT 200
 ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA 250
 AGAAGAACGT TGGGCGATT ACCGTCCAGC GCCAAGCTAC GAAGATTTGT 300
 CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT 350
 TGTCCGTTCC CTAAGGGCGG TAAAGTTGGT CTGTTCCGGTG GTGCTGGTGT 400
 60 TGGTAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450

ACTCCGGTTA TTCCGTGTTT GCAGGCGTGG GTGAGCGTAC TCGTGAGGGT 500
 AACGACTTCT ACCACGAAAT GAACGACTCC AACGTACTGG ACAAAGTATC 550
 CCTGGTTTAC GGCCAGATGA ACGAGCCACC GGGTAACCGT CTGCGCGTTG 600
 CTCTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA AGGCCGCGAC 650
 5 GTTCTGCTGT TCGTTGATAA CATTTACCGT TATACCCTGG CCGGTACCGA 700
 AGTGTCCGCA CTTCTGGGCC GTATGCCATC TCGGGTAGGT TATCAGCCAA 750
 CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC CTCTACCAAG 800
 ACCGGTTCTA TCACTTCCG 819

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

TCAGGATGCC GTACCGAAAG TGTACGACGC CCTTGAGGTA GAAAACGGCA 50
 CCGAAAAACT GGTGTTGGAA GTTCAGCAAC AGCTGGGCGG TGGCGTGGTT 100
 30 CGCTGTATCG CAATGGGGAC CTCCGACGGT CTGCGTCGCG GTCTGAAAGT 150
 GAACAACCTG GACCACCCGA TTGAAGTGCC GGTGGGTAAA GCTACCCTGG 200
 GTCGTATCAT GAACGTATTG GGTCAACCGA TCGACATGAA AGGCGACATC 250
 GGCGAAGAAG AGCGTTGGGC GATTCACCGC GCGGCGCCAA GCTACGAAGA 300
 GCTGTCAAGC TCTCAGGAAC TGCTGGAAAC CGGTATCAAG GTAATGGACC 350
 35 TGATTTGTCC GTTCGCCAAG GGCGGTAAAG TCGGTCTGTT CGGCGGTGCG 400
 GGCGTAGGTA AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT 450
 CGAGCACTCC GGTTATTCCG TGTTTGCGGG CGTGGGCGAG CGTACTCGTG 500
 AGGGTAACGA CTTCTACCAC GAAATGACCG ACTCCAACGT TCTGGACAAA 550
 GTATCCCTGG TTTACGGCCA GATGAACGAG CCACCAGGTA ACCGTCTGCG 600
 40 CGTTGCGCTG ACCGGTCTGA CCATGGCGGA GAAATTCCGT GACGAAGGCC 650
 GTGACGTTCT GCTGTTCGTT GACAACATCT ACCGTTACAC CCTGGCCGGT 700
 ACCGAAGTGT CCGCACTTCT GGGCCGTATG CCATCCGCGG TAGGTTATCA 750
 GCCAAGCTG GCGGAAGAGA TGGGCGTTCT GCAAGAACGT ATCACCTCGA 800
 CCAAG 805

45

2) INFORMATION FOR SEQ ID NO: 358

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia odorifera*
 60 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	AACTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTGGTTCGTT	100
	GTATCGCTAT	GGGCACCTCC	GACGGTTTGC	GTCGCGGCCT	GAAAGTGAAC	150
	GATCTGCAAC	ACCCAATCGA	AGTCCCGGTT	GGCAAGGCAA	CGCTGGGTCTG	200
	TATCATGAAC	GTATTGGGTC	AACCAATCGA	CATGAAAGGC	GACATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCAAGCTA	CGAAGAAGTCTG	300
10	TCCAACCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTTA	TGGACCTGAT	350
	CTGCCCCTTT	GCCAAGGGTG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGTG	400
	TTGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCAAGTGT	TGCGGGCGTG	GGTGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTACTG	GACAAGGTTT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CGGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCCGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCTGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCT	ATCACCTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 359

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: ATCC 183

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

40	GTGTACAACG	CTCTTGAGGT	AGAAAACGGT	GCCAATAAGC	TGGTGCTGGA	50
	AGTTCAGCAA	CAGCTGGGCG	GTGGCGTGGT	TCGCTGTATC	GCGATGGGGA	100
	CCTCTGATGG	TCTGCGTCGC	GGTCTGAAAG	TGATCGACCT	GGATCACCCG	150
	ATTGAAGTAC	CGGTAGGTAA	AGCTACCCTG	GGCCGTATCA	TGAACGTATT	200
	GGGTGAACCA	ATCGACATGA	AAGGCGACAT	CGGCGAAGAA	GAACGTTGGG	250
45	CAATTCACCG	TCCAGCGCCA	AGCTACGAAG	ATTTGGCCAA	CTCCCAGGAT	300
	CTGCTGGAAG	CCGGTATCAA	GGTTATGGAC	CTGATCTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTGGGTCTGT	TCGGCGGTGC	GGGCGTGGGT	AAAACCGTAA	400
	ACATGATGGA	GCTGATCCGT	AACATCGCGA	TCGAACACTC	CGGTTATTCC	450
	GTGTTTGCGG	GCGTGGGTGA	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
50	CGAAATGAAC	GACTCCAACG	TACTGGACAA	AGTATCCCTG	GTTTACGGCC	550
	AGATGAACGA	GCCACCGGGT	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCGG	AGAAATTCCG	TGACGAAGGC	CGCGACGTTT	TGCTGTTCGT	650
	TGATAACATC	TACCGTTATA	CCCTGGCCGG	TACCGAAGTG	TCCGCACTTC	700
	TGGGCCGTAT	GCCATCTGCG	GTAGGTTATC	AGCCAACGCT	GGCGGAAGAG	750
55	ATGGGCGTTC	TGCAAGAACG	TATCACCTCT	ACCAAGACCG	GTTCTATCAC	800
	CTCCG					805

60 2) INFORMATION FOR SEQ ID NO: 360

215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

15 TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA 50
 CGGTAACGAA AAAGTGGTGC TGGAGTTTCA GCAGCAGCTG GCGGCGGCG 100
 TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG 150
 AAAGTTAACG ACCTCGAGCA CCAATCGAA GTGCCAGTTG GTAAAGCAAC 200
 20 GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG 250
 ACATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCAAGCTAC 300
 GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT 350
 GGACCTGATC TGCCCGTTCG CCAAGGGTGG TAAAGTTGGT CTGTTCCGGT 400
 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC 450
 25 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG 550
 ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG 700
 30 CCGGTACCGA AGTGTCCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT 750
 TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC 800
 CTCGACCAAG ACCGGTTCAA TCACCTCCGT A 831

35

2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
 (B) STRAIN: LCDC D7172

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

CCGTAAACAT GATGGAAGT ATCCGTAACA TCGCCATCGA GCACAGCGGT 50
 TATTCCGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 100
 CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT 150
 55 ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC 200
 GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT 250
 GTTCGTCGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG 300
 CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCCTGGCT 350
 GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC 400
 60 GATCAC 406

2) INFORMATION FOR SEQ ID NO: 362

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

20	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	50
	TGGTAATGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	200
	TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	250
25	AGATCGGTGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAACTCTCA	GGAAGTGTCT	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
30	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ACAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
35	TATCAGCCGA	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACTGGTTCTA	TCACCTCCGT	A		831

40 2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55	GCCGTACCGC	GCGTGTACGA	TGCTCTTGCG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCAATGGG	TTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
60	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGTGAAG	250

	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTCATTC	GTAACATCGC	GATCGAGCAC	450
5	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CG					802

15

2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCCGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
35	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	GTGCGGGTGT	400
40	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
45	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
	ACTGGTTCTA	TCACCTCCG				819

50

2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

218

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

GTACCGCGCG TGTACGATGC TCTTGAGGTG CAAAATGGTA ATGAGCGTCT 50
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATCGTG CGTACCATCG 100
 10 CAATGGGTTC CTCCGACGGT CTGCGTCGCG GTCTGGATGT AAAAGACCTC 150
 GAACACCCGA TCGAAGTCCC GGTAGGTAAA GCGACTCTGG GCCGTATCAT 200
 GAACGTA CTG GGTGAACCGG TCGACATGAA AGGCGAGATC GGTGAAGAAG 250
 AGCGTTGGGC GATTCAACGC GCAGCACCTT CCTACGAAGA GCTGTCAAAC 300
 TCTCAGGAAC TGCTGGAAAC CGGTATCAAA GTTATCGACC TGATGTGTCC 350
 15 GTTCGCTAAG GGC GGTAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTCATTCGTA ACATCGCGAT CGAGCACTCC 450
 GGTTACTCTG TGTTTGC GGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGACAAA GTATCCCTGG 550
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCTCTG 600
 20 ACCGGTCTGA CCATGGCTGA GAAATTCCGT GACGAAGGTC GTGACGTTCT 650
 CCTGTTCTGTT GACAACATCT ATCGTTACAC CCTGGCCGGT ACGGAAGTAT 700
 CCGCACTGCT GGGCCGTATG CCTTCAGCGG TAGGTTATCA GCCGACCCTG 750
 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAACTGG 800
 TT 802

25

2) INFORMATION FOR SEQ ID NO: 366

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

TAACGCCTTG GTTATTGATG TGCCTAAAGA AGAAGGTACA ATACA ACTAA 50
 CATTAGAAGT TGCGCTGCAA TTAGGTGACG ACGTTGTTCG TACAATTGCG 100
 45 ATGGATTCAA CTGATGGTGT CCAAAGAGGC ATGGATGTAA AAGATACAGG 150
 CAAAGAAATT AGTG TACCTG TTGGTGATGA AACATTAGGT CGTGTATTTA 200
 ATGTACTAGG TGAAACAATT GACCTTAAAG AAGAAATTAG TGATTCTGTT 250
 CGCCGCGATC CTATCCATCG TCAAGCACCA GCATTGATG AACTTTCAAC 300
 AGAAGTTCAA ATTTTAGAAA CAGGTATTAA AGTAGTAGAT TTACTAGCAC 350
 50 CTTATATTAA AGGTGGTAAA ATCGGATTGT TCGGTGGTGC CGGTGTAGGT 400
 AAAACAGTAT TAATCCAAGA ATTAATTAAC AACATCGCTC AAGAGCACGG 450
 TGGTATTTCT GTATTGCGCG GTGTAGGTGA ACGTACTCGT GAAGGTAACG 500
 ATTTATACTT CGAAATGAGT GATAGTGGTG TAATTAAGAA AACAGCCATG 550
 GTATTGCGGC AAATGAATGA GCCACCTGGT GCACGTATGC GTGTTGCATT 600
 55 ATCTGGTTTA ACAATGGCTG AATATTCCG TGACGAACAA GGTCAAGACG 650
 TATTATTATT CATCGATAAC ATTTTCAGAT TTACACAAGC TGGTTCCTGAG 700
 GTATCTGCAT TATTAGGTCG TATGCCTTCT GCAGTAGGTT ACCAACCAAC 750
 ACTTGCTACT GAAATGGGAC AATTACAAGA ACGTA 785

60

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA 50
 AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG 100
 20 GCGATGACGT TGTTCGTACC ATTGCAATGG ATTCAACTGA TGGTGTTAAA 150
 CGTGGTAAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAGTCGG 200
 AGACGAAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT 250
 TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCTAT ACATAGAGAA 300
 GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG 350
 25 AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAAGTTG 400
 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTTAAT CCAAGAATTA 450
 ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTTCACTCT TTGCCGGTGT 500
 AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA 550
 GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA 600
 30 CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAACAA TGGCTGAATA 650
 TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT 700
 TCCGTTTCAC ACAAGCCGGT TCAGAAAGTT CTGCCTTACT AGGTCGTTTA 750
 CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT 800
 ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA 843

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2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 50 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA 50
 55 GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA 100
 ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG 150
 TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT 200
 GTTGGTGATG CAACTTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT 250
 CGATTTAGAT GAAAAGATTG ATGATTCACT ACGTCGTGAT CCTATTCATA 300
 60 GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA 350

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTGG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTT	AGTATTCGCC	500
	GGTGTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTTGCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

2) INFORMATION FOR SEQ ID NO: 369

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCT	GCTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCGT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTCT	400
	GTGGTGCCGG	TGTTGGTAAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAAAC	ATGGCTGAAT	ATTTCGGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAGAAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAACATAAG	GTTTCAGTAAC			830

50 2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Staphylococcus epidermidis*

(B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

5
 AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT 50
 AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG 100
 CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA 150
 GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTCTAG GAAGAGTGTT 200
 10 TAACGTACTA GGAGAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG 250
 TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA 300
 ACAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC 350
 ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG 400
 GTAAAACCGT ACTAATCCAA GAACTTATTA ATAACATCGC TCAAGAACAC 450
 15 GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA 500
 TGATCTTTAC TATGAAATGA GTGACAGTGG TGTTATCAAG AAAACTGCAA 550
 TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA 600
 TTATCCGGAT TAACAATGGC CGAATATTCG CGAGATGAAG AAGGCCAAGA 650
 TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG 700
 20 AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT 750
 ACACCTTGCTA CAGAAATGGG TCAATTACAA GAACGTA 787

25 2) INFORMATION FOR SEQ ID NO: 371

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

40
 GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA 50
 TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAATA GGTGATGACG 100
 TTGTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG 150
 GAAGTTCAGA ACACTGGAAA AGACATTTCA GTACCAGTTG GCCAAGTAAC 200
 45 TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA 250
 AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC 300
 TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT 350
 TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAATC GGTCTATTTG 400
 GTGGTGCCGG TGTGGTAAA ACCGTTTTAA TCCAAGAATT GATTAATAAT 450
 50 ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG 500
 TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTGA 550
 TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA 600
 CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA 650
 TGAACAAGGA CAAGACGTTT TGTATTTCAT CGATAACATT TTCAGATTGA 700
 55 CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT 750
 GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG 800
 TATTACATCA ACGAATAAAG GTTCAGTAAC 830

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2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

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TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA      50
CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT      100
AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTT      150
AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTCCTGTGA      200
GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA      250
TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC      300
GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA      350
GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT      400
TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT      450
TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT      500
GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA      550
TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC      600
CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA      650
TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTATTCA TTGACAATAT      700
TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATT TTAGGACGTA      750
TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA      800
TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA          846

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2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

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TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA      50
CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT      100
AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTT      150
AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTCCTGTGA      200
GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA      250
TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC      300
GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA      350
GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT      400

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TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
 TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
 TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
 5 CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
 TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTATTCA TTGACAATAT 700
 TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATT TTAGGACGTA 750
 TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
 TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846
 10

2) INFORMATION FOR SEQ ID NO: 374

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus lugdunensis*
 25 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

30 ATAATGAAGT GCCTGAAATA AATAATGCGC TCATTGTTGA AATTCCTAAA 50
 AGTGATACAA CAATCAGTTT AACACTTGAA GTTGCTTTGC AATTAGGTGA 100
 CGATGTTGTA CGTACTATTG CAATGGATTC AACTGATGGC GTTCAACGTG 150
 GTATGGAAGT TCAAAACACA GGTAAAGACA TCAGTGTACC TGTGAGAGAT 200
 GAAACATTAG GAAGAGTATT TAACGTTTTA GGAGAATCTA TTGATTTAGA 250
 AGAAAAGCTA GATGACTCTG TGCCTAGAGA TCCAATTCAT AGACTAGCAC 300
 35 CTAAATTTGA TGAATTATCT ACAGAAAGTAG AAATTCTTGA AACTGGTATT 350
 AAAGTTGTTG ATTTATTAGC ACCATATATT AAAGGTGGTA AAGTTGGATT 400
 GTTTGGTGGT GCCGGAGTAG GTAAACGGT ATTAATTCOA GAATTAATCA 450
 ACAATATTGC TCAAGAACAT GGTGGTATTT CTGTGTTTGC CGGAGTAGGT 500
 GAACGTACAC GTGAAGGTAA TGAATTATAT TATGAAATGA GCGATAGTGG 550
 40 CGTAATTAAG AAAACAGCGA TGGTATTTGG CCAAATGAAT GAACCACCTG 600
 GTGCACGTAT GAGAGTTGCG TTATCTGCCT TAACAATGGC TGAATATTTT 650
 CGTGACGAGC AAGGACAAGA CGTATTGCTG TTTATCGATA ATATATTCCG 700
 TTTTACACAA GCAGGTTTCA AGATATCTGC ATTACTTGA CGTATGCCAT 750
 CTGCCGTTGG TTATCAACCA ACATTGGCTA CAGAAATGGG ACAATTGCAA 800
 45 GAAAGAATTA CATCTACAAA TAAAGGTTCT GTAAC 835

2) INFORMATION FOR SEQ ID NO: 375

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

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5  GAGCACAATG AAGTTCCAGA AATTAACAAT GCCTTAGTTCG TAGACGTTGA      50
   AAGAGATGAA GGTACAGTAT CTCTTACATT AGAAGTGGCA TTACAACCTG      100
   GCGATGATGT CGTACGTACA ATTGCAATGG ATTCTACTGA TGGTGTAA      150
   CGTGGTACAG AAGTTTCGAGA TAGCGGAGAT AGCATCAGTG TTCCAGTTGG      200
   TGATGCTACG TTAGGACGTG TGTTTAATGT TCTTGGTGAT ACAATTGACT      250
10 TAGACGAGAA GCTTGATACT TCTGTCAAAC GTGATCCAAT TCATAGAGAA      300
   GCACCTGCAT TCGATCAATT ATCAACAAAA GTTGAATCT TAGAAACAGG      350
   TATTAAAGTA ATTGATTTAC TTGCACCATA TATTAAAGGT GGTAAAATCG      400
   GTTTATTTCG TGGCGCTGGT GTAGGTAAAA CAGTATTAAT TCAAGAATTA      450
   ATTAATAATA TAGCTCAAGA ACATGGTGGT ATTTCAGTAT TTGCCGGCGT      500
15 AGGTGAACGT ACGCGTGAAG GTAATGACTT ATACTACGAA ATGAGTGATA      550
   GTGGTGTTAT TAAGAAAACA GCTATGGTCT TCGGACAAAT GAATGAGCCA      600
   CCTGGTGCGC GTATGCGTGT TGCTTTATCA GGCTTAACAA TGGCTGAACA      650
   CTTCCGTGAT GTACAAGGAC AAGATGTTTT ACTATTTATT GATAACATAT      700
   TCAGATTTAC GCAAGCTGGT TCAGAAGTAT CAGCACTATT AGGTCGTATG      750
20 CCATCAGCCG TTGGTTATCA ACCTACCCTT GCTACTGAAA TGGGTCAATT      800
   ACAAGAACGT ATTACATCAA CAACTAAAGG ATCTGTAACG TC          842

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25 2) INFORMATION FOR SEQ ID NO: 376

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 842 bases
      (B) TYPE: Nucleic acid
30    (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Staphylococcus simulans
      (B) STRAIN: ATCC 27848

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

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40 TGATGAACCTG CCTAAGATTA ATAACGCATT AGTGCTAGAT GTACCTAAGA      50
   AAGATGGCAC GACTGAATCT CTTACATTAG AAGTAGCACT TGAATTAGGC      100
   GACGACGTAG TTAGAACTAT CGCCATGGAC TCTACAGACG GAATTAAACG      150
   TGGTGACGAC GTTAAAGACA CTGGTCGTCC AATCAGTGTA CCTGTCCGGTG      200
45 AAGATACGTT AGGAAGAGTA TTTAACGTTT TAGGTGATCC AATCGATAAT      250
   GATGGACCGA TTTCTGAATC AGTTCCACGT GAACCAATTC ATAGACAACC      300
   ACCTAAATTT GATGAATTAT CAACAAAAGT TGAACTACTT GAAACTGGTA      350
   TCAAAGTAGT AGACTTATTA GCACCATATA TCAAAGGTGG TAAAGTTGGT      400
   TTATTCCGTG GTGCCGGAGT AGGTAAACT GTATTAATCC AAGAATTAAT      450
50 TAATAACATC GCTCAAGAAC ACGGCGGTAT TTCAGTATTC GCAGGTGTTG      500
   GTGAACGTAC ACGTGAAGGT AACGACTTGT ACTTCGAAAT GAGCGACAGT      550
   GGTGTTATCA AGAAAACAGC GATGGTATTC GGACAAATGA ACGAACCACC      600
   TGGTGCACGT ATGCGTGTAG CTTTATCAGG TTTAACAATG GCTGAATACT      650
   TCCGTGATGT TAAAGGACAA GACGTTCTTT TATTCATCGA TAACATTTTC      700
55 CGCTTCACAC AAGCAGGTTT TGAGGTATCA GCATTGCTTG GCCGTATGCC      750
   ATCAGCCGTT GGTTACCAAC CAACATTGGC AACAGAAATG GGTCAATTAC      800
   AAGAACGTAT CACTTCTACA ATGAAAGGTT CTATCACATC TA          842

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60

2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA 50
 AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG 100
 ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA 150
 20 GGCATGGATG TTAAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCGA 200
 TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG 250
 AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA 300
 CCAGGTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT 350
 TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC 400
 25 TATTCGGTGG TGCCGGAGTA GGTAAAACCG TTTTAATCCA AGAATTAATT 450
 AACAATATTG CACAAGAACA TGGTGGTATT TCAGTATTCG CGGGTGTAGG 500
 TGAACGTA CTGTAAGGTA ATGATTTATA CTATGAAATG AGTGATAGTG 550
 GTGTAATTAA GAAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACCT 600
 GGCGCACGTA TGCCTGTAGC TTTATCTGGT TTAACATATG CTGAATACTT 650
 30 CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCAATCGAT AATATTTTCA 700
 GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT 750
 TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA 800
 AGAACGAATT ACATCTACAA ATAAAGGTTC TGTAACATCT A 841

35

2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA 50
 CAAAGACAGT GAGAAAAAAC ATAAATCGT TCTTGAAGTA GCTCTTGAAC 100
 55 TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAATCAAC TGATGGTTTG 150
 ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT 200
 TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCTTGGT GATGCTATCG 250
 ATCTTGAAGA ACCATTTGGA GAAGATGCAG AACGTCACCC CATTATAAG 300
 AGTGCCCAA CTTTTGATGA ATTATCAACG TCAACAGAAA TCCTTGAAAC 350
 60 AGGGATTAAA GTTATCGACC TACTTGCCCC TTACTTAAAA GGAGGGAAGG 400

TTGGACTTTT CGGTGGTGCC GGAGTTGGTA AGACCGTTCT TATCCAAGAG 450
 TTGATTCATA ACATTGCTCA AGAGCATGGT GGTATTTTCAG TATTTACCGG 500
 AGTTGGTGAA CGTACACGTG AAGGTAATGA CCTCTATTGG GAAATGAAAG 550
 AATCAGGCGT TATTGAAAAA ACAGCTATGG TATTTGGTCA GATGAATGAG 600
 5 CCACCTGGTG CACGTATGCG TGTAGCCCTT ACTGGTTTGA CAATCGCTGA 650
 ATATTTCCGT GATGTTGAAG GACAGGACGT GCTTCTCTTT ATTGATAACA 700
 TTTTTCGTTT CACACAAGCA GGTCTGAAG TTTCAGCTCT TCTTGGACGT 750
 ATGCCATCAG CCGTTGGTTA TCAACCAACC TTGGCAACTG AAATGGGTCA 800
 ATTGCAAGAA CGTATCACGT CAACTAAAAA AGGTTCTGTT ACATCA 846
 10

2) INFORMATION FOR SEQ ID NO: 379

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 25 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
 30 AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTA CTCTTGAAGT 100
 TGGTGACGGC CTCGTTCTGA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
 CCTTGAAGAG CTTTTGTCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
 35 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA 350
 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 40 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 45 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCAA 846

2) INFORMATION FOR SEQ ID NO: 380

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Streptococcus agalactiae*

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

```

5  TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
   GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
10 TCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
   GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
   TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT      500
15 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
   CTTCCGTTTC ACACAAGCTG GGTCAGAAAGT GTCAGCGCTT TTAGGTCGTA      750
20 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCCTGTTA CCTCAA      845

```

25 2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Streptococcus agalactiae
(B) STRAIN: ATCC 12973

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

```

40 TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GTGCAATTAG TGTGCCGGTT      200
45 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
   CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC ATTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA      350
   GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
50 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT      500
   GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
55 CTTCCGTTTC ACACAAGCTG GGTCAGAAAGT GTCAGCGCTT TTAGGTCGTA      750
   TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCCTGTTA CCTCA      845

```

60

2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

```

5      TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
      AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
      TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
20     CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
      GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
      CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
      AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
      GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
25     TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACC GTTCTT ATTCAAGAAT      450
      TAATCCACAA CATCGCCCAA GAACATGGTG GTATTT CAGT ATTTACTGGT      500
      GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
      ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
      CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
30     TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
      CTTCCGTTTC ACACAAGCTG GGTGAGAAGT GTCAGCGCTT TTAGGTCGTA      750
      TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
      TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA      845

```

35

2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ss1073

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

```

55     TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
      AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
      TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
      CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
      GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
      CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
      AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
60     GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400

```

TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCACT ATTTACTGGT 500
 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
 ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
 5 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
 CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
 TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCCTGTTA CATCA 845
 10

2) INFORMATION FOR SEQ ID NO: 384

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus dysgalactiae*
 25 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

TTGCTAGTGG GGACAAACTT CCAGAGATTA ATAATGCATT GATTGTTTAT 50
 30 AAAGATAGTG ATAAAAAGCA AAAAATCGTC CTTGAAGTTG CTCTGGAAGT 100
 TGGTGACGGT ATGGTGCGAA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
 CACGTGGGTT AGAAGTTCTT GACACTGGTC GTGCGATTAG TGTACCAGTA 200
 GGTAAAGAAA CTTTGGGACG CGTCTTTAAT GACTTTGGAG AAACCATTGA 250
 CTTGGAAGAA CCATTTGCAG AAGACGTTGA CCGTCAGCCA ATCCATAAAA 300
 35 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT TCTTGAAACT 350
 GGTATCAAGG TAATTGACCT TCTTGCCCCCT TACCTTAAAG GTGGTAAAGT 400
 TGGACTTTTC GGGGGTGCCG GAGTTGGTAA GACTGTCCTT ATCCAAGAAT 450
 TAATCCACAA TATCGCCCAA GAACACGGAG GTATTTCACT ATTTACCGGT 500
 GTTGGTGAGC GAACACGTGA AGGAAATGAC CTTTACTGGG AAATGAAAGA 550
 40 ATCAGGCGTT ATTGAGAAAA CTGCCATGGT TTTTGGTCAG ATGAATGAGC 600
 CGCCTGGGGC ACGTATGCGT GTAGCCCTTA CTGGTTTAAC CATTGCTGAG 650
 TATTTCCGTG ATGTAGAAGG CCAAGATGTT TTGCTCTTTA TTGATAATAT 700
 CTTCCGTTTC ACTCAGGCAG GTTCAGAAGT ATCAGCCCTC TTAGGCCGTA 750
 TGCCTTCTGC TGTTGGTTAC CAACCGACCC TTGCTACTGA AATGGGACAA 800
 45 TTGCAAGAAC GTATTACGTC AACTCAAAAA GGATCTGTTA CTTCT 845

2) INFORMATION FOR SEQ ID NO: 385

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

```

5  TTGCGAGTGG GGACAAACTA CCAGAGATTA ATAATGCGTT GATAGTTTAT      50
   AAAGATGGCG ATAAAAAGCA AAAAATCGTT CTCGAGGTTG CCCTAGAGCT      100
   TGGAGACGGT ATGGTACGTA CAATTGCTAT GGAATCAACC GATGGGCTTA      150
   CACGTGGATT AGAGGTTCTT GATACTGGTC GTGCCATTAG TGTACCAGTT      200
   GGTAAAGAGA CTCTAGGTCG TGTTTTCAAC GTTCTTGGTG AAACCATCGA      250
10  CCTAGAAGCA CCATTTGCAG ATGATGTTAA TCGTGAACCG ATCCATAAAA      300
   AAGCACCAGC CTTTGTATGAA TTGTCAACAT CATCAGAAAT TCTTGAAACA      350
   GGTATCAAGG TTATTGACCT GCTTGCCCTT TACTTAAAGG GTGGTAAGGT      400
   CGGTCTTTTC GGTGGTGCCG GAGTTGGTAA AACCGTTCTT ATCCAAGAAT      450
   TAATCCACAA TATCGCTCAA GAGCATGGTG GGATCTCGGT ATTTACCGGT      500
15  GTTGGTGAGC GTACGCGTGA AGGAAATGAC CTTTACTGGG AAATGAAGGA      550
   ATCAGGCGTT ATTGAAAAAA CAGCCATGGT TTTTGGTCAG ATGAATGAAC      600
   CACCAGGAGC CCGTATGCGT GTTGCCCTGA CCGGCTTGAC AATTGCTGAA      650
   TATTTCCGCG ATGTTGAAGG CCAAGACGTC CTGCTCTTCA TTGACAATAT      700
   TTTCCGCTTT ACTCAAGCAG GCTCAGAGGT ATCAGCCCTT CTAGGTCGTA      750
20  TGCCTTCAGC CGTTGGTTAC CAGCCAACAC TTGCCACTGA AATGGGACAA      800
   TTGCAAGAGC GTATCACCTC AACGAAAAAA GGCTCTGTTA CCTCTA      846

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25 2) INFORMATION FOR SEQ ID NO: 386

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Streptococcus anginosus
(B) STRAIN: ATCC 27335

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

```

40  TTGCAGCTGG TGATAAATTA CCTGAGATAA ATAATGCACT TGTAGTCTAT      50
   AAAAATGACG AAAATAAATC AAAAATCGTC CTTGAAGTAG CTCTTGAGCT      100
   TGGTGATGGA GTGGTTCGAA CTATTGCCAT GGAATCCACT GATGGGTTGA      150
   CTCGTGGCAT GGAAGTTCTA GATACTGGTC GACCAATTTT TGTTCCAGTT      200
45  GGGAAAGAAA CACTTGGTGCG CGTCTTTAAC GTTTTAGGCG ATACCATTGA      250
   TTTGGATACT CCATTGCGCG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCTCCAAC TTTTGTATGAG TTATCTACTT CATCAGAAAT CTTAGAAACA      350
   GGAATAAAGG TTATTGACCT TTTAGCCCCC TACCTCAAAG GTGGGAAAGT      400
   CGGCCTCTTC GGTGGTGCTG GCGTTGGGAA AACTGTCTTG ATTCAAGAGT      450
50  TGATTCATAA TATCGCCCAA GAACACGGCG GGATTTCACT CTTTACTGGT      500
   GTTGGGGAAC GAACTCGTGA AGGGAATGAC CTGTACTGGG AAATGAAAGA      550
   ATCTGGTGTT ATCGAAAAGA CGGCTATGGT CTTTGGGCAA ATGAATGAAC      600
   CGCCTGGAGC ACGTATGCGT GTAGCTTTGA CTGGGTTAAC GATTGCAGAG      650
   TATTTCCGTG ATGTGGAAGG TCAAGATGTT CTTTGTGTTA TTGATAATAT      700
55  TTTCCGTTTC ACTCAAGCTG GTTCTGAAGT GTCAGCCCTT CTTGGTCGTA      750
   TGCCATCAGC TGTTGGTTAC CAACCAACCT TGGCTACTGA AATGGGGCAA      800
   TTACAAGAAC GTATTACATC AACGAAAAAA GGTTCTGTTA CCTCAA      846

```

60

2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

```

GCAGCTGGTG ATAAACTTCC TGAGATTAAAC AATGCATTGG TCGTTTATAC      50
TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG      100
GAGAAGGTGT GGTTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT      150
CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG      200
TAAAGATAACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT      250
TGGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA      300
GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG      350
GATTAAAGTT ATCGACTTGC TAGCCCCTTA CCTTAAGGGT GGTAAGTTCG      400
GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG      450
ATTCAACAAC TTGCCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT      500
TGGTGAACGT ACACGTGAAG GTAATGACCT TTACTGGGAA ATGAAAGAAT      550
CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA      600
CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA      650
CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT      700
TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG      750
CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT      800
GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT              843

```

2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

```

TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT      50
AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAGT      100
TGGTGATGGC GTTGACGGA CCATTGCCAT GGAATCAACG GATGGATTGA      150
CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCCAGTC      200
GGTAAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA      250
CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA      300
AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA      350
GGGATTAAGG TTATCGACCT CTTAGCACCT TATCTAAAAG GTGGTAAGGT      400

```

TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCTT ATCCAAGAAT 450
 TGATTCACAA TATTGCCCAA GAACACGGTG GTATCTCTGT ATTTACCGGA 500
 GTTGGCGAGC GTACCCGTGA AGGGAACGAT CTTTACTGGG AAATGAAAGA 550
 ATCAGGTGTT ATTGAAAAAA CGGCCATGGT ATTTGGTCAG ATGAATGAGC 600
 5 CACCAGGAGC CCGTATGCGT GTTGCTCTTA CTGGTTTGAC TATTGCGGAA 650
 TACTTCCGTG ATGTGGAAGG GCAGGATGTT CTTCTGTTCA TCGATAATAT 700
 CTTCCGTTTC ACACAGGCTG GTTCAGAAGT GTCTGCCCTC TTGGGTCGTA 750
 TGCCATCAGC CGTTGGTTAT CAGCCAACAC TTGCGACGGA GATGGGACAA 800
 TTGCAGGAGC GTATTACCTC AACCAAGAAG GGTCTCTGTTA C 841
 10

2) INFORMATION FOR SEQ ID NO: 389

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus uberis*
 25 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

GCAAACGGTG AAAAATTACC AGAGATTAAT AATGCATTGA TAGTTTATAA 50
 30 AGGTAGCGAT AAAAACAACAA AGATTGTTCT TGAAGTTGCT TTGGAACCTG 100
 GGGACGGAAT GGTTCGTACA ATCGCTATGG AATCAACTGA TGGGCTTACA 150
 CGTGGAATTAG AAGTTT TAGA TACTGGCCGT GCCATTAGTG TACCAGTCGG 200
 AAAAGAAACT TTGGGTCGTG TTTTCAATGT GCTTGGTGAA ACCATTGATT 250
 TGGATGAACC ATTTGCCGCT GATGCTGCAA GAGAACCCAT CCATAAAAAA 300
 35 GCCCCAGCAT TTGATGAACT ATCAACGTCT TCAGAAATTC TTGAAACCGG 350
 AATAAAAGTT ATTGACTTAT TAGCCCCCTTA TCTCAAAGGT GGTAAAGTTG 400
 GTTTATTTGG TGGTGCCGGA GTAGGTAAAA CGGTTTAAAT TCAAGAATTA 450
 ATTCATAATA TTGCACAAGA ACATGGTGGT ATTTCAGTAT TTACCGGTGT 500
 TGGTGAAAGA ACTCGTGAAG GTAATGACCT TTATTGGGAA ATGAAAGAAT 550
 40 CTGGCGTTAT TGAAAAACA GCCATGGTAT TTGGACAAAT GAACGAACCA 600
 CCAGGAGCAG GTATGCGCGT TGCTTTAACA GGTTTAACCA TTGCTGAATA 650
 TTTCCGGGAT GTTGAAGGTC AAGATGTTTT GCTCTTTATT GACAACATTT 700
 TCCGTTTCAC GCAAGCTGGT TCAGAAAGTTT CAGCCCTATT GGGTCGTATG 750
 CCTTCAGCGG TAGGATACCA ACCAACACTT GCTACCGAAA TGGGACAATT 800
 45 GCAAGAAAGA ATTACCTCAA CTAACAAGGG ATCTGTTACT TCTA 844

2) INFORMATION FOR SEQ ID NO: 390

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Tatumella ptyseos*
 233

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

```

5  TTCCCTCAGG ACGCTGTACC ACAGGTGTAC AACGCTCTTG AGGTTGAAAA    50
   TGGTGATACC CGTCTGGTGC TGGAAAGTTCA GCAGCAGCTG GCGGGTGGTG    100
   TCGTTTCGTAC GATTGCAATG GGAACCTCTG ACGGCCTGAA ACGTGGCCTT    150
   AAGGTGACCG ATCTGCAAAA ACCGATTTCAG GTACCGGTCTG GTAAAGCGAC    200
   GCTGGGCCGT ATCATGAACG TACTGGGTCA GCCAATCGAT ATGAAAGGCG    250
10  ACCTGAAGAA CGAAGATGGT AGCAATGTTG AGGTGAACTC TATTCACCGT    300
   GCAGCGCCAA GCTACGAAGA ACTGGCTAAC TCTACTGAGC TGCTGGAAAC    350
   GGGTATCAAG GTTATCGACC TGATCTGTCC GTTTGCAAAA GCGGGTAAAG    400
   TGGGTCTGTT CGGTGGTGCG GGTGTAGGTA AGACCGTCAA CATGATGGAA    450
   CTGATCCGTA ACATCGCTAT CGAGCACTCT GGTTACTCTG TATTTGCAGG    500
15  GGTGGGTGAG CGTACCCGTG AAGGTAACGA CTTCTACCAC GAAATGACCG    550
   AGTCTAACGT TCTGGATAAA GTTGCTCTGG TTTATGGCCA GATGAACGAG    600
   CCACCAGGAA ACCGTCTGCG CGTTGCGCTG ACCGGTCTGA CTATGGCTGA    650
   AAAATTCCGT GACGAAGGCC GTGACGTACT GCTGTTTCGTT GATAACATCT    700
   ATCGTTATAC CCTGGCCGGT ACTGAAGTTT CAGCACTGCT GGGTCGTATG    750
20  CCTTCTGCGG TAGGTTATCA GCCAACACTG GCCGAAGAAA TGGGTGTTCT    800
   TCAGGAACGT ATCACGTCAA CCAAACCGG TTCAATCACT TCCGTA        896

```

25 2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 829 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Trabulsiella guamensis
   (B) STRAIN: ATCC 49490

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

```

40  TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTTATGAA    50
   TGGTAGTGAG CGTCTGGTGC TGGAAAGTTCA GCAGCAGCTC GGTGGTGGTA    100
   TCGTACGTAC TATCGCCATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG    150
   GATGTAAAAG ATCTCGAGCA TCCGATCGAA GTCCCGGTAG GTAAAGCAAC    200
45  GCTGGGTCGT ATCATGAACG TGCTGGGTCA GCCGATCGAT ATGAAAGGCG    250
   ACATCGGCGA AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCGTCCTAC    300
   GAAGAGCTGT CCAGCTCTCA GGAAGTGTCT GAAACCGGCA TCAAAGTTAT    350
   CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT    400
   GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTGAT TCGTAACATC    450
50  GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAACGTAC    500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTCTGG    550
   ACAAAGTATC CCTGGTGTAT GGACAGATGA ACGAGCCGCC GGGAAACCGT    600
   CTGCGCGTTG CACTGACCGG TCTGACCATG GCTGAGAAGT TCCGTGACGA    650
   AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTACCGT TACACCCTGG    700
55  CGGGTACTGA AGTATCTGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT    750
   TACCAGCCGA CCCTGGCGGA AGAGATGGGT GTTCTTCAGG AACGTATCAC    800
   CTCAACCAAA ACCGGTCTA TCACCTCCG        829

```

60

2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
 (B) STRAIN: ATCC 43970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

```

CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG      50
AAGGCACAGC TCAGAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT      100
GGTGTTGTTC GTTGATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG      150
GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT      200
CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA      250
GGTCCTATCG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC      300
TTACGAAGAG CTTGCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG      350
TAATGGATCT GATTGTCCG TTCGCTAAGG GCGGTAAAGT CCGTCTGTTC      400
GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTCGTAA      450
TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC      500
GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT      550
CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA      600
CCGTCTGCGC GTTGCACTGA CCGGCTTGAC CATGGCGGAG AAATTCGGTG      650
ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATACC      700
CTGGCCCGTA CAGAGGTATC TGCCTGCTA GGTCGTATGC CATCAGCGGT      750
AGGCTATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA      800
TCACTTCCAC CAAGACGGGT TCAATCACCT CCGTA                        835

```

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

```

GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA      50
GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CGGTGGTGTT GTTCGTTGTA      100
TCGCAATGGG CTCTCCGAT GGTCTGAGCC GTGGGTGAA AGTCATCAAC      150
CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT      200
CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGCGAAG      250
AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC      300
AGCTCGCAAG ACTTGTTAGA AACCGGTATC AAGGTAATGG ACTTGATTTG      350
TCCGTTGCTG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400

```

GTAAAACGGT AAACATGATG GAGCTTATTC GTAACATTGC GATTGAGCAC 450
 TCAGGTTATT CCGTATTTGC TGGCGTGGGT GAGCGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT 550
 TGGTTTATGG CCAAATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
 5 CTGACCGGCT TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
 ATTGCTGTTC ATCGATAACA TCTATCGCTA TACCTTAGCC GGTACGGAAG 700
 TTTCCGCACT GCTGGGTCGT ATGCCATCTG CCGTAGGTTA CCAGCCAACG 750
 CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACCAAGAC 800
 GGGTTCAATC AC 812
 10

2) INFORMATION FOR SEQ ID NO: 394

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia frederiksenii*
 25 (B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

AAAGTGACAC ACGCCCTTGA GGTGAAGGT ACTGCTGAGA AGTTAGTACT 50
 30 GGAAGTTCAG CAACAGCTGG GCGGTGGTGT TGCTCGTTGT ATCGCCATGG 100
 GCTCTTCCGA TGGTTTGAGC CGCGGGTTGA AAGTTGTCAA CCTGGAACAC 150
 CCAATTGAAG TACCGGTTGG TAAATCAACT CTGGGCCGTA TCATGAACGT 200
 ATTGGGTGAC CCAATCGACA TGAAAGGTCC TATCGGTGAA GAAGAGCGTT 250
 GGGCAATCCA CCGCGAAGCG CCTTCTTACG AAGAGCTTGC CAGCTCGCAA 300
 35 GATCTGTAG AAACCGGTAT CAAGGTAATG GATCTGATTT GCCCGTTTCGC 350
 TAAAGGCGGT AAAGTCGGTC TGTTCCGGTGG TGCGGGTGTA GGTAACCGG 400
 TAAACATGAT GGAGCTGATC CGTAATATCG CGATCGAGCA CTCAGGTTAT 450
 TCCGTATTTG CGGGTGTTGG TGAACGTACC CGTGAGGGTA ACGACTTCTA 500
 CCACGAGATG ACTGACTCCA ACGTTCTGGA CAAAGTATCC TTGGTTTATG 550
 40 GCCAGATGAA TGAGCCACCA GGTAACCGTC TTCGCGTTGC ACTGACCGGT 600
 CTGACCATGG CGGAGAAATT CCGTGATGAA GGTGCTGACG TATTGCTGTT 650
 CATCGATAAC ATCTATCGTT ATACCTTGGC CGGTACGGAA GTATCCGCAC 700
 TGCTGGGTCTG TATGCCATCT GCGGTAGGCT ATCAGCCAAC GCTGGCAGAA 750
 GAGATGGGTG TGTTGCAGGA ACGTATTACT TCCACCAAGA CGGGTTCAAT 800
 45 CA 802

2) INFORMATION FOR SEQ ID NO: 395

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Yersinia intermedia*
 236

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

```

5  GCTGTACCAA GAGTGTACAA CGCCCTTGAG GTTGAAGGCA CTGCTGAGAA      50
   GCTGGTGCTG GAAGTTCAGC AACAGCTAGG CGGTGGTGTT GTTCGTTGTA      100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GCGGGTTGAA AGTCATCAAC      150
   CTGGAACACC CAATTGAAGT GCCGGTTGGT AAATCAACTC TGGGCCGTAT      200
   CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGTGAAG      250
10  AAGAGCGTTG GGCAATCCAC CGCGAAGCGC CTTCTTACGA AGAGCTTGCC      300
   AGCTCACAAG ATTTGTTAGA AACC GGATC AAGTAATGG ACTTGATTTG      350
   CCCGTTTCGT AAGGGCGGTA AAGTGGGTCT GTTCGGTGTT GCGGGTGTAG      400
   GTAAACAGT AAACATGATG GAGCTTATTC GTAACATCGC GATTGAGCAC      450
   TCAGGTTATT CTGTATTTGC TGGTGTGGGT GAGCGTACTC GTGAGGGTAA      500
15  CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT      550
   TGGTGTATGG CCAGATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA      600
   CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT      650
   ACTGTTGTTT ATCGATAACA TCTATCGCTA TACCTTGGCC GGTACGGAAG      700
   TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACG      750
20  CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACGT CCACCAAGAC      800
   GGGTTC

```

25 2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Yersinia pseudotuberculosis
(B) STRAIN: ATCC 29833

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

```

40  GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTAGAAGGCA CAACTGAAAA      50
   GTTAGTGCTG GAAGTTCAGC AACAGTTGGG CGGTGGTGTT GTTCGTTGTA      100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTTGAA AGTAACCAAC      150
   CTGGAACACC CGATCGAAGT ACCGGTTGGT AAAGCGACCC TTGGCCGTAT      200
45  CATGAACGTA TTGGGTGAAC CAATCGACAT GAAAGGTCCT ATCGGTGAAG      250
   AAGAGCGTTG GGCAATCCAT CGCGAAGCGC CTTCTTATGA AGAGCTTGCT      300
   AGCTCACAAG ATCTGTTAGA AACC GGATC AAGGTTATGG ACCTGATTTG      350
   TCCGTTTGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGTT GCGGGTGTAG      400
   GTAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
50  TCTGGGTATT CTGTATTTGC CGGTGTAGGT GAGCGTACCC GTGAGGGTAA      500
   TGA CTTCTAC CATGAAATGA CTGACTCCAA CGTTTTGGAC AAAGTATCCT      550
   TGGTTTACGG CCAGATGAAT GAGCCACCAG GTAACCGTCT ACGCGTTGCA      600
   CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT      650
   ACTGCTGTTT ATCGATAATA TCTATCGTTA TACCCTAGCT GGTACGGAAG      700
55  TATCCGCATT GCTGGGTCGT ATGCCATCAG CGGTAGGTTA TCAGCCAACA      750
   CTGGCTGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACTAAGAC      800
   GGGTTC

```

60

2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

```

TTCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG      50
TGCAGCTGAG AAGCTTGTGC TGGAAGTTCA GCAGCAGCTG GGCGGTGGTG      100
TTGTTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG      150
AAAGTTATCA ACCTGGAACA CCAATTGAA GTGCCAGTTG GTAAATCAAC      200
TCTGGGCCGT ATCATGAACG TATTGGGTGA CCAATCGAC ATGAAAGGCC      250
CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC      300
GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT      350
GGATCTGATT TGTCCGTTCG CTAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
GTGCGGGTGT TGGTAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC      450
GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC      500
TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG      550
ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT      600
CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA      650
AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG      700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGC      750
TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC      800
TTCCACTAAG ACGGGTTCAA TCACCTCCG      829

```

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

```

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG      50
AAACTGGTGC TGGAAGCTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC      100
TATCGCCATG GGTTCCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG      150
ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCCGT      200
ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA      250
AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT      300
CCAGCTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTAAT GGATCTGATC      350
TGCCCGTTTCG CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT      400

```

AGGTAAACT GTAAACATGA TGGAGCTTAT CCGTAACATC GCGATTGAGC 450
 ACTCCGGTTA CTCTGTGTTT GCAGGCGTGG GTGAACGTAC TCGTGAGGGT 500
 AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG ATAAAGTATC 550
 CCTGGTGTAC GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
 5 CGCTGACCGG CCTGACCATG GCTGAGAAAT TCCGTGACGA AGGCCGTGAC 650
 GTTCTGCTGT TCGTCGATAA CATCTACCGT TATACCCTGG CCGGTACGGA 700
 AGTATCCGCA CTGCTGGGTC GTATGCCTTC TCGCGTAGGT TATCAGCCAA 750
 CTCTGGCGGA AGAGATGGGT GTTCTTCAGG AACGTATCAC CTCTACCAA 800
 ACCGGTTCTA TCACCTCCG 819
 10

2) INFORMATION FOR SEQ ID NO: 399

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1097 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yarrowia lipolytica*
 25 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

AAGCTTAAGG CTGAGCGAGA GCGAGGTATC ACCATTGATA TCGCTCTCTG 50
 30 GAAGTTCCAG ACCCCTAAGT ACTACGTCAC CGTTATTGAT GCTCCCGGTC 100
 ACCGAGATTT CATCAAGAAC ATGATTACCG GTACTTCCCA GGCTGACTGC 150
 GCCATCCTCA TCATTGCTGG TGGTGTGGT GAGTTCGAGG CTGGTATCTC 200
 CAAGGATGGT CAGACCCGAG AGCACGCCCT GCTCGCTTTC ACCCTCGGTG 250
 TTAAGCAGCT CATTGTTGCT ATCAACAAGA TGGACTCCGT CAAGTGGTCT 300
 35 CAGGATCGAT ACCTCGAGAT TTGCAAGGAG ACTGCCAACT TCGTCAAGAA 350
 GGTGCGTTAC AACCCCAAGG CTGTCCCCTT CGTCCCATT TCCGGATGGA 400
 ACGGTGACAA CATGATCGAG CCCTCTACCA ACTGTGACTG GTACAAGGGA 450
 TGGACCAAGG AGACCAAGGC CGGCGAGATC AAGGGTAAGA CCTCCTCGA 500
 GGCCATTGAT GCCATTGAGC CCCCCGTGCG ACCCCACGAC AAGCCCCTCC 550
 40 GACTTCCCCT CCAGGATGTC TACAAGATCG GTGGTATCGG CACAGTGCCC 600
 GTTGGCCGAG TCGAGACCGG TGTTATCAAG GCCGGTATGG KTGTTACCTT 650
 CGTCCCCGCC AACGTGACCA CTGAGGTCAA GTCTGTGAG ATGCACCACG 700
 AGATCCTCCC CGATGGAGGT TTCCCCGTG ACAACGTCGG TTCAACGTC 750
 AAGAACGTTT CCGTCAAGGA TATCCGACGA GGTAACGTTG CTGGTGA CTC 800
 45 CAAGAACGAC CCCCCCAAGG GCTGCGACTC TTTCAACGCT CAGGTCATTG 850
 TTCTTAACCA CCCC GGTCAG ATCGGTGCTG GTTACGCTCC CGTCCTTGAT 900
 TGCCACACTG CCCACATTGC TTGCAAGTTC GACACCCTGA TCGAGAAGAT 950
 CGACCGACGA ACCGGTAAGA AGATGGAGGA CTCCCCCAAG TTCATCAAGT 1000
 CTGGTGATGC TGCCATTGTC AAGATGGTTC CCTCCAAGCC CATGTGTGTC 1050
 50 GAGGCCTTCA CTGAGTACCC CCCTCTTGGT CGATTGCGCC TCCGAGA 1097

2) INFORMATION FOR SEQ ID NO: 400

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1233 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

```

10 CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT 50
   GGAAGTTCGA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCCTGGC 100
   CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG 150
   CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTTCGAA GCTGGTATCT 200
   CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT 250
15 GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC 300
   TGAGGCCCCG TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA 350
   AGATTGGTTT CAACCCCAAG TCCGTTTCCT TCGTCCCTAT CTCTGGCTGG 400
   AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAGGG 450
   ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG 500
20 AAGCCATTGA CAACATTGAT CCCCCTGTTT GCCTTCCGA CAAGCCCCTT 550
   CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC 600
   TGTCGGTCGT GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTACCT 650
   TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC 700
   GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGTT TCAACGTCAA 750
25 GAACGTTTCC GTCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA 800
   AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC 850
   TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGGATTG 900
   CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG 950
   ATYGTCTGTC CGGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC 1000
30 TTAATCTYTG GATTTTGCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT 1050
   ACTTTTTGAT CATTTGCTAA TCCAAACCCT TTCCATTTYA TTGAAAACAG 1100
   GTAAGAAGTT GGAAGACTCC CCAAAGTTCG TCAAGWSYGG TGACTCTGCY 1150
   ATCGTCAAGA TGGTTCCTTC CAAGCCCATG TCGGTTGAAG CCTACACTGA 1200
   ATATCCTCCT CTTGGTCGTT TCGCTGTCCG TGA 1233
35

```

2) INFORMATION FOR SEQ ID NO: 401

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

```

55 CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT 50
   GGAAGTTCGA GACTCCCAAG GTTAGTACCC CTCTGCCTAC TACATCAAGT 100
   TCTTTACAAT GCTAACATGT TGTACTCAGT ACTATGTCAC CGTCATTGAC 150
   GCCCCCGGTC ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA 200
   GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG 250
   CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC 300
60 ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC 350

```

	CAAGTGGTCC	GAGGAGCGTT	ACCAGGAGAT	CATCAAGGAG	ACCTCCAAC T'	400
	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCC	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
10	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCACAA	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
15	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCACTGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

20

2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
40	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCACCCTC	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
45	AACTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCGG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
50	TCGGTACTGT	GCCCGTCGGT	CGTGTCGAGA	CTGGTGTCAT	CAAGCCTGGT	700
	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
55	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
60	GTCCGTGACG	TAAGTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTCACAT	1200

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250
TTTTTGCC TG CAAGTTCTCT ATAGCTAACA TGA 1283

5

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1103 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: DAL95

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
GACTCCCAAG TATGAGGTCA CTGTATCGG TAAGCTCGAC TCGCCCCGAT 100
ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT 150
25 GACTTCATCA AGAATATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
CCTCATCATT GCCTCCGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCTG 400
30 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT 450
GACAACATGC TTGAGCCCTC CTCCAACCTG CCCTGGTACA AGGGATGGGA 500
GAAGGAGACC AAGGCCGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550
TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCTG 650
35 CCGTGTCTGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC 700
CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTTCAACG TCAAGAACGT 800
TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
40 CACCCCGGTC AGGTCGGCGC TGGTACGCC CCCGTCCTCG ACTGCCACAC 950
TGCCCAATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
GTACCGGCAA GTCTGTTGAG AACAACCCCA AGTTCATCAA GTCCGCTGAT 1050
GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
CAC 1103

45

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1149 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
5	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
10	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
15	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTGAGGA	CCGGTATCAT	CAAGCCCGGC	ATGGTCTGTA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
20	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
25	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

30 2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTTCATCA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCAAC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
50	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGCTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAAC TTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCCTTTCGT	CCCCATCTCC	450
55	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATTGCCCCT	GGTATGGTCG	700
60	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750

	CACCACCAGC	AGCTCAAGGA	AGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	800
	CGTCAAGAAC	GTTTCCGTCA	AGGAGGTTCCG	CCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCT	CTTGGCTGTG	AGAGCTTCAC	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCCGG	TCAGGTCGGC	GCTGGTTACG	CTCCCGTCTT	950
5	GGACTGCCAC	ACTGCTCACA	TTGCTTGCAA	GTTTCGCTGAG	CTCCTTGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AATCTTCCCC	CAAGTTCATC	1050
	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	ATTCCCTCCA	AGCCCATGTG	1100
	TGTTGAGGCT	TTCACTGACT	ACCCCCCTCT	TGGTCGTTTC	GCCGTCCGCG	1150
	A					1151

10

2) INFORMATION FOR SEQ ID NO: 406

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1093 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*

25 (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

	GCTTAAAGCT	GAACGTGAAC	GTGGTATCAC	CATTGATATC	GCTCTCTGGA	50
30	AGTTCGAAAC	TCCTAAGTAC	TACGTTACTG	TTATTGATGC	TCCAGGTCAC	100
	CGTGATTTCA	TCAAGAACAT	GATTACTGGT	ACTTCCCAAG	CCGATTGCGC	150
	CATTCTTATC	ATTGCTGCCG	GTGTCGGTGA	ATTCTGAAGCT	GGTATCTCCA	200
	AGGAAGGTCA	AACCAGAGAA	CACGCTCTTC	TCGCTTTCAC	CCTTGGTGTC	250
	AGACAACCTA	TCATTGCCAT	CAACAAGATG	GACTCTGTCA	AGTGGGACCA	300
35	AAAGAGATAC	GAAGAAATCG	TCAAGGAGGC	TTCCAACCTC	GTCAAGAAGG	350
	TTGGTTACAA	CCCCAAGTCT	GTTCCATTCG	TTCTATCTC	TGGTTGGAAC	400
	GGTGACAACA	TGTTGGAACC	TACCACCAAC	GCCCCATGGT	ACAAGGGATG	450
	GACCAAGGAA	ACCAAGGCTG	GTGCCACTAA	GGGTATGACT	CTTATTGAAG	500
	CCATTGACGC	CATTGAACCA	CCAGTAAGAC	CATCCGACAA	GCCACTCCGT	550
40	CTCCCACTCC	AAGATGTTTA	CAAGATTGGT	GGTATCGGAA	CTGTGCCAGT	600
	CGGCCGTGTC	GAAACCGGTA	TCATCAAGGC	CGGTATGGTC	GTTACCTTTG	650
	CTCCACCAAT	GGTCACAACT	GAAGTTAAGT	CCGTTGAAAT	GCACCACGAA	700
	CAACTTGCTC	AAGGTAACCC	AGGTGACAAC	GTTGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTT	AAGGAAATCA	GACGTGGTAA	CGTCTGTGGT	GACTCCAAGA	800
45	ACGATCCACC	AAAGGGCTGC	GAATCTTTCA	ACGCTCAAGT	TATCGTCTTG	850
	AACCACCCTG	GTCAAATCTC	TGCTGGTTAC	TCTCCAGTTC	TCGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	GATTCGACGA	ACTCCTTGAA	AAGATCGACC	950
	GTCGTTCTGG	TAAGAAGATT	GAAGACTCTC	CAAAGTTTGT	CAAGTCTGGT	1000
	GATGCCGCTA	TCGTCAAGAT	GATCCCAACC	AAGCCAATGT	GCGTTGAAAC	1050
50	CTTCACTGAA	TACCCACCAC	TTGGTCGTTT	CGCCGTCCGT	GAT	1093

2) INFORMATION FOR SEQ ID NO: 407

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 10231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

```

10 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
15 TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA      300
   ATGGGACAAA AACAGATTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTYGT TCCAATCTCT      400
   GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
   CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
20 TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAAGTGGTAT CATCAAAGCC GGTATGGTTG      650
   TTACTTTTCG CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
25 CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCOA TGCCCAAGTC      850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
   GGATTGTCAC ACTGCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA      950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC     1000
30 AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
   TGTGAAGCT TCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
   A                                                                1101

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35

2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1089 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

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   GAAGGCTGAA AGAGAAAGAG GTATCACCAT TGATATCGCT TTGTGGAAAT      50
   TCGAAACTCC AAAATACCAC GTTACCGTCA TTGATGCTCC AGGTCACAGA      100
   GATTTTCATCA AGAATATGAT CACTGGTACT TCTCAAGCTG ATTGTGCTAT      150
55 TTTGATTATT GCTGGTGGTA CTGGTGAATT CGAAGCCGGT ATTTCTAAGG      200
   ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACTTT GGGTGTCAAA      250
   CAATTGATTG TTGCTGTCAA CAAGATGGAC TCTGTCAAAT GGGACAAAAA      300
   CAGATTTGAA GAAATCATCA AGGAAACCTC CAACTTCGTC AAGAAGGTTG      350
   GTTACAACCC AAAGACTGTT CCATTGCTTC CAATCTCTGG TTGGAATGGT      400
60 GACAACATGA TTGAACCATC CACCAACTGT CCATGGTACA AGGGTTGGGA      450

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	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550
	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	ATTGGTACTG	TGCCAGTCGG	600
	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	TATGGTTGTT	ACTTTCGCCC	650
5	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TTGAAATGCA	TCACGAACAA	700
	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	750
	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	800
	ATCCACCAAA	GGGTTGTGAC	TCTTTCATG	CCCAAGTCAT	TGTTTTGAAC	850
	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTCTTGG	ATTGTCACAC	900
10	TGCCCACATT	GCTTGTAAT	TCGACACTTT	GGTTGAAAAG	ATTGACAGAA	950
	GAACTGGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGTGAT	1000
	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	CCAATGTGTG	TTGAAGCTTT	1050
	CACTGACTAC	CCACCATTAG	GTAGATTTCG	TGTCAGAGA		1089

15

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1101 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 56884

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTGCAAAC	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
35	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
40	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
45	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
50	ATTGTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCACCA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
55	A					1101

2) INFORMATION FOR SEQ ID NO: 410

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

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15  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
    GTATTCTCAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
20  TTGGGTGTCA AACAATTGAT TGTGCTGTC AACAGATGG ACTCTGTCAA      300
    ATGGGACAAA AACAGATTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
    TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT      400
    GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
    CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
25  TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
    CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AAAC TGGTAT CATCAAAGCC GGTATGGTTG      650
    TTA CTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
    CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
30  CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
    ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
    ATTGTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
    GGATTGTCAC ACTGCCCACA TTGCTTGTA ATTTCGACACT TTGGTTGAAA      950
    AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGTC     1000
35  AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
    TGTTGAAGCT TCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
    AT                                                                1102
  
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40

2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

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    CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
60  TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
  
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	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGTTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
5	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
10	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
15	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
20						

2) INFORMATION FOR SEQ ID NO: 412

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3108

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
40	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
45	ATGGGACAAA	AACAGATTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGTTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
50	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
55	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
60	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100

5 2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
 (B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20 GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50
 TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100
 GGTACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150
 CTGTGCTATC TTGATCATTG CTTCCGGTGT CGGTGAGTTC GAGGCTGGTA 200
 25 TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTGGC CTACACCTTG 250
 GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300
 GGACAAGAAC AGATTGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350
 AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC 400
 TGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA 450
 30 GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500
 TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550
 TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600
 GCCCGTCGGC CGTGTGAGG CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA 650
 CCTTCGCCCC CGCTGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700
 35 CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTCAACGT 750
 CAAGAACGTC TCTGTAAAG AGATCAGACG TGGTAACGTC TGCGGTGACT 800
 CCAAGAACGA CCCCCCATG GGTGCTCTT CTTTCAACGC CCAGGTTATC 850
 GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTTACTCTC CCGTCTTGGA 900
 CTGCCACACC GCCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950
 40 TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000
 TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050
 TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA 1098

45

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTTCGAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
5	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTCTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
10	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
15	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
20	GGATTGTGAC	ACTGCCACACA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
25						

2) INFORMATION FOR SEQ ID NO: 415

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1102 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - (B) STRAIN: CBS 7987
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
45	CTTTGTGGAA	ATTTCGAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
50	ATGGGACAAA	AACAGATTYG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
55	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
60	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAGTC	850

	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCAC	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAGATG	GTCCCAACCA	AACCAATGTG	1050
5	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102

10 2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

25	AATTGAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATTGATAT	CGCTTTATGG	50
	AAATTGCAAA	CTCCAAAATA	CCACGTTACC	GTTATTGATG	CTCCAGGTCA	100
	CAGAGATTTC	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGATTGTG	150
	CTATTTTTRAT	TATTGCTGGT	GGTGTGCGTG	AATTCGAAGC	CGGTATCTCT	200
30	AAGGATGGTC	AAACCAGAGA	ACACGCTTTA	TTGGCTTACA	CCTTAGGTGT	250
	TAGACAATTG	ATTGTTGCCG	TCAACAAGAT	GGACTCTGTT	AAATGGGACA	300
	AGGCTAGATT	CGAAGAAATC	ATCAAGGAAA	CCTCTAACTT	CGTCAAGAAG	350
	GTTGGTTACA	ACCCTAAGAC	TGTTCCTTTC	GTGCCAATTT	CTGGATGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCTCCACCAA	CTGTCCATGG	TACAAGGGTT	450
35	GGGAAAAGGA	AACCAAGGCT	GGTAAATCTA	CTGGTAAGAC	TTTGTTAGAA	500
	GCCATTGATG	CCATTGAACC	ACCAACCAGA	CCAACCGAAA	AGCCATTGAG	550
	ATTACCATTA	CAAGATGTCT	ACAAGATCGG	TGGTATTGGT	ACTGTGCCAG	600
	TCGGTAGAGT	TGAAACCGGT	GTTATCAAGG	GTGGTATGGT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTCCTAC	CGAAGTCAAA	TCCGTTGAAA	TGCACCACGA	700
40	ACAATTAAGT	GAAGGTGTTT	CAGGTGACAA	TGTTGGTTTC	AACGTCAAGA	750
	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTTTGTGG	TGACTCCAAG	800
	AACGACCCAC	CAAAGGGTGC	TGAATCTTTC	ACCGCTCAAG	TTATTGTCTT	850
	GAACCACCCA	GGTCARATCT	CTGCTGGTTA	CTCTCCAGTC	TTAGATTGTC	900
	ACACCGCCCA	CATTGCTTGT	AAATTTCGATG	CTTTACTCGA	AAAGATTGAC	950
45	AGAAGATCCG	GTAAGAAATT	AGAAGACGAA	CCAAAATTTCG	TCAAGTCCGG	1000
	TGATGCTGCT	ATCGTCAAGA	TGGTCCCAAC	CAAACCAATG	TGTGTTGAAG	1050
	CTTTCCTACTGA	ATACCCACCA	TTAGGTAGAT	TCGCTGTTAG	AGAT	1094

50

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

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TTTGGACAAG TTGAAGGCTG AAAGAGAAAG AGGTATCACT ATCGATATCG      50
CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCT      100
CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC      150
10 TGA CTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG      200
GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTTACC      250
CTAGGTGTTA GACAATTGAT TGTYGCTGTC AACAAGATGG ACTCTGTCAA      300
GTGGGATGAA TCCAGATTCG CTGAAATCGT TAAGGAAACC TCCAATTCA      350
TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT      400
15 GGT TGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCTGGTA      450
CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT      500
TGTTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG      550
GCTTGAGAT TGCCATTGCA AGATGTCTAC AAGATCGGTG GTATCGGTAC      600
GGTGCCAGTC GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG      650
20 TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
CACCACGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA      750
CGTTAAGAAC GTTTCCGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG      800
ACTCCAAGAA CGACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC      850
ATTGTCTTGA ACCACCCAGG TCAAATCTCT GCTGGTACT CTCCAGTTTT      900
25 GGA CTGTCAC ACCGCCACA TTGCTTGTA GTTCGAAGAA TTGTTGGAAA      950
AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG      1000
AAGTCCGGTG ACGCTGCTTT GGTAAAGTTC GTTCCATCCA AGCCAATGTG      1050
TGTCGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG      1100
A
1101

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2) INFORMATION FOR SEQ ID NO: 418

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
 45 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

```

AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC      50
50 AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTCACAGA GATTTCATCA      100
AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT      150
GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC      200
CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTTAGA CAATTGATTG      250
TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYAG      300
55 GAAATCATCA AGGAAACCTC TAACTTCGTC AAGAAGGTTG GTTACAACCC      350
TAAGACTGTG CCATTCGTTC CTATCTCTGG ATGGAAYGGT GACAACATGA      400
TTGAGGCTTC TACCAACTGT CCTTGGTACA AGGGATGGGA GAAGGAGACC      450
AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT      500
TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG      550
60 ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA      600

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	ACCGGTATCA	TYAAGGCCGG	TATGGTTGTT	ACCTTTGCCC	CAGCTGGTGT	650
	YACCACTGAA	GTCAAGTCCG	TGGAAATGCA	CCACGAACAA	TTGGTTGAAG	700
	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAAA	800
5	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCTGGTC	850
	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	ACTGTCACAC	CGCCCACATT	900
	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
10	CCACCATTTG	GAAGATTCGC	CGTCAGAGAC			1080

2) INFORMATION FOR SEQ ID NO: 419

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

30	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACCTTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTTCGTCC	100
	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
35	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGGT	300
	ATCGGAAGTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCGG	350
	TATGGTTGTC	ACCTTCGCCC	CAGCTGGTGT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
40	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	CACCCAGGTC	AGATCTCTTC	TGGTTACTCT	600
	CCAGTTTGG	ACTGTCACAC	TGCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
45	C					751

2) INFORMATION FOR SEQ ID NO: 420

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 253

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(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

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5  TCTTGACAAG TTAAAGGCTG AAAGAGAAAG AGGTATCACT ATTGATATTG      50
   CTTTATGGAA ATTCGAAACT CCAAAGTATC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTCAT TAAGAACATG ATTACTGGTA CTTCTCAAGC      150
   AGATTGTGCT ATTTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
   GTATTTCCAA GGATGGTCAA ACTAGAGAAC ACGCTTTATT AGCATTACAC      250
10  TTAGGTGTTA AGCAATTGAT TGTTGCTATC AACAAGATGG ATTCTGTTAA      300
   GTGGGATGAA AAGAGATTTG AAGAAATTGT CAAGGAAACC CAAAACCTTCA      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCGT TCCAATTTCT      400
   GGTGGAATG  GTGACAACAT GATTGAACCA TCTTCTAACT GTCCATGGTA      450
   CAAGGGTTGG ACTAAGGAAA CCAAGGCAGG TGTTGTCAAG GGTAAGACCT      500
15  TATTAGAAGC TATTGATGCT ATTGAACCAC CTGTCAGACC AACTGATAAG      550
   CCATTAAGAT TACCATTACA AGATGTTTAC AAGATTGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAACCGGTAT TATTAAGCCA GGTATGGTTG      650
   TTGTTTTCGC ACCATCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
   CACCATGAAC AATTAGAAGA AGGTGTCCCA GGTGACAATG TTGGTTTCAA      750
20  CGTCAAGAAC GTCTCTGTTA AGGATATCAA GAGAGGTAAC GTTTGTGGTG      800
   ACTCCAAGAA TGACCCACCA CAAGGTTGTG CTTCTTCAA TGCTCAAGTC      850
   ATTGTCTTGA ACCACCCTGG TCAAATTTCT GCTGGTTACT CTCCAGTTTT      900
   AGATTGTGCT ACTGCCACCA TTGCATGTAA ATTCGATGAA TTAATTGAAA      950
   AGATTGACAG AAGAACTGGT AAGTCCGTTG AAGACCATCC AAAGTCTGTT     1000
25  AAGTCTGGTG ATGCAGCTAT CGTTAAGATG GTTCCAACCA AGCCAATGTG     1050
   TGTTGAAGCT TTCACTGAAT ACCCACCATT AGGTAGATTC GCAGTCAGAG     1100
   AT

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2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

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35  (A) LENGTH: 1099 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

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   (A) ORGANISM: Candida kefyr
   (B) STRAIN: ATCC 28838

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45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

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   TGGACAAGTT AAAGGCTGAA AGAGAAAGAG GTATCACCAT CGATATCGCT      50
   TTGTGGAAGT TCGAAACTCC AAAGTACCAA GTTACCGTTA TCGATGCTCC      100
   AGGTCACAGA GATTTTCATCA AGAACATGAT TACTGGTACT TCTCAAGCTG      150
50  ACTGTGCTAT CTTGATTATT GCTGGTGGTG TCGGTGAATT CGAAGCCGGT      200
   ATCTCCAAGG ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACCTT      250
   GGGTGTTAGA CAATTGATTG TTGCTATCAA CAAGATGGAC TCTGTTAAGT      300
   GGGATGAATC TCGTTACCAA GAAATTGTTA AGGAAACCTC CAACTTCATC      350
   AAGAAGGTCG GTTACAACCC AAAGAATGTT CCATTCGTCC CAATCTCTGG      400
55  TTGGAACGGT GACAACATGA TTGAAGCCAC CACCAACGCT CCATGGTACA      450
   AGGGTTGGGA AAAGGAAACC AAGGCTGGTA CCGTCAAGGG TAAGACCTTG      500
   TTGGAAGCTA TTGACGCTAT CGAACCACCA ACCAGACCAA CTGACAAGCC      550
   ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT ATTGGTACTG      600
   TGCCAGTCGG TAGAGTCGAA ACCGGTGTC AAGGCCAGG TATGGTTGTT      650
60  ACCTTCGCCC CAGCCGGTGT CACTACCGAA GTTAAGTCCG TCGAAATGCA      700

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	CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
	TCAAGAACGT	TTCCGTAAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
	TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTTGG	900
5	ATTGTACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTGGGAAAAG	950
	AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCG	TGTCAGAGA	1099

10

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1095 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(B) STRAIN: ATCC 34135

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
30	ACAGAGATT	CATCAAGAAC	ATGATTACCG	GTACTTCTCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTGTCCGG	GAATTCGAAG	CTGGTATCTC	200
	CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC	TCATCAAGAA	350
35	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCAT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
40	GTCCGGTAG	TCGAAACCGG	TGTCATTAAG	CCAGGTATGG	TTGTCACCTT	650
	TGCTCCAGCA	GGTGTCAACA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
45	TGAACCAACC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
	GCTTTCACTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1104 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 5 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

```

10 CTTGGACAAG CTTAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTATGGAA GTTCGAAACT CCAAAGTACC ACGTTACCGT CATTGACGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCTCAAGC      150
   AGATTGTGCT ATTTTTRATYA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
   GTATCTCTAA GGATGGTCAA ACCAGAGAAC ACGCTCTTCT TGCATTCACT      250
   CTTGGTGTTA GACAATTGAT TGTTGCTATC AACAAGATGG ACTCTGTCAA      300
15 GTGGGACGAA TCCAGATTCG ATGAAATTG TAAGGAAACC GCWAACTTCA      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT      400
   GGTTGGAACG GTGACAACAT GATTGAACCA TCTGCTAACT GTCCATGGTA      450
   CAAGGGATGG ACTAAGGAAA CCAAGGCTTC CGGTGTCGTC AAGGGTAAGA      500
   CCCTTCTTGA AGCAATTGAT GCTATTGAGC CACCTGTCAG ACCAACTGAC      550
20 AAGGCTTTGA GATTGCCATT RCAAGATGTC TACAAGATTG GTGGTATTGG      600
   TACTGTGCCA GTCGGTAGAG TTGAAACCGG TATCATCAAG CCAGGTATGA      650
   TTGTCGTTTT CGCTCCAACC GGTGTTACTA CTGAAGTTAA GTCCGTTGAA      700
   ATGCACCATG AACAATTAGA AGAAGGTGTC CCAGGTGACA ATGTTGGTTT      750
   CAACGTCAAG AACGTCTCTG TTAAGGATAT TAAGAGAGGT AACGTCTGTG      800
25 GTGACTCCAA GAACGACCCA CCAATGGGTT GTGCTTCCTT CAATGCTCAA      850
   GTCATTGTTC TTAACCACCC AGGTCAAATT TCTGCTGGTT ACTCACCAGT      900
   TCTTGACTGT CACACTGCCC ACATTGCATG TAAGTTCGAY GAATTACTCG      950
   AAAAGATTGA CAGAAGAACC GGTAAGGCTA CTGAAGACCA TCCAAAGTCT     1000
   GTCAAGTCTG GTGATGCAGC TATCGTCAAG ATGGTTCCAA CCAAGCCAAT     1050
30 GTGTGTYGAA GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTYA      1100
   GAGA                                                                1104

```

35 2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

```

50 GGACAAGTTG AAGGCTGAGA GAGAAAGAGG TATCACCATC GATATCGCTT      50
   TGTGGAAGTT CGAGACTCCA AAGTACCACG TTACCGTCAT TGACGCTCCA      100
   GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACTT CCCAAGCTGA      150
   CTGTGCTATC TTGATTATCG CTGGTGGTGT CGGTGAGTTC GAAGCCGGTA      200
55 TCTCTAAGGA CGGTCAAACC AGAGAGCACG CTTTGTTGGC TTACACCTTG      250
   GGTGTCAAGC AGTTGATTGT TGCTGTCAAC AAGATGGACT CCGTCAAGTG      300
   GGACCAATCT AGATTGAGG AAATCATCAA GGAAACCTCT AACTTCGTCA      350
   AGAAGGTTGG TTACAACCCT AAGACTGTTC CATTCGTCCT AATCTCTGGT      400
   TGAACGGTG ACAACATGAT TGAGCCATCY ACCAACTGCC CATGGTACAA      450
60 GGGTTGGGAG AAGGAGACCA AGTCYGGTAA GTCCACCGGT AAGACCTTGT      500

```

	TGGAGGCCAT	TGACGCCATT	GAGCCACCTT	CGAGACCAAC	CGACAAGCCA	550
	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTCAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
5	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGA	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACGTC	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTACTCTC	CAGTYTTGGA	900
	CTGTCACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
10	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTCGCT	GTCAGAGA	1098

15

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
35	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTACAC	250
	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
40	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTAAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
45	TTGTTTTTCG	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCAGGTTACT	CTCCAGTTTT	900
50	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	GTTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	A					1101

55

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

257

(A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

15	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
	GGAAATTCGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
20	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
	AGGTTGGTTA	CAACCCATAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
25	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGTGTGCC	600
	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
30	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
	TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCGA	CACTTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCACT	GACTACCCAC	CATTGGGAAG	ATTGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

55	CTCCGTCAAG	TGGTCTCAGT	CTCGTTTCGA	GGAGATCGTC	AAGGAGGTTT	50
	CCAACTTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTCGTC	100
	CCCATCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
	GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCGTCCT	250
60	ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300

	TATCGGTACG	GTACCTGTCG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCC	350
	GCATGGTCGT	CACTTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400
	GTCGAGATGC	ACCACGAGCA	GATCCCCGAG	GGTCTCCCCG	GTGACAACGT	450
	CGGTTTCAAC	GTCAAGAACG	TTACCGTCAA	GGATATCCGC	CGTGGTAACG	500
5	TCTGCGGTGA	CTCCAAGAAC	GACCCCCCA	AGGGCTGCTC	TTCCTTCACT	550
	GCCCAGGTCA	TCGTTTTCAA	CCACCCCGGT	CAGATCTCCA	ACGGTTACTC	600
	CCCCGTTTGT	GACTGCCACA	CCGCCACAT	TGCCTGCCGC	TTCGACGAGA	650
	TCCAGTCCAA	GATGGACCGT	CGTACTGGTA	AGACCCTTGA	GGAGAACCCC	700
	AAGTTCATCA	AGGCTGGTGA	CTCCGCTATC	GTCAAGATGG	TTCCCTCCAA	750
10	GC					752

2) INFORMATION FOR SEQ ID NO: 428

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

30	AGTTAAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATCGATAT	CGCTTTGTGG	50
	AAGTTCGAAA	CTCCAAAGTA	CCAAGTTACC	GTTATCGATG	CTCCAGGTCA	100
	CAGAGATTTC	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGACTGTG	150
	CTATCTTGAT	TATTGCTGGT	GGTGTCGGTG	AATTCGAAGC	CGGTATCTCC	200
	AAGGATGGTC	AAACCAGAGA	ACACGCTTTG	TTGGCTTTCA	CCTTGGGTGT	250
35	TAGACAATTG	ATTGTTGCTG	TTAACAAGAT	GGATTCGGTT	AAGTGGGATG	300
	AATCTCGTTT	CCAAGAAATT	GTCAAGGAAA	CCTCTAATT	CATCAAGAAG	350
	GTCGGTTACA	ACCCAAAGAC	TGTTCCATTC	GTCCCAATCT	CTGGTTGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCACCACCAA	TGCTTCATGG	TACAAGGGTT	450
	GGGAAAAGGA	AACCAAGTCC	GGTGTCGTCA	AGGGTAAGAC	CTTGTTGGAA	500
40	GCTATTGACG	CTATCGAACC	ACCATCCAGA	CCAAC TGACA	AGCCATTGAG	550
	ATTGCCATTG	CAAGATGTCT	ACAAGATTGG	TGGTATCGGA	ACTGTGCCAG	600
	TCGGTAGAGT	CGAAACCGGT	GTTATCAAGC	CAGGTATGAT	TGTTACCTTT	650
	GCCCCAGCCG	TGTGTACTAC	TGAAGTTAAG	TCCGTCGAAA	TGCACCACGA	700
	ACAATTGGAA	GAAGGTCTAC	CAGGTGACAA	CGTCGGTTTC	AACGTCAAGA	750
45	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTCGTGG	TGACTCCAAG	800
	AACGATCCAC	CAAAGGCTGC	TGCTTCTTTC	AACGCCACTG	TTATCGTCTT	850
	GAACCATCCA	GGTCAAATCT	CTGCTGGTTA	CTCTCCAGTT	TTGGATTGTC	900
	ACACTGCTCA	CATTGCTTGT	AAGTTCGACG	AATTGTTGGA	AAAGAACGAT	950
	AGAAGATCCG	GTAAGAAGTT	GGAAGACTCT	CCAAAGTTCT	TGAAGTCCGG	1000
50	TGATGCTGCT	TTGGTTAAGT	TCGTTCCATC	TAAGCCAATG	TGTGTTGAAG	1050
	CCTTCTCTGA	CTACCCACCT	CTAGGTAGAT	TCGCTGTCAG	AGA	1093

55 2) INFORMATION FOR SEQ ID NO: 429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

259

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

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10 AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG      50
   GAAATTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC      100
   ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT      150
   GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTT      200
15 TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG      250
   TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC      300
   AAAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA      350
   GGTGTTGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA      400
   ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT      450
20 TGGGAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTTGGA      500
   AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA      550
   GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA      600
   GTCGGTAGAG TTGAAACTGG TGTCATCAA GCGGTATGG TTGTTACTTT      650
   CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG      700
25 AACAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG      750
   AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA      800
   GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT      850
   TGAACCACCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT      900
   CACACTGCTC ATATTGCTTG TAAATTCGAC ACCTTGGTTG AAAAGATTGA      950
30 CAGAAGAACT GGTAAGAAAT TGGAAGAAAA TCCAAAATTC GTCAAATCCG      1000
   GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA      1050
   GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA            1094

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35

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

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40 (A) LENGTH: 1095 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*

(B) STRAIN: Csp 388

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

```

   CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT      50
   GGAAGTTCGA GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT      100
   CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG      150
55 TGCTATTCTT ATCATTGCCG GTGGTGTGG TGAGTTCGAG GCTGGTATCT      200
   CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT      250
   GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA      300
   CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA      350
   AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG      400
60 AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG      450

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	TTGGGAGAAG	GAGACCAAGG	CTGGTGTGTG	CAAGGGTAAG	ACCTTGCTCG	500
	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAACGTGTTCC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTGTGTACCT	650
5	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCCGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTTAA	750
	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
10	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCT	CTCCAAAGTT	CGTCAAGTCT	1000
	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTGCTGTGC	AGAGA	1095

15

2) INFORMATION FOR SEQ ID NO: 431

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1085 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
- (B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
35	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATYT	CTAAGGATGG	200
	TCAAACCAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
40	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AAC TGCCCAT	GGTACAAGGG	TTGGGAAAAG	450
	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAACGTGACC	AGTCGGTAGA	600
45	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACTT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
50	CAGGTCAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGGTT	GAAAAGATTG	ACAGAAGAAC	950
	CGGTAAGAAG	TTGGAAGAAA	ACCCAAAGTT	TGTCAAGTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCAC	1050
	GACTACCCAC	CATTGGGTAG	ATTGCTGTGC	AGAGA		1085

55

2) INFORMATION FOR SEQ ID NO: 432

- 60 (i) SEQUENCE CHARACTERISTICS:

261

(A) LENGTH: 1072 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTCGAGACC	CCCAAGTACC	50
15	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCTG	AGGAGATTGT	300
20	CAAGGAGACC	TCCAACCTTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTGGTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
25	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCCTACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCCC	AAGGCTGCTG	800
30	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCGG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCCACA	TTGCTTGCA	900
	ATTTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCCCTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCCTGACT	ACCCTCCCTT	1050
35	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

55	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTCTG	GATACAACCC	CAAGGCTGTT	CCATTCGTCC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
60	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300

	ATCGGAACAG	TCCCAGTCGG	CCGTGTCGAA	ACCGGTGTTA	TCAAGCCTGG	350
	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400
	TCGAAATGCA	CCACCAGCAG	CTCACCAGG	GTAACCCTGG	TGACAACGTT	450
	GGCTTCAACG	TCAAGAACGT	CTCTGTCAAG	GAAGTCCGCC	GCGGTAACGT	500
5	CGCTGGTGAC	TCCAAGAACG	ACCCACCAAA	GGGCTGCGAC	TCCTTCAACG	550
	CCCAGGTCAT	CGTCCTCAAC	CACCCTGGTC	AAGTCGGTGC	TGGTTATGCC	600
	CCAGTCCTTG	ACTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCCGAGCT	650
	CCTCGAGAAG	ATCGACCGCC	GTACCGGTAA	ATCCGTTGAG	AACAACCCCA	700
	AGTTCATCAA	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCATCCAAG	750
10	C					751

2) INFORMATION FOR SEQ ID NO: 434

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus albidus*
 (B) STRAIN: ATCC 66030

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

30	AAGCTCAAGG	CCGAGCGAGA	GCGAGGTATC	ACCATCGACA	TCGCCTTGTG	50
	GAAGTTCGAG	ACCCCCAAGT	ACAATGTCAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGAGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	GGCCGACTGT	150
	GCCATCCTCA	TCATCGCCTC	CGGTATCGGA	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGACGGT	CAGACCCGAG	AGCACGCCCT	TTTGGCCTTC	ACCCTCGGTG	250
35	TCCGACAGCT	CATCATTGCC	ATCAACAAGA	TGGACACCTG	CAAGGTTAGT	300
	TCGCAGGTCC	TGGTCTCTGT	ACGAATCTTG	CTGACCCCTT	TTACAGTGGT	350
	CCGAAGACCG	ATACAACGAA	ATCGTCAAGG	AGGCTTCCGG	TTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GACCGTTCCC	TTCGTCCCCA	TCTCCGGATG	450
	GCACGGAGAC	AACATGTTGG	AGGAGTCCAC	CAACATGCCC	TGGTACAAGG	500
40	GATGGCACAA	GGAGTCCAAG	GCCGGTGTG	TCAAGGGAAA	GACCTTGCTC	550
	GAGGCCATCG	ACGCCATCGA	GCCCCCTACC	CGACCTTCCG	ACAAGCCCTT	600
	GCGATTGCCC	CTCCAGGATG	TCTACAAGAT	CGGTGGTATC	GGTACGGTGC	650
	CCGTGCGTCG	AGTCGAGACC	GGTGTCAATCA	AGGCTGGTAT	GGTCGTCAAC	700
	TTCGCCCCTG	CCAACGTCAC	CACCGAAGTC	AAGTCCGTCG	AAATGCACCA	750
45	CGAACAGCTC	GCTGAGGGTG	TTCCCGGTGA	CAACGTCGGT	TTCAACGTCA	800
	AGAACGTTTC	CGTCAAGGAC	ATCCGACGAG	GAAACGTCTG	CTCCGACTCG	850
	AAGAACGACC	CCGCTATGGA	GTCTGCTTCC	TTCAACGCTC	AGGTCATTGT	900
	CTTGAACCAC	CCGGGTCAGA	TCGGTGCCGG	CTACTCCCCC	GTTTTGGACT	950
	GCCACACCGC	TCACATTGCC	TGCAAGTTTCG	CTGAGCTCGT	TGAGAAGATC	1000
50	GACCGACGAA	CCGGTAAGGT	CATGGAGGCC	GCCCCCAAGT	TCGTCAAGTC	1050
	CGGTGACGCC	GCCATCGTCA	AGTTGATCCC	GTCCAAGCCC	ATGTGTGTGC	1100
	AGTCCTACTC	CGAGTACCCC	CCCTTGGGTC	GATTCGCCGT	CCGAGA	1146

55

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exophiala jeanselmei*
(B) STRAIN: ATCC 64755

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

	CAAGCTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCTTGT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CTGTCATCGA	CGCCCCTGGT	100
	CATCGTGA	TTATCAAGAA	CATGATCACT	GGTACTTCCC	AGGCTGACTG	150
15	CGCCATTCTC	ATCATTGCCG	CCGGTACTGG	TGAATTCGAA	GCCGGTATCT	200
	CCAAGGATGG	TCAGACTCGT	GAGCACGCTC	TGCTCGCCTA	CACCCTGGGT	250
	GTCAAGCAGC	TCATTGTGCG	CATCAACAAG	ATGGACACCA	CCAAGTGGTC	300
	CGAGGATCGT	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	350
	AGGTCGGCTA	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	400
20	AACGGTGACA	ACATGATCGA	TGTCTCCACC	AACTGCCCCT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTCG	500
	AGGCCATCGA	CGCCATCGAC	CCCCCCTCTC	GTCCCACCGA	CAAGCCTCTC	550
	CGTCTTCCCT	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	GAACGGTGCC	600
	CGTCGGTCGT	GTTGAGACTG	GTGTCATCAA	GGCCGGTATG	GTCGTTACCT	650
25	TCGCTCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	700
	GAACAACTCG	CCGAGGGTGT	TCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	750
	GAACGTCTCC	GTCAAGGAGG	TTCGTCGTGG	AAACGTCTGC	GGTGACTCCA	800
	AGAACGACCC	ACCCAAGGGT	GCTGATTCTT	TCAACGCCCA	GGTCATCGTC	850
	TTGAACCACT	CTGGTCAAGT	CGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	900
30	CCACACTGCC	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATTG	950
	ACCGCCGTAC	CGGTAAATCC	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	1000
	GGTGACGCTG	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CTCTTGGTG	TTTCGCCGTC	CGTGA	1095

35

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTTCGAG	ACTCCTCGCT	ACTATGTCAC	CGTCATTGGT	ATGTTGTTCGC	100
55	TCATGCTTCA	TTCTACTTCT	CTTCGTACTA	ACACATCACT	CAGACGCTCC	150
	CGGTCACCGT	GATTTTCATCA	AGAACATGAT	CACTGGTACT	TCCCAGGCCG	200
	ATTGCGCCAT	TCTCATCATT	GCCGCCGGTA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTTCTTG	CCTACACCCT	300
	TGGTGTCAAG	AACCTCATCG	TCGCCATCAA	CAAGATGGAC	ACCACCAAGT	350
60	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CTCTTTCATC	400

	AAGAAGGTCG	GCTACAACCC	CAAGGCTGTC	GCTTTCGTCC	CCATCTCCGG	450
	TTTCAACGGT	GACAACATGC	TTACCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGTTGGGA	GCGTGAGATC	AAGTCCGGCA	AGCTCACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TTGACTCCAT	CGAGCCCCCC	AAGCGTCCCG	TTGACAAGCC	600
5	CCTTCGTCTT	CCCCTTCAGG	ATGTCTACAA	GATCGGTGGT	ATTGGAACGG	650
	TTCCCGTCGG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCGG	TATGGTCGTT	700
	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACGAGCAA	CTCACTGAGG	GCCAGCCCGG	TGACAACGTT	GGTTTCAACG	800
	TGAAGAACGT	CTCCGTCAAG	GACATCCGAC	GTGGTAACGT	CGCTGGTGAC	850
10	TCCAAGAACG	ACCCCCCTAT	GGGTGCCGCT	TCTTTCACCG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGTC	AGGTCGGTGC	TGGTTACGCT	CCCGTCCTCG	950
	ATTGTACAC	TGCCACATT	GCCTGCAAGT	TCGCCGAGAT	CCAGGAGAAG	1000
	ATCGACCGCC	GAACCGGTAA	GGCTACTGAG	GCCGCCCCCA	AGTTCATCAA	1050
	GTCTGGTGAC	TCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCCATGTGTG	1100
15	TTGAGGCTTT	CAC				1113

2) INFORMATION FOR SEQ ID NO: 437

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: LEV-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

35	GGTCCGAGGA	CAGATTCAAC	GAGATTGTCA	AGGAGACTTC	CAACTTCATC	50
	AAGAAGGTTG	GTTAYAACCC	CAAGACTGTT	GCTTTCGTCC	CCATCTCTGG	100
	TTGGAACGGT	GACAACATGA	TTGAGCCCTC	CACCAACTGC	CCCTGGTACA	150
	AGGGATGGCA	GAAGGAGACC	AAGGCTGGTG	TACTAAGGG	TAAGACCCTC	200
	CTTGAGGCCA	TCGATGCCAT	TGAGCCCCCT	GTCAGACCTT	CCGACAAGCC	250
40	CCTCCGTCTT	CCCCTCCAGG	ATGTCTACAA	GATCGGTGGT	ATCGGAACATG	300
	TGCCCCGTCCG	CCGTGTCGAA	ACCGGTGTCA	TCAAGCCCGG	TATGGTCGTC	350
	ACCTTCGCCC	CCGCTGGTGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	400
	CCACGAGCTC	CTCACTGAGG	GTCTCCCCCG	TGACAACGTT	GGTTTCAACG	450
	TCAAGAACGT	CTCCGTTAAG	GATATCAGAC	GTGGTAACGT	CTGCGGTGAC	500
45	TCCAAGAACG	ATCCCCCCTA	GGCTTGCGCT	TCTTTCACCG	CCCAGGTCAT	550
	TATCTTCAAC	CACCCTGGTC	AGATCTCTGC	TGGATACTCT	CCCGTCCTTG	600
	ATTGCCACAC	CGCCCATATT	GCTTGCAAGT	TCGACACTTT	GATCGAGAAG	650
	ATTGACCGTC	GTA CTGGTAA	GAAGACTGAG	GACTCCCCCA	AGTTCGTCAA	700
	GGCCGGTGAT	GCTGCTATCG	TCAAGA			726

50

2) INFORMATION FOR SEQ ID NO: 438

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 5 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

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10 CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
   CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
   CCAATCTCTG GTTTCGAGGG TGACAAACATG ATTGAACCCT CCCCCAACTG      150
   CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG      200
   GTAAAACCTT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT      250
   ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG      300
15 TATTGGCACT GTTCCCGTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCCG      350
   GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
   GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTACCCTG GCGACAACGT      450
   CGGCTTCAAC GTCAAGAACG TTTCAGTCAA GGAAGTCCGC CGTGGCAACG      500
   TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
20 GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC      600
   CCCAGTCCTC GACTGCCACA CTGCCCACAT TGCTTGCAAG TTCTCTGAGC      650
   TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
   AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
   GCCC
25

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2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Issatchenkia orientalis*
 40 (B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

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45 TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
   CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG      100
   GTTGGAATGG TGACAAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
   AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
   ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
   CATTAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
50 GTGCCAGTCG GTAGAGTCGA AACCGGTGTC ATTAAGCCAG GTATGGTTGT      350
   CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
   ACCATGAACA ATTAGAACAA GGTGTTCCAG GTGATAACGT TGTTTTC AAC      450
   GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA      500
   CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA      550
55 TTGTCTTGAA CCACCCTGGT CAAATTTCCT CTGGTTACTC TCCAGTCTTG      600
   GATTGTCACA CTGCCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA      650
   GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
   AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC          743

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60

2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

CAAGCTCAAG GCTGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTGT 50
 GGAAGTTCGA GACCCCTAAG TACCACGTTA CCGTCATTGA CGCTCCTGGT 100
 20 CACCGTGACT TCATCAAGAA CATGATTACG GGTACCTCGC AGGCTGACTG 150
 CGCTATCCTC ATCATTGCCG GTGGTACCGG TGAGTTCGAG GCTGGTATCT 200
 CGAAGGACGG TCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTGGGT 250
 GTGCGTCAGC TCATTGTGGC CGTCAACAAG ATGGACACCA CCAAGTACTC 300
 GGAGGACCGC TTCAACGAGA TTGTCCGCGA AGTGTCGAAC TTCATCAAGA 350
 25 AGGTCGGTTT CAACCCCAAG ACTGTTGCCT TCGTCCCAT CTCGGGCTGG 400
 CACGGTGACA ACATGATCGA GGCCACCACC AACATGCCTT GGTACAAGGG 450
 CTGGGAGAAG GAGACCAAGT CGGGCAAGGT CACTGGTAAG ACTCTGCTGG 500
 ACGCCATCGA CGCCATCGAG CCCCCGACCC GCCCCACTGA CAAGCCCCTG 550
 CGTCTCCCTC TGCAGGATGT GTACAAGATC GGTGGTATCG GTACTGTCCC 600
 30 TGTCCGTCGT GTTGAGACCG GTGTGATCAA GCCCGGTATG GTTGTGACCT 650
 TCGTCCCTC GAACGTCACC ACTGAAAGTTA AGTCGGTTGA GATGCACCAC 700
 GAGTCGCTCC CTGAGGGTCT CCCCCTGAC AACGTTGGTT TCAACGTGAA 750
 GAACGTCTCG GTTAAGGACA TTCGCCGTGG TAACGTTGCC TCGGACTCGA 800
 AGAACGACCC CGCTCAGGAG GCTGCTTCGT TCAACGCGCA GGTCAATTGTC 850
 35 ATGAACCACC CTGGTCAGAT CAGCAACGGT TACTCGCCCG TGCTTGACTG 900
 CCACACTGCG CACATTGCCT GCCGCTTCAA CAACATCCTC CAGAAGATCG 950
 ACCGTCGCTC GGGTAAGGTG CTTGAGGAGA ACCCCAAGTT CATCAAGTCG 1000
 GGTGACGCTG CCATGGTGGA GATGATCCCC ACCAAGCCCA TGTGTGTGGA 1050
 40 GTCGTTCAAC GAGTACCCCC CTCTGGGTCG TTTCGCTGTG C 1091

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 55 (B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

ACCACCAAGT ACTCGGAGGA CCGCTTCAAC GAGATTATTC GCGAGACTTC 50
 60 GAACTTCATC AAGAAGGTCG GTTACAACCC GAAGACTGTT GCCTTCGTCC 100

	CGATCTCGGG	CTGGCACGGT	GACAACATGA	TTGAGGCGAC	CACCAACATG	150
	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCTTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCGA	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
5	ATCGGTACYG	TCCC GGTCGG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCGG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTTAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTCGCC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
10	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRG TGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTTCGACATG	100
35	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
40	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCT	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGCCA	AGAGCACCGG	CAAGACCCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCCG	GTCCGTCCCA	CCGACAAGCC	600
45	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCCTGTCGG	TCGTGTTGAG	ACTGGTGTC	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
50	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCCGGTG	TGGATACGCT	CCCGTCCTCG	950
	ATTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CACTGACTAC	CCTCCCCTTG	GTCGTTTCGC	CGTCCGTGAC	1150

2) INFORMATION FOR SEQ ID NO: 443

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

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15  GGACAAGTTG AAGGCTGAGA GAGAGAGAGG TATCACCATC GACATTGCCT      50
    TGTGGAAGTT CGAGACTCCT AAGTACCACG TCACCGTYAT TGACGCCCCA      100
    GGTACAGAG  ATTTCATCAA GAACATGATC ACTGGTACTT CCCAGGCTGA      150
    CTGTGCYATC TTGATTATCG CYGGTGGTGT TGGTGAGTTC GAGGCTGGTA      200
    TCTCCAAGGA TGGCCAGACC AGAGAGCACG CTTTGTGTCG YTACACCTTG      250
20  GGTGTTAGAG ARTTGATTGT TGCCGTCAAC AAGATGGAAT CTGTCAAGTG      300
    GGACAAGAAC AGATTTGAGG AGATCATCAA GGAGACCTCT AACTTCGTCA      350
    AGAAGGTTGG TTACAACCCT AAGACYGTGC CATTCGTGCC AATYTCTGGT      400
    TGAACCGGTG ACAACATGAT TGAGGCTYTC ACTAAGTACC CATGGTACAA      450
    GGGTTGGGAG AAGGAGACCA AGGCCGGTAA GTCTWCCGGT AAGACCTTGT      500
25  TGGAGGCCAT TGACGCCATT GAGCCACCAA CCAGACCTAC CGACAAGGCC      550
    TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TCGGAACGGT      600
    GCCAGTCGGC CGTGTGAGGA CCGGTGTCAT TAAGGCCGGT ATGGTTGTYA      650
    CCTTYGCCCC AGCTGGTGTC ACCACTGAGG TCAAGTCCGT CGAGATGCAC      700
    CACGAGCAGT TGGTCGAGGG TCTTCCAGGT GACAAYGTTG GTTTCAACGT      750
30  CAAGAACGTC TCCGTTAAGG AGATCAGAAG AGGTAACGTC TGTGGTGACT      800
    CCAAGCAGGA CCCACCAAAG GGTGCCGCTT CTTTCACCGC YCAGGTTATT      850
    GTGTTGAACC ACCCTGGTCA GATCTCCTCT GGTACTCTC CAGTGTTGGA      900
    CTGYCACACC GCCCACATTG CCTGTAARTT CGACACCTTG TTGGAGAAGA      950
    TTGACAGAAG AACTGGTAAG TCCTTGGAGT CYGAGCCTAA GTTCGTCAAG     1000
35  TCYGGTGACG CCGCCATTGT CAAGATGGTG CCAACCAAGC CAATGTGTGT     1050
    TGAGGCTTTC ACCGACTACC CACCTTTGGG TAGATTGCCG GTCAGAGAC     1099
  
```

2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

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55  CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT      50
    GGAAGTTCGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGACT      100
    CGCGCGAGAC TGGTCGCAAT TTCCACGTCG CTAACGTGCT TGAACAGACG      150
    CTCCCGGCCA CCGTGACTTC ATCAAGAACA TGATCACTGG TACCTCCAG      200
60  GCTGACTGCG CTATCCTCAT TATCGCTGCC GGCCTGGTG AGTTCGAGGC      250
  
```

	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	300
	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	350
	AAGTGGTCTG	AGGCCCCGTTT	CCAGGAGATC	ATCAAGGAGA	CCTCCAACCTT	400
	CATCAAGAAG	GTCGGCTACA	ACCCCAAGAC	CGTCGCTTTC	GTCCCCATCT	450
5	CTGGTTTCCA	CGGCGACAAC	ATGCTTTCCC	CCTCCACCAA	CTGCCCCCTGG	500
	TACAAGGGCT	GGGAGAAGGA	GACCAAGGCT	GGCAAGTCCA	CCGGCAAGAC	550
	CCTCCTTGAG	GCCATCGACT	CCATCGAGCC	CCCCAAGCGC	CCCAGCGACA	600
	AGCCCCCTCG	CCTTCCCCCTT	CAGGATGTGT	ACAAGATCGG	CGGTATCGGC	650
	ACAGTCCCTG	TCGGCCGTAT	CGAGACTGGT	GTCATCAAGC	CCGGCATGGT	700
10	CGTGACCTTC	GCTCCTTCCA	ACGTCAACCAC	CGAAGTCAAG	TCCGTTGAGA	750
	TGCACCACGA	GCAGCTCTCC	GAGGGTGTC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTCTCCGT	CAAGGAGATC	CGTCGTGGCA	ACGTCGCCCG	850
	TGACTCCAAG	AACGACCCCC	CTCTGGGTGC	CGCTTCTTTC	GATGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGGTGC	GTGCTGGCTA	CGCCCCCGTC	950
15	CTCGACTGCC	ACACCGCCCA	CATTGCCTGC	AAGTTCGCCG	AGATCAAGGA	1000
	GAAGATCGAC	CGCCGTACCG	GCAAGTCTGT	CGAGTCCGCC	CCCAAGTTCA	1050
	TCAAGTCTGG	CGACTCTGCC	ATCGTCAAGA	TGATTCCCTC	CAAGCCCATG	1100
	TGCGTTGAGG	CTTTCACCGA	CTACCCTCCT	CTGGGCCGCT	TCGCCGTCCG	1150
20	TGA					1153

2) INFORMATION FOR SEQ ID NO: 445

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32071

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
40	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
45	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCCG	GTGACAACGT	450
	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
50	GCCCAGGTCA	TCGTCTCTAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
55	GCCCATGTGC	GTC				763

2) INFORMATION FOR SEQ ID NO: 446

60 (i) SEQUENCE CHARACTERISTICS:

270

(A) LENGTH: 1346 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
10 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
15	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GGCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
20	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTCTT	TTCGTTCCCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCTCCTC	550
25	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
30	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCCGGT	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
35	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	TTCGCGAGTA	AGTTTATCT	CCGTTGTCTA	TTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
55 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

60	AAGTTAAAAG	CTGAACGTGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
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	GAAATTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGTG	250
5	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
10	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
15	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
20	GTGATGCTGC	TATTGTTAAA	TTTGTTCCAT	CAAAACCATT	ATCAGTTGAA	1050
	GCTTTCCTG	ACTACCCACC	ATTAGGTCGT	TTCGCTGTCA	GAGA	1094

25 2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTTCGAACT	CCAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
45	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACCTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAACGTG	TCCATTCGTT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
50	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACCTT	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
55	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
60	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000

AATCAGGTGA TGCTGCTATT GTTAAATTTG TTCCATCAAA ACCATTATCA 1050
 GTTGAAGCTT TCACTGACTA CCCACCATTA GGTCGTTTCG CTGTCAGAGA 1100

5

2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT 50
 GGAAGTTCGA GACCCCAAG TACCAGGTCA CCGTCATTGG TATGTCTTTG 100
 TGCTTTTGTG GCTTTTGTG CCTGTGCCTC GCACAATTCC AGCCCTCGAT 150
 AATTATGAAC CTCGTACTAA TATGTCGTTT TCCCACTACC CACAGACGCC 200
 CCCGGCCATC GTGATTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC 250
 TGATTGCGCC ATTCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG 300
 GCATCTCCAA GGATGGCCAG ACCCGTGAGC ACGCTCTTCT CGCCTTCACC 350
 CTCGGTGTCA AGAACCTCAT TGTTGCCATC AACAAGATGG ACACCAACAA 400
 CTGGTCCGAG GACCGATACA AGGAGATCAT CAAGGAGACC TCCAAC TTCA 450
 TCAAGAAGGT CGGCTACAAC CCCAAGGCCG TTCCTTTTCGT CCCCATCTCC 500
 GGTTCACACG GAGACAACAT GCTTACCCCC TCCACCAACT GCCCCTGGTA 550
 CAAGGGTTGG GTCCGTGAGG TCAAGGGTAA CACCCTTACC GGCAAGACCC 600
 TTCTCGAGGC CATCGACTYC ATCGAGCCCC CCAAGCGTCC CACCGAGAAG 650
 CCCCTCCGTC TTCCCCTTCA GGACGTCTAC AAGATCGGTG GTATTGGCAC 700
 TGTGCCCCGTC GGCCGTATCG AGACCGGTAT CCTCAAGCCC GGTATGGTCG 750
 TCACCTTCGC TCCCTCCAAC GTCACCACTG AAGTCAAGTC CGTCGAGATG 800
 CACCACGAGC AGCTTACCGA GGGTGTCCCC GGTGACAACG TTGGTTTCAA 850
 CGTGAAGAAC GTCTCCGTCA AGGATATCCG CCGTGGAACG GTCTGCGGTG 900
 ACTCCAAGAA CGACCCCCCG GCTGCTGCCG CCTCTTTCCA GGCCCAAGTC 950
 ATTGTCCTCA ACCACCCCGG CCAGATCGGT GCTGGTTACG CTCCCGTTCT 1000
 TGACTGCCAC ACTGCCACA TTGCTTGCAA GTTCGCCGAG CTCCTTGAGA 1050
 AGATCGACCG CCGTACCGGT AAGTCGGTCG AGAACAACCC CAAGTTCGTC 1100
 AAGTCTGGTG ATGCCGCCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG 1150
 TGTTGAGTCC TTCACCGAGT ACCCCCCTCT CGGTCGTTTC GCCGTCCGTG 1200
 A 1201

2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*

(B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

5 CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT 50
 GGAAGTTCGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT 100
 CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG 150
 TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTCGAA GCTGGTATCT 200
 10. CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT 250
 GTCCGTCAAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC 300
 CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA 350
 AGATTGGTTA CAACCCCAAG TCTGTTCCCT TCGTCCCCAT CTCTGGTTGG 400
 CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GGTACAAGGG 450
 15. ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG 500
 ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC 550
 CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC 600
 CGTCGGTCGT GTCGAAACTG GTGTCATCAA GGCTGGTATG GTTGTACACT 650
 TCGCTCCTGC TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC 700
 20. GAAACCCCTCA CTGAAGGTCT CCCCCTGAC AACGTCGGTT TCAACGTCAA 750
 GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA 800
 AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC 850
 TTGAACCAACC CTGGTCAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG 900
 TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG 950
 25. ACAGACGTTC CGGTAAGTCC TTGGAAGCTA CTCCCAAGTT CGTCAAGTCT 1000
 GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA 1050
 AGCTTACACT GACTACCCTC CTCTCGGTCT TTTCTGCTGT CGTGA 1095

30

2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1092 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
 (B) STRAIN: ATCC 10658

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA 50
 AGTTCGAGAC CCCCAGTAC AACGTCACCG TCATTGACGC TCCAGGACAT 100
 CGTGATTTC AAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA 150
 50. CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTACTTCCCA 200
 GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTGTTG GAGTTCGAGG 250
 CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC 300
 ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT 350
 CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC 400
 55. CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC 450
 GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTCT ACCCCAAGGG 500
 TGTTCCCTTC GTCCCATCT CAGGATGGCA CGGAGACAAC ATGATCGAGG 550
 AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC 600
 GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC 650
 60. CCCACCCGT CCTACCGACA AGCCTCTCCG ACTTCCCCTC CAGGATGTCT 700

	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCAACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTTC	AACATCAAGA	ACGTTTTCAGT	CAAGGATATC	900
5	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
10	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

15

2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
35	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCGC	CGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCCTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCGTT	TGAGGAGAT	CATCAAGGAG	ACCTCCAACT	400
40	TCATCAAGAA	GGTCGGCTTC	AACCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TGCGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCCTC	GTCTTCCCCT	CCAGGTTCGT	TTCCCTGCTC	GCGGTTTACG	650
45	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTGCTCGGC	900
50	CATTTTTTCA	GTCCTGACCC	CGTTTTGCCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTTAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCAAA	GGAGGCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCACATT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
55	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

60

2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1070 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: WSA-148

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTTCATCAA 100
GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
20 CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
CGTGAGCACG CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
25 TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
GAGCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCGGC CGTATCGAGA 600
CTGGTGTCTT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC 650
30 ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG 800
GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGGCCA 850
GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCATTG 900
35 CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
CCCCTCTGGG CCGTTTCGCC 1070

40

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1092 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
(B) STRAIN: ATCC 52550

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
ATTTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
60 GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC 150

	ATCCTTATCA	TTGCTGGTGG	TGTCGGTGAG	TTCGAGGCTG	GTATCTCCAA	200
	GGACGGTCAG	ACCAGAGAGC	ACGCTCTTCT	TTCTTTCACC	CTTGGTGTCA	250
	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
5	TGGTTACAAC	CCTAAGAATA	TTGCTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGAGGGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCCTCTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
10	GGTCGTGTTG	AGACTGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
	AGATCCCAGA	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
15	ACCACCCTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTCACA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTCGTC	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
	TTCACTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092
20						

2) INFORMATION FOR SEQ ID NO: 455

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
40	GACCCCCAAG	TACAATGTCA	CCGTCATTGG	TATGTTTTCT	CTTTACCTTT	100
	CCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCTTGG	300
45	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGGTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
50	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCTACAA	GATCTCTGGT	ATCGGAACTG	650
	TACCAGTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCGTC	700
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
55	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTCGAA	GCCAACCCCA	AGTTCGTCAA	1050
60	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC' CGTCCGTGA' f149

5 2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
 CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
 CCAGGTCACC GTGATTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
 CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200
 25 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
 CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAGATGG ACTCTGTCAA 300
 GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACCTCG 350
 TCAAGAAGGT TGGTTACAAC CCAAGTCTG TTCCATTCGT TCCTATCTCT 400
 GGTGGAACG GTGACAACAT GTTGGAACCT ACCACCAACG CCCCATGGTA 450
 30 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
 TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
 CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
 TGTGCCAGTC GGCCGTGTCTG AAACCGGTAT CATCAAGGCC GGTATGGTCTG 650
 TCACCTTTGC TCCACCAATG GTCACAACCTG AAGTTAAGTC CGTTGAAATG 700
 35 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
 CGTCAAGAAC GTTTCCTGTTA AGGAAATCAG ACGTGGTAAC GTCTGTGGTG 800
 ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
 ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTTACT CTCCAGTTCT 900
 CGATTGCCAC ACTGCCCACA TTGCCTGCAG ATTGACGAA CTCCTTGAAA 950
 40 AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTCT 1000
 AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
 CGTTGAAACC TTCCTGAAT ACCCACCCTT TGGTCGTTTC GCCGTCCGTG 1100
 A 1101

45

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 60 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

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5   GTTGAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA      50
    AGTTCGAGAC CCCCAGGTAC TATGTCACCG TCATCGACGC CCCGGGTCAT      100
    CGTGACTTTA TCAAGAACAT GATCACTGGT ACCTCGCAGG CCGACTGCGC      150
    CATCTTGATC ATTGCCGCCG GTACCGGTGA ATTCTGAAGCC GGTATCTCCA      200
    AGGATGGTCA GACCCGTGAG CACGCTCTGC TCGCCTACAC CTTGGGTGTC      250
    AAGCAGCTCA TCGTCGCCAT CAACAAGATG GACACCACCA AGTGGTCCGA      300
    GGAGCGTTTC AACGAAATCA TCAAGGAGAC TTCCAACCTT ATCAAGAAGG      350
10  TCGGCTACAA CCCCAGGCC GTTCCTTTCG TCCCCTCTC CGGCTTCAAC      400
    GGTGACAACA TGATTGAGGT CTCCACCAAC TGCCCGTGGT ACAAGGGATG      450
    GGAGAAGGAG TCCAAGGCTG GCAAGGCCAC CGGCAAGACC CTCCTCGAGG      500
    CCATTGACGC CATCGACCCA CCCACCCGTC CCACCGACAA GCCTCTCCGT      550
    CTCCCTCTCC AGGATGTCTA CAAGATCTCT GGTATCGGAA CGGTTCTCTG      600
15  CGGTCGTGTC GAGACCGGTA CCATCAAGGC CGGTATGGTC GTCACCTTCG      650
    CTCCGGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAAAT GCACCACGAG      700
    CAGCTCGCCG AGGGTCTGCC AGGTGACAAC GTTGGCTTCA ACGTCAAGAA      750
    CGTCTCCGTC AAGGAGGTTC GTCGTGGTAA CGTTGCCGGT GACTCCAAGA      800
    ACGACCCGCC CAAGGGTGCC GAGTCCTTCA ACGCCAGGT CATTGTCCTC      850
20  AACCACCTG GTCAGATCGG TGCCGGCTAC GCTCCAGTCT TGGATTGCCA      900
    CACTGCCAC ACATTGCTGCA AGTTCGCCGA GTTGCTCGAG AAGATCGACC      950
    GTCGTACCGG AAAGTCCATC GAGAACAACC CCAAGTTCAT CAAGTCTGGT     1000
    GATGCTGCCA TCGTCAAGAT GATTCCCAGC AAGCCCATGT GTGTCGAGGC     1050
    TTTCACCGAC TATCCTCCTC TGGGTCGTTT CGCTG                      1085
25

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2) INFORMATION FOR SEQ ID NO: 458

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30  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 492 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
35
    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Aspergillus fumigatus
40  (B) STRAIN: DAL-95

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

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45  TGTCTTCATC CGGAATTGAT TGTGAGTCGT TCCACATGCT CACCTAGTTT      50
    TCGCTCGATC TTTTCACTAA CGCAAACCAT GTAGAACAAC ATTGCCAAGG      100
    CCCACGGTGG TTA CTCCGTC TTA CTGGTG TTGGTGAGCG TACTCGTGAG      150
    GGTAACGATC TGTACCACGA AATGCAGGAG ACTGGTGTCA TTCAGCTCGA      200
    GGGTGAATCC AAGGTGCGAC TGGTGTTCGG ACAGATGAAC GAGCCCCCCG      250
    GTGCCCCGTC CCGTGTGCGC CTTACCGGTC TGACCATTGC CGAGTACTTC      300
50  CGTGACGAGG AGGGTCAGGA CGTGCTGCTC TTCATTGACA ACATTTTCCG      350
    TTTCACCCAG GCCGGTCTG AGGTGTCTGC CCTTCTCGGT CGTATCCCCT      400
    CTGCCGTCGG TTACCAGCCC ACCCTGGCCG TCGACATGGG TGGTATGCAG      450
    GAGCGTATCA CCACCACCAA GAAGGGTCTT ATTACCTCCG TC                      492
55

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2) INFORMATION FOR SEQ ID NO: 459

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60  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1154 bases

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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

	GTCCGTGGTC	AAGAAGTTAT	TGACACTGGT	GCCCCAATTA	CCATTCCTGT	50
	TGGTCGTGGT	ACTCTTGGA	GAATTATCAA	CGTCATTGGT	GAACCAATTG	100
15	ACGAACGTGG	TCCTATCAAG	GCTTCTAAGT	ATGCTCCTAT	CCATACTGAA	150
	CCACCAACCT	TTGCTGAACA	ATCTACTTCT	GCTGAAGTTC	TTGAAACTGG	200
	TATCAAGGTT	GTCGATCTTC	TTGCTCCTTA	CGCCCGTGGT	GGTAAGATTG	250
	GTCTTTTCGG	TGGTGCTGGT	GTCGGTAAGA	CTGTCTTCAT	TCAAGAACTT	300
	ATTAACAACA	TTGCCAAGGC	TCACGGTGGT	TTCTCTGTCT	TCACTGGTGT	350
20	CGTGAAAGA	ACCCGTGAAG	GTAACGATCT	TTACCGTGAA	ATGAAGGAAA	400
	CTGGTGTCAT	CAACCTCGAA	GGTGACTCCA	AGGTCGCTCT	CGTTTTTCGGT	450
	CAAATGAACG	AACCTCCAGG	TGCCCGTGCC	CGTGTCGCTT	TGACTGGTCT	500
	TACCATTGCC	GAATACTTCC	GTGATGAAGA	AGGACAAGAT	GTCTTGCTTT	550
	TCGTTGACAA	CATTTTCAGA	TTCACCCAAG	CCGGTTCTGA	AGTCTCTGCT	600
25	CTTTTGGGTC	GTATTCCATC	TGCCGTCGGT	TACCAACCTA	CCCTTGCTAC	650
	CGATATGGGT	GCCCTCCAAG	AACGTATTAC	CACCACCCAA	AAGGGTTCCTG	700
	TCACATCTGT	CCAAGCCGTC	TATGTCCCAG	CAGACGATTT	GACTGATCCT	750
	GCCCCAGCCA	CCACTTTCGC	TCACTTGGAC	GCCACCACTG	TCTTGCTCTCG	800
	TTCCATTTC	GAATTGGGTA	TCTACCCAGC	TGTGATCCT	CTCGATTCCA	850
30	AGTCTCGTCT	TTTGGATCCT	GAAGTTATTG	GACACGAACA	CTACGAAGTT	900
	GCCACTCAAG	TTCAACAAAC	CCTCCAAGCT	TACAAGTCTC	TCCAAGATAT	950
	CATTGCCATT	TTGGGTATGG	ATGAATTGTC	TGAAGCTGAT	AAGCTTACTG	1000
	TCGAACGTGC	CCGTAAGATC	CAAAGATTCC	TTTCCCAACC	ATTGCTGTGTT	1050
	GCCGAAGTTT	TCACTGGTAT	CGAAGGTCGT	CTCGTTCCAT	TGAAGGAAAC	1100
35	CGTCAGATCT	TTCAAGGAAA	TCCTTGAAGG	TAAGTACGAT	CACCTTCCAG	1150
	AAGC					1154

40 2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

55	CCAATTCGAC	GAAGGAAACT	TGCCAGCTAT	TTTGAATGCT	TTGACTTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCTCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCTATTGC	TATGGATGGT	ACTGAAGGTT	TAGTCAGAGG	150
	TACCGAAGTC	AACGATACCG	GTGCCCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
60	GTACTTTAGG	TAGAATCATC	AATGTTGTTG	GTGAACCAAT	TGATGACAGA	250

	GGTCCAATTG	AATGTAAGGA	AAAGAAACCA	ATTCACGCTG	AACCACCATC	300
	ATTGCTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAACC	GGTATCAAGG	350
	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
5	CATTGCCAAA	GCCCCATGGT	GTTTCTCTGT	CTTTACCGGT	GTYGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTTGAAGTGG	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTCAATTGAT	700
10	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCT	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTT	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTC	GCCCCATTTG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
15	CTGAATTGGG	TATCTACCCA	GCTGTGCGAT	CATTGGATTG	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTCGCTG	TTGCTGAAGT	1200
20	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

25 2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAAGTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
45	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
50	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCGG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTG	700
55	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTTCCTGTA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTCGCCCA	900
	TTTGGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
60	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000

	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTC	AAACAACTTT	1050
	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100
	AATTGTCTGA	AGCTGATAAA	TTGACTGTCTG	AAAGAGCCCG	TAAGATTCAA	1150
	AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTCA	CTGGTATTCC	1200
5	AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAAATCATTC	AAGGATGTTT	1250
	TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

10 2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACTTGCC	AGCTATTTTG	AACGCTTTGA	CCTTGAAGAA	CGGTGAAAAC	50
	GACTTAGTTT	TAGAAGTTGC	CCAACATTTG	GGTGAAAACA	CCGTCAGAGC		100
	TATTGCTATG	GATGGTACTG	AAGGTTTAGT	TAGAGGTACT	CCAGTTACCG		150
	ATTCTGGTGC	TCCAATTTCT	GTCCAGTCG	GTAGAGGTAC	TTTAGGTAGA		200
30	ATCTTGAACG	TTATTGGTGA	ACCAATTGAT	GAACAAGGTC	CAGTTGATGC		250
	CAAGGAAACC	AGACCAATTC	ACCAAGACCC	ACCAGCATTC	GTTGATCAAT		300
	CCACCAAGGC	TGAAGTTTTG	GAAACTGGTA	TCAAGGTTGT	CGATTTATTA		350
	GCCCCTTACG	CTAGAGGTGG	TAAGATTGGT	TTATTCGGTG	GTGCCGGTGT		400
	CGGTAAGACC	GTCTTTATCC	AAGAATTGAT	TAACAACATT	GCCAAGGCCC		450
35	ATGGTGGTTT	CTCTGTTTTC	ACTGGTGTCTG	GTGAAAGAAC	CAGAGAAGGT		500
	AACGATTTAT	ATAGAGAAAT	GAAGGAAACT	GGTGTCTATTA	ACTTGAAGG		550
	TGACTCCAAG	GTCGCCTTGG	TTTTCGGTCA	AATGAACGAA	CCACCAGGTG		600
	CTAGAGCTAG	AGTTGCTTTA	ACCGGTTTAA	CCATTGCCGA	ATACTTCAGA		650
	GACGAAGAAG	GTCAAGATGT	GTTATTGTTC	GTCGATAACA	TTTTTAGATT		700
40	CACCCAAGCC	GGTTCCGAAG	TGTCTGCTTT	GTTAGGTCGT	ATTCCATCGG		750
	CTGTCCGGTTA	TCAACCAACC	TTAGCCACTG	ATATGGGTCT	TTTACAAGAA		800
	AGAATTACCA	CCACCACCAA	GGGTTCCGTT	ACTTCTGTCC	AAGCTGTCTA		850
	CGTCCCAGCC	GATGATTTAA	CCGATCCTGC	TCCAGCTACC	ACTTTCGCCC		900
	ACTTGGATGC	TACCACTGTG	TTGTCTCGTG	GTATCTCTGA	ATTGGGTATT		950
45	TACCCAGCTG	TCGATCCATT	GGATTCCAAA	TCCAGATTGT	TAGATGCTGA		1000
	TATCGTTGGT	AAAGAACACT	ACGAAGTTGC	CACTGGTGTC	CAACAAACCT		1050
	TACAAGCTTA	CAAATCTTTA	CAAGATATCA	TTGCTATTTT	AGGTATGGAT		1100
	GAATTGTCTG	AAGCCGATAA	ATTGACTGTC	GAAAGAGCCA	GAAAGATCCA		1150
	AAGATTCTTG	TCTCAACCAT	TCGCCGTTGC	CGAAGTTTTT	ACCGGTATCC		1200
50	CAGGTAGATT	AGTTAGATTG	CAAGACACTG	TTAAATCTTT	CAAGGAAGTC		1250
	TTAGAAGGTA	AATATGATCA	CTTACCAG				1278

55 2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

10 TCTGGTCAGA GGCGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC 50
CTGTCGGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CCGTGAACCT 100
ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC 150
CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA 200
15 CAGGTATCAA GGTCGTCGAC TTGTGGCCCC CTTACGCCAG AGGTGGTAAG 250
ATCGGTCTGT TCGGTGGTGC CGGTGTCTGGT AAGACCGTGT TCATCCAAGA 300
ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTACAG 350
GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG 400
GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CTTGGTCTT 450
20 CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG 500
GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG 550
CTGTTTCGTCG ACAACATTTT CAGATTCACC CAAGCCGGTT CAGAAGTCTC 600
CGCTTTGCTA GGTCGTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG 650
CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT 700
25 TCCGTCACTT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA 750
TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT 800
CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCGA CCCATTGGAC 850
TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA 900
CGTCGCCACA AAGGTCCAAG AAACTTTACA AACTTACAAG TCTCTGCAAG 950
30 ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCGGAACA AGATAAGCTA 1000
ACTGTGCGAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCC AACCATTTCG 1050
TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG 1100
ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT 1150
CCAG 1154

35

2) INFORMATION FOR SEQ ID NO: 464

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

50 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

55 CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA 50
AGAACGGTGA CCAAAACTTG GTTTTGGGAAG TTGCCAGCA TTTGGGTGAA 100
AACACCGTCA GAACCATTCG TATGGATGGT ACTGAAGGTT TGGTTAGAGG 150
TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG 200
GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT 250
GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTACGCTG AACCACCATC 300
60 GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAACC GGTATCAAGG 350

	TTGTCGACTT	GTTGGCTCCA	TACGCCAGAG	GTGGTAAGAT	TGGATTGTTCT	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTGTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	GTTCAACGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
5	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTCG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTCGTGAC	700
	AACATTTTCA	GATTCACTCA	AGCTGGTTCT	GAAGTGTGCG	CTTTGTTGGG	750
	TCGTATTCCCT	TCGGCTGTCTG	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
10	GTTTGTGTC	AGAGCGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTCGATC	CTTTGGATTTC	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
15	CGTTCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
	GCCCCGTAAGA	TCGAGAGATT	CTTGCTCTCA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATCACTTGCC	AGA	1293
20						

2) INFORMATION FOR SEQ ID NO: 465

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1293 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Candida haemulonii*
- (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
40	GAACGGTGAC	CAGGACTTGG	TCTTGAGAGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTGAC	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
45	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCTT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTCG	400
	GTGGTGCCGG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
50	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTGC	650
	CGAATACTTC	AGAGATGAAG	AAGGTCAGGA	TGTGTTGTTG	TTCGTTGACA	700
	ACATTTTTCAG	ATTCACTCAG	GCTGGTTCCT	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTCTG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
55	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTC	GTCACCTCTG	850
	TCCAGGCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
	ACCACTTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTT	950
	CGAGTTGGGT	ATCTACCCAG	CTGTCGACCC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
60	GTCCAGCAGA	CCTTGCAGGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100

TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCGAGAGAG	1150
CTAGAAAGAT	TCAGAGATTC	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCAGTGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

2) INFORMATION FOR SEQ ID NO: 466

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear.

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
25 CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTAGAGGTC	100
AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	CGGTAGAGGT	150
ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	ATGAAAGAGG	200
TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	CCTCCTGCTT	250
TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAACCGG	TATTAAGGTT	300
30 GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	GTTTATTCCG	350
TGGTGCTGGT	GTCGGTAAAA	CCGTTTTTCAT	TCAAGAATTA	ATTAACAATG	400
TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCACTGGTGT	CGGTGAAAGA	450
ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	CTGGTGTTAT	500
TAACCTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTCCGT	CAATGAATG	550
35 AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	AACTATTGCT	600
GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCATTGATAA	650
CATTTTCAGA	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	TTGTTAGGTA	700
GAATTCCATC	CGCTGTCCGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	750
CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCCG	TTACTTCTGT	800
40 CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	GCTCCAGCAA	850
GTACTTTTCG	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	AGGTATTTCC	900
GAATTAGGTA	TTTACCCAGC	TGTGATCCCA	TTAGATTCTA	AATCTAGATT	950
ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	GCAACTCAAG	1000
TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	TATTGCTATT	1050
45 TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	TTGAAAGAGC	1100
AAGAAAGATT	C				1111

50 2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida kefyr*

(B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

5
 TCGAACAAGG TCAATTGCCA GAAATTTTGA ACGCTTTGGA GATTGAWACT 50
 CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTTGG GTGAAAACAC 100
 CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA 150
 AGGTTTTTGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAACT 200
 10 TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCC 250
 AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG 300
 TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACCGGTAT CAAGGTTGTC 350
 GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCCGTGG 400
 TGCCGGTGTC GGTAAAGACCG TTTTCATCCA AGAGTTGATT AACAACATTG 450
 15 CCAAGGCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC 500
 AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACCG GTGTCATCAA 550
 CTTGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCGGTCAA ATGAACGAAC 600
 CACCTGGAGC TAGAGCCAGA GTTGCCTTGA CCGGTTTGAC TATCGCTGAA 650
 TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT 700
 20 TTTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750
 TTCCATCCGC TGTCGGTTAC CAACCTACTT TGGCCACCGA TATGGGTTTG 800
 TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCCGTTA CCTCCGTCCA 850
 AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA 900
 CTTTCGCCCA TTTGGACGCC ACCACCGTGT TGTCAGAGG TATCTCCGAA 950
 25 TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT 1000
 GGACGCTGCC GTTGTGCGTC AAGAACATTA CGACGTCGCT ACTCAAGTTC 1050
 AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG 1100
 GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCG AAAGAGCCAG 1150
 AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTCA 1200
 30 CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC 1250
 AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTG 1283

35 2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1287 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

50
 CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA 50
 ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC 100
 ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA 150
 AACCCTTAAC GATACCGGTG CTCCAATCTC TGTCCCAGTT GGTAGAGGTA 200
 55 CCTTAGGTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT 250
 CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT 300
 CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAACTGGT ATTAAGGTTG 350
 TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCGGT 400
 GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT 450
 60 YGCAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA 500

	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTATT	550
	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTCGGTC	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTGCAG	650
	AATATTTCAG	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
5	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTCGCC	CACTTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
10	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
15	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

20 2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCCAGTTGG	TAGAGGTACT	200
40	TTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTCC	300
	TTGACCAATC	CACTGAAGCT	GAAGTTTGG	AAACCGGTAT	TAAGGTTGTC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTCATCCA	AGAAATTGATT	AACAATGTTG	450
45	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTCA	CTGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
50	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCCGTCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTTCGCCA	CTTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
55	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
	GGATGTCGCT	GTTGTCCGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCCTTT	CCCAACCTTT	CTCCGTCGCA	GAAGTTTTCA	1200
60	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTC	1250

5 2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20 AGGTGCCTCT GTCACTGACA CTGGTTCTCC AATCTCTGTC CCTGTTGGTC 50
GTGAAACCTT GGGTAGAATT ATCAACGTTG TTGGTGAGCC AATTGACGAG 100
AGAGGCCCAA TCAACTCCAA GAAGAGAAAC CCAATTCACA CTGAGCCACC 150
ATCGTTTGTT GAACAATCCA CTTCTGCTGA AGTTTGGAG ACTGGTATCA 200
25 AGGTTGTCGA CTTGTTGGCC CTTACGCCA GAGGTGGTAA GATTGTTTGT 250
TTCGGTGGTG CCGGTGTCGG TAAGACCGTT TTCATCCAAG AGTTGATTAA 300
CAACATTGCC AAGGCCACG GTGGTTTCTC TGTTTTCCT GGTGTCGGTG 350
AAAGAACCAG AGAAGGTAAC GATTGTACC GTGAAATGCA AGAGACCGGT 400
GTCATCAACT TCGAGGGTGA CTCCAAGGTC GCCTTGGTCT TCGGTCAAAT 450
30 GAACGAACCA CCAGGAGCCA GAGCTAGAGT TGCTTTGACC GGTTTGACTA 500
TTGCCGAGTA CTTCAGAGAC GAAGAGGGCC AAGATGTCTT GTTGTTCGTT 550
GACAACATTT TCAGATTCAC CCAGGCCGGT TCTGAAGTGT CTGCTTTGTT 600
GGGTGCTATT CCATCCGCTG TCGGTTACCA ACCAACCTTG GCCACCGATA 650
TGGGTGCTTT GCAAGAGAGA ATTACCACCA CCAAGAAGGG TTCCGTCACC 700
35 TCTGTCCAAG CCGTTTATGT TCCAGCTGAT GACTTGACTG ACCCTGCTCC 750
AGCCACCACC TTCGCCACT TGGACGCCAC CACTGTGTTG TCCAGAGGTA 800
TCTCTGAATT GGGTATCTAC CCAGCTGTCG ACCCATGGA CTCCAAGTCT 850
AGATTGTTGG ACGCTTCTAT TGTTGGTAAG GAGCACTACG AAGTTGCTTC 900
TAACGTTCAA CAACTTTGC AAGCTTACAA GTCTTTGCAA GATATCATTG 950
40 CCATTTTGGG TATGGATGAA TTGTCTGAGG CTGACAAGTT GACCGTTGAG 1000
AGAGCCAGAA AGATCCAAAG ATTCTTGCTT CAACCATTCG CTGTTGCCGA 1050
GGTTTTCACT GGTATCCCAG GTAGATTGGT CAGATTGGAG GACACTGTCA 1100
GATCCTTCAA GGAAGTTTGT GACGGTAAGT ACGACCACTT 1140

45

2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
60 (B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTGCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAG	TTGCTCAACA	TTTAGGTGAA	100
5	AACACCGTCA	GAACCATGTC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTACTTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
10	TTGTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAC TAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTCG	GTCAAATGAA	600
15	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGCTCTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTT	TGTTACTTCC	850
20	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTGATC	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
25	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	AACTTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
50	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTACTTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAACC	GGTATTAAAG	350
55	TTGTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTCG	GTCAAATGAA	600
60	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTTGAAGGTT	TTGACCATTC	650

	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCCGCTGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACTACCA	AAAAGGGTTC	AGTTACTTCA	850
5	GTCCAAGCCG	TTTACGTGCC	AGCTGATGAT	TTAACCGATC	CTGCTCCAGC	900
	TACCACTTTC	GCTCACTTGG	ATGCCACCAC	TGTGTTGTCT	AGAGGTATTT	950
	CGGAGTTGGG	TATTTACCCA	GCTGTGATC	CATTGGATTC	CAAATCCAGA	1000
	TTGTTGGATG	CTGCCGTTGT	TGGTCAAGAA	CATTACGACG	TTGCCACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAGTC	CTTGCAAGAT	ATCATTGCTA	1100
10	TCTTGGGTAT	GGATGAATTG	TCCGAACAAG	ATAAATTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TTCAAAGATT	CTTGTCTCAA	CCATTTGCTG	TCGCTGAAGT	1200
	TTTCACTGGT	ATTCCAGGTA	AATTGGTTAG	ATTGTCTGAA	ACTGTCAAGT	1250
	CATTCAAGGA	AGTCTTGAA	GGTAAGTACG	ATAACTTGCC	AGAAAAT	1297

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2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1285 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida rugosa*

(B) STRAIN: ATCC 96275

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

	CCAGTTTGGC	AACGACCTCC	CTGCCATTTT	GAACGCCCTC	ACTCTTCAGC	50
	GTGAAGACGG	TAACAAGCTT	GTTCTTGAGG	TTGCCCAGCA	TCTCGGTGAG	100
35	AACACCGTCC	GTACCATTGC	TATGGACGGT	ACCGAGGGTT	TGGTGCGTGG	150
	CACTGGTGTC	CACGACACCG	GACACCCCAT	CATGACTCCC	GTCGGTGACG	200
	GTACCCTGGG	ACGTATTCTT	AACGTCACCG	GTGACCCTGT	AGACGAGCGT	250
	GGTCCCGTCA	AGACTGACAA	GTTCCGCCCC	ATCCACGCCG	AGGCCCTGTC	300
	CTTCGATGAG	CAGGCTACCA	GTGCCGAGGT	TCTTGAGACC	GGTATCAAGG	350
40	TTGTCGACTT	GCTCGCTCCT	TACGCCAAGG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGCAA	GACCGTCTTC	ATCCAGGAGC	TGATTAACAA	450
	CATCGCCAAG	GCCCACGGTG	GTTACTCCGT	GTTCACTGGT	GTCGGTGAGC	500
	GTA CTCTGTA	GGGTAACGAT	TTGTACAAGG	AAATGATCGA	GTCCGGTGTC	550
	ATCAACCTCG	ATGGTGAGTC	CAAGGTCGCC	TTGGTGTTTCG	GTCAGATGAA	600
45	CGAGCCCCCT	GGAGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTTACCATCG	650
	CTGAGTATTT	CCGTGATGAG	GAGGGTAAGG	ATGTCTTGTT	GTTTCGTTGAC	700
	AACATTTTCC	GCTTCACTCA	GGCCGGTTCT	GAGGTGTCCG	CCTTGCTTGG	750
	TCGTATTCTT	TCCGCTGTCG	GTTACCAGCC	TACCCTGGCC	ACCGATATGG	800
	GTGCCCTTCA	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	CGTTACATCC	850
50	GTCCAGGCCG	TCTACGTCCC	TGCCGATGAT	TTGACTGATC	CCGCCCCCTGC	900
	CACCACCTTC	GCCCATTGTT	ATGCCACCAC	TGTCTTGTCT	CGTGCCATCT	950
	CTGAGTTGGG	TATCTACCCC	GCTGTGACCC	CTCTCGACTC	CAAGTCCCGT	1000
	CTTCTTGACG	CCGCTGTCTG	TGGTCAGGAG	CACTACGATA	CTGCCACCTC	1050
	CGTTCAGCAG	ACTTTGCAGG	CTTACAAGTC	TTTGCAGGAT	ATCATTGCCA	1100
55	TTCTTGGTAT	GGATGAGTTG	TCCGAGTCTG	ACAAGCTCAC	CGTCGAGCGT	1150
	GCTCGTAAGA	TCCAGCGTTT	CCTCTCCCAG	CCTTTCGCTG	TTGCTGAGGT	1200
	CTTCACTGGT	ATTCAAGGCC	GTCTTGTTCC	TCTCAAGGAC	ACTGTCCGCT	1250
	CCTTCAAGGA	GATTCTCGAA	GGTAAGTACG	ATGCT		1285

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2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

TTGAACAAGG TCAATTGCCA GCTATTTTGA ACGCTTTGGA AATCGACACT 50
 CCAGAAGGAA AGTTGGTTTT GGAAGTCGCT CAACATTTGG GTGAAAACAC 100
 20 TGTCAGAACCC ATTGCTATGG ATGGTACTGA AGGTTTAGTC CGTGGTGAAA 150
 ACGTTTCTGA CACTGGTGCT CCAATTTCCG TCCCAGTTGG TAGAGAAACC 200
 TTGGGTAGAA TTATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGTCC 250
 AATCAACTCC AAGATGAGAA AGCCAATTCA TGCTGATCCT CCATTATTCTG 300
 TTGAACAATC CACTGCTGCT GAAGTTTTGG AAAGTGGTAT CAAGGTTGTC 350
 25 GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCGGTGG 400
 TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAATTGATT AACAACATTG 450
 CCAAGGCTCA TGGTGGTTTC TCTGTCTTCA CTGGTGTCGG TGAAAGAACC 500
 AGAGAAGGTA ACGATTGTGA CCGTGAAATG AAGGAAACTG GTGTTATCAA 550
 CTTGGAAGGT GATTCTAAGG TCGCGTTGGT TTTCGGTCAA ATGAACGAAC 600
 30 CTCCTGGAGC TAGAGCTAGA GTCGCCTTGA CTGGTTTGAC CATCGCTGAA 650
 TACTTCAGAG ATGAAGAAGG TCAAGATGTC TTGTTGTTTA TCGACAACAT 700
 TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750
 TTCCATCCGC TGTCGGTTAT CAACCAACTT TGGCCACCGA TATGGGTTTG 800
 TTGCAAGAAA GAATTACTAC CACCAAGAAG GGTTCCGTCA CTTCTGTCCA 850
 35 AGCCGTTTAC GTGCCAGCTG ATGATTTGAC TGATCCTGCT CCAGCTACCA 900
 CTTTCGCGCA TTTGGATGCC ACCACTGTGT TGTCCAGAGG TATCTCTGAA 950
 TTGGGTATCT ACCCAGCTGT CGATCCTTTG GATTCCAAAT CTAGATTGTT 1000
 GGATGCTGCC GTCGTTGGTC AAGAACATTA CGATGTCGCT ACTCAAGTTC 1050
 AACAACTTT GCAAGCTTAC AAGTCTTTC AAGATATCAT TGCCATTTTG 1100
 40 GGTATGGATG AATTGTCCGA ACAAGATAAG TTGACCGTCG AAAGAGCTAG 1150
 AAAGATTCAA AGATTCTTGT CTCACCTTT CGCTGTCGCT GAAGTCTTCA 1200
 CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CTCTTCTTTC 1250
 AAGGCTGTCT TGGACGGTAA GTACGATCAC TTG 1283

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2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGTTTGT	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
5	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTCTG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCTG	350
10	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTGT	GTTCGGTGGT	400
	GCTGGTGTCTG	GTAACACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCCGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTGTGAC	CGTGAAATGA	AAGAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
15	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTCAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTTAC	TTCTGTCCAA	850
20	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGCTCAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTC	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
25	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCGA	AAGAGCTCGT	1150
	AAGATTCAAA	GATTCTTGTC	CCAACCATTC	GCTGTTGCCG	AAGTTTTTCAC	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

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2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
50	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCGTATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCGA	CCTTCTCGCC	CCATACGCCA	350
55	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACAG	GTGGTTTCTC	450
	TGTTTTTACC	GGTGTCCGGT	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCCTGT	600
60	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650

	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTCAC	CCAGGCCCGT	700
	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGTT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCAC	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
5	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCACT	TGGACGCCAC	900
	CACTGTGTTG	TCCCGTGGTA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCTG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
10	CTGACAAGTT	GACTGTCGAG	AGAGCCAGAA	AGATTCAGCG	TTTCCTTTCC	1150
	CAGCCATTCTG	CTGTCTGCTGA	GGTTTTCACC	GGTATCCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTTG	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

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2) INFORMATION FOR SEQ ID NO: 477

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1296 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
- (B) STRAIN: ATCC 28269

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTCGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
35	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGGG	TAGAATCATC	AACGTTGTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGGAAGACC	GGTATCAAGG	350
40	TTGTCTGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCTGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCC	TTGGTTTTCG	GTCAAATGAA	600
45	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTTGAAGGTT	TTGACCATTG	650
	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCCGGTTCC	GAAGTGCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCTGCCGTCG	GTTATCAACC	AACCTTGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
50	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGCT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTTGGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TCCAAAGATT	CTTGTCGCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTGGCT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

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2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

	TCAATTCGAG	CAAGGCAACC	TCCCTGCCAT	CTTGAACGCT	CTCACCTTGA	50
	AGAATGGTGA	CAACGACTTG	GTTTTGGAAG	TTGCCCAGCA	CTTGGGTGAG	100
20	AACACCGTCA	GAGCCATTGC	CATGGATGGT	ACCGAGGGTT	TGGTTAGAGG	150
	TGCGTCCGTC	AAGGACACTG	GCGCCCCTAT	CTCGGTCCCC	GTTGGCCGCG	200
	GGACTTTGGG	TCGTATCATC	AACGTCACCG	GTGACCCCAT	TGACGAGAGA	250
	GGTCCCATCG	AGCTGACCCA	GAGAAACCCT	ATCCACGCCG	ACCCCCCCTC	300
	GTTTCGTTGAG	CAGTCCACCA	ACGCTGAGGT	TTTGGAGACT	GGTATCAAGG	350
25	TTGTCGATTT	GTTGGCTCCC	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACCGTCTTC	ATTGAGGAGT	TGATCAACAA	450
	CATCGCCAAG	GCCCACGGTG	GGTTCTCGGT	CTTCACTGGT	GTCGGTGAGA	500
	GAAC TAGAGA	GGGTAACGAC	TTGTACCGTG	AGATGAAGGA	GACCGGTGTC	550
	ATCAACTTGG	AGGGTGACTC	CAAGGTGGCC	TTGGTGTTTCG	GTCAGATGAA	600
30	CGAGCCCCCT	GGAGCCAGAG	CCAGAGTCGC	CTTGACCGGG	TTGACCATTG	650
	CCGAATACTT	TAGAGACGAG	GAGGGTCAGG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATCTTCA	GATTCACCCA	AGCTGGTTCG	GAGGTGTCGG	CCTTGTTGGG	750
	TCGTATTCCC	TCTGCCGTCG	GTTACCAGCC	CACCTTGGCA	ACTGATATGG	800
	GATTGTTGCA	GGAGCGTATC	ACCACGACCA	AGAAGGGTTC	CGTCACCTCA	850
35	GTGCAGGCCG	TCTACGTCCC	CGCTGATGAC	TTGACTGACC	CTGCTCCCGC	900
	CACCACCTTT	GCCCACTTGG	ACGCCACCAC	CGTGTGTGCC	AGAGGTATCT	950
	CTGAGTTGGG	TATCTACCCC	GCCGTCGACC	CCTTGGAATC	CAAATCGAGA	1000
	TTGTTGGACG	CTGCCGTGGT	CGGTCAGGAG	CACTACGATG	TTGCCTCGAA	1050
	CGTCCAGCAG	ACCTTGCAGG	CCTACAAGTC	CTTGCAGGAT	ATCATTGCCA	1100
40	TTTGGGGTAT	GGATGAGTTG	TCCGAGGCTG	ACAAGTTGAC	CGTTGAGAGA	1150
	GCCAGAAAGA	TCCAGAGATT	CTTGTCGCTG	CCCTTCGCTG	TTGCCGAGGT	1200
	TTTCACTGGT	ATCAAGGGTA	GATTGGTCAG	ATTGGAGGAC	ACCGTCAGAT	1250
	CTTCAAGGA	GGTTTTGGAG	GGTAAGTACG	ACCACTTGCC	CGAGA	1295

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2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

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TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
CTGATATGCT CTAGAACAAAC ATTGCTAAGG CTCACGGTGG TTACTCCGTG      100
5  TTCACTGGTG TCGGTGAGCG TACCCGTGAG GGTAAACGATT TGTACCATGA      150
AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC      200
TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCCTGC CCGTGTGTC      250
CTTACCGGTT TGACCATTCG TGAATACTTC CGTGACGAGG AAGGCCAAGA      300
CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA      350
10 TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTTCACTCAA      400
GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCCTT CCGCTGTCGG      450
TTACCAACCT ACTCTCGCCG TCGACATGGG TGTTATGCAG GAACGTATCA      500
CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                          534

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2) INFORMATION FOR SEQ ID NO: 480

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 494 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Cryptococcus albidus
    (B) STRAIN: ATCC 66030

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

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CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTG GTT      50
ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG      100
35 TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA      150
CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC      200
GAGGGTGA CT CCAAGGTCGC CTTGGTCTTC GGTGAGATGA ACGAGCCCCC      250
TGGAGCCCGA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT      300
TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTCAATTGA CAACATTTTC      350
40 CGATTCACCC AAGCCGGTTC CGAAGTGTC GCCTTGTTGG GTCGTATCCC      400
CTCCGCCGTC GGTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC      450
AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC              494

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45

2) INFORMATION FOR SEQ ID NO: 481

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50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 415 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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55 (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Fusarium oxysporum
    (B) STRAIN: WSA-212

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60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

	TTCAGGAGCT	TATCAACAAC	ATCGCCAAGG	CCCACGGTGG	TTACTCCGTC	50
	TTCACTGGTG	TCGGTGAGCG	AACTCGTGAG	GGTAACGATC	TGTACCACGA	100
	AATGCAGGAG	ACTTCCGTCA	TTCAGCTTGA	TGGCGAGTCC	AAGGTCGCCC	150
5	TGGTCTTCGG	TCAGATGAAC	GAGCCCCCTG	GAGCTCGTGC	CCGTGTCGCC	200
	CTTACCGGTC	TTACTGTAGC	TGAATACTTC	AGAGATGAGG	AGGGTCAGGA	250
	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	ATTCACTCAG	GCCGGTTCCG	300
	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	CTGCCGTCGG	TTACCAGCCC	350
	ACCCTCGCCG	TCGACATGGG	TGGTATGCAA	GAGCGTATTA	CCACCACCAC	400
10	CAAGGGTTCC	ATTAC				415

2) INFORMATION FOR SEQ ID NO: 482

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: Lev-4

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30	AGGACAACCT	CCCCGCTATT	CTTAACGCTC	TTGAGCTTAA	GAGAGATAAC	50
	GGTGAGAAGC	TCGTTCTCGA	GGTTGCCCAG	CATCTGGGTG	AGAACACTGT	100
	CCGTACTATT	GCTATGGACG	GTA CTGAGGG	TCTCGTCCGT	GGTCAGCCCCG	150
	TTGTTGACAC	CGGTGCCCCC	ATTACCATT C	CCGTTGGTGC	TGGTACTCTT	200
	GGTAGAATTA	TCAACGTCAT	TGGTGAGCCC	ATCGATGAGC	GTGGACCCAT	250
35	TGAGGCTACC	AAGTACCTCC	CCATCCACAC	CGAGCCCCCC	ACCTTCGCTG	300
	AGCAGTCTAC	CTCCGCTGAG	GTTCTTGAGA	CTGGTATCAA	GGTTGTGCAT	350
	CTCCTTGCCC	CCTACGCCCG	TGGTGGAAG	ATTGGTCTCT	TCGGTGGTGC	400
	CGGTGTGCGT	AAGACCGTTT	TCATT CAGGA	GCTGATTAAC	AACATTGCCA	450
	AGGCCCATGG	TGGTTTCTCC	GTTTT CACCG	GTGTCGGTGA	GAGAACCCGT	500
40	GAGGGTAACG	ATTTGTACCG	TGAGATGAAG	GAGACCGGTG	TCATCAACCT	550
	CGAGGGTGAG	TCTAAGGTCC	CTCTCGTTTT	CGGTCAGATG	AACGAGCCCC	600
	CTGGAGCCCG	TGCCCCGTGT	GCTCTTACTG	GTCTTACCAT	TGCTGAGTAC	650
	TTCCGTGATG	AGGAGGGTCA	GGATGTGTTG	CTCTTCGTTG	ACAACATTTT	700
	CCGTTTCACT	CAGGCCGGTT	CCGAGGTGTC	TGCCCTTTTG	GGTCGTATTC	750
45	CCTCCGCTGT	CGGTTACCAG	CCCACCCTTG	CCACTGATAT	GGGTGCCCTG	800
	CAAGAGCGTA	TTACCACCAC	CCAGAAGGGT	TCCGTCACTT	CCGTCCAGGC	850
	CGTCTACGTC	CCTGCCGATG	ATTTGACCGA	TCCTGCCCCT	GCTACCACCT	900
	TCGCCCATTT	GGATGCCACC	ACCGTCTTGT	CGCGTTCCAT	TTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCGA	TCCCCTTGAT	TCCAAGTCTC	GTCTTTTGGA	1000
50	TATCACCGTC	GTTGGCCAGG	AGCACTACGA	TGTTGCTACC	CAGGTCCAGC	1050
	AGACCCTCCA	GTCCTACAAG	TCTCTTCAGG	ATATCATTGC	CATTTTGGGT	1100
	ATGGATGAGT	TGTCTGAGGC	TGATAAGCTT	ACTGTCGAGC	GTGCCC GTAA	1150
	GATCCAGAGA	TTCCTTTCCC	AGCCCTTCAC	TGTCGCTGAG	GTTTTCACTG	1200
	GTATCGAGGG	CCGTCTCGTT	CCTTTGAAGG	ACACTGTTTCG	CTCTTTCAAG	1250
55	GAGATCCTTG	AGGGCAAGTA	CGACCACCTC	C		1281

2) INFORMATION FOR SEQ ID NO: 483

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

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15  ATTCAAGAAT TGATCGTACG TTCCTCCGCC, CCACACACGA TCAATGGAGA      50
    AAGAAACAAA TTTTGTGGGA GTGGTCATTT TTTCTAATAA TTCGAATAGA      100
    ACAACATTGC CAAAGCCCAC GGTGGTTACT CCGTGTTTAC TGGTGTCCGC      150
    GAGCGGACCC GTGAAGGAAA TGACTTGATC CACGAAATGC AGGAAACCCG      200
    TGTATCCAG CTCGATGGAG AGTCCAAGGT CGCCCTCGTT TTCGGTCAGA      250
20  TGAACGAGCC TCCCGGAGCC CGTGCCCGTG TTGCCCTCAC TGGTCTGACC      300
    GTTGCCGAGT ACTTCCGTGA CGAGGAAGGC CAAGACGGTA TGTATAAGTA      350
    TACACCGTAG CAAATCAACA CAGAGCTTCA CTCACGCTCG GATTTAGTGC      400
    TTCTCTTCAT CGACAACATT TTCCGCTTCA CTCAGGCCGG TTCCGAAGTG      450
    TCTGCCCTGC TCGGCCGTAT TCCCTCCGCC GTCGGTTACC AACCCACCCT      500
25  CGCCGTGGAC ATGGGTGGTA TGCAGGAACG TATCACCCT ACCACCAAGG      550
    GCTCCATCAC CTCTGTGCAR GCCGTCTACG TCCCCG      586
  
```

2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

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45  GCGTGGCCAG AAGGTCATTG ACACTGGTGC TCCCATCACC ATCCCCGTCTG      50
    GTGGTGCCAC ACTGGGTCGT ATTCTGAACG TCACGGGTGA CCCTATTGAC      100
    GAGCGTGGCC CCGTTAAGAC TGACGTTTTC CGCCCCATTC ACCGTGACCC      150
    CCCTGCCTTT GTCGAGCAGT CGACTGATGC CGAGATTCTC GAGACTGGTA      200
50  TCAAAGTCGT TGACCTGATT GCCCCTTACG CCCGTGGTGG TAAGATTGGT      250
    CTGTTCCGGT GTGCCGGTGT CGGTAAGACC GTGCTTATCC AGGAGCTCAT      300
    CAACAACATC GCCAAGGCCC ACGGTGGTTT CTCCGTGTTT ACTGGTGTCTG      350
    GTGAGCGTAC TCGTGAGGGT AACGATTGTG ACCACGAGAT GATTGAAACC      400
    GGTGTCATTA ACCTCGAGGG TGAAGTGAAG GTGGCTCTGG TGTTCCGGTCA      450
55  GATGAACGAG CCCCCGGGTG CCCGTGCGCG TGTCGCTCTT ACTGGTCTGA      500
    CTGTGGCCGA GACTTCCGT GACGACGAGG GCCAGGATGT GCTGCTGTTT      550
    ATTGACAACA TTTTCCGTTT CACCCAGGCC GGTTCGGAGA CTTCCGGCTCT      600
    GCTGGGTCGT ATCCCTTCGT CGGTCGGTTA CCAGCCCACT TTGTCGACCG      650
    ATATGGGTGC CATGCAGGAG CGTATCACCA CCACCAAGAA GGGTTCGATT      700
60  ACGTCGGTGC AGGCCGTCTA CGTGCCCGCC GATGATGTCA CTGACCCTGC      750
  
```

	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACCTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
5	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
	GAGCGTGCCC	GTAAGATGCA	GCGTTTCATG	TCGCAGCCTT	TCGCTGTCCG	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCGGGCA	AGCACGACAA	CCTCC	1145

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2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1261 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTTGCC	CAGCACCTTG	GTGAGAACAC	TGTTTCGTTGC	100
30	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCTTGA	150
	CACTGGTGCC	CCGATCACTA	TCCCTGTCCG	TAACGGTACC	TTGGGCCGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACC	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTTC	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
35	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGGTG	TGCYGGTGT	400
	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTCA	CTGGTGTCGG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTCCGGTCAG	ATGAACGAGC	CCCCGGGTGC	600
40	CCGTGCCCGT	GTCGCCCTGA	CYGGCTCTGAC	CATCGCCGAG	TACTTCCGTG	650
	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCCGGAGAC	TTCGGGCTCTG	CTGGGTCGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
45	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCA	900
	CTTGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGCGYAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACTCGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
50	AGTTGTCCGA	GGAGGACAAG	CTCACTGTCT	AGCGTGCCCG	TAAGATGCAG	1150
	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCGTCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTC	1250
	TGTCCGGTAA	G				1261

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2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1282 bases

298

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 486

	AGGAGGGCAA	CTTGCCAGCT	ATCTTCAACG	CTTTGACGTT	GAAGAACGGC	50
	GACCAGAACT	TGGTCTTGGA	GGTGGCCCAG	CACTTGGGTG	AGAACACCGT	100
15	CAGAACCATT	GCCATGGACG	GTACCGAGGG	TTTGGTCAGA	GGCGCCTCTG	150
	TCACCGACAC	YGGTGCCCCCT	ATCTCCGTGC	CTGTCGGCCG	TGAGACCTTG	200
	GGTCGTATTA	TCAATGTTGT	TGGTGAGCCA	ATCGACGAGA	GAGGCCCAAT	250
	CAACACCAAG	AAGAGAAACC	CTATTACAC	CGACCCACCT	TCGTTTGTCC	300
	AGCAATCCAC	TTCCGCCGAG	GTCTTGAGGA	CTGGTATCAA	GGTTGTCTGAC	350
20	TTGTTGGCCC	CTTACGCCAG	AGGTGGTAAG	ATTGGTTTGT	TCGGTGGTGC	400
	CGGTGTCTGGT	AAGACCGTGT	TCATCCAGGA	GTTGATTAAC	AACATTGCCA	450
	AGGCCACCGG	TGGTTTCTCC	GTTTTACCG	GTGTCGGTGA	GAGAACCAGA	500
	GAGGGTAACG	ATTTGTACCG	TGAAATGCAG	GAGACTGGTG	TCATCAACTT	550
	CGAGGGTGAC	TCCAAGGTCG	CCTTGTTTT	CGGTCAGATG	AACGAGCCTC	600
25	CAGGAGCTAG	AGCYAGAGTT	GCCTTGACCG	GTTTGACCAT	CGCCGAGTAC	650
	TTCAGAGACG	AGGAGGGTCA	GGATGTGTTG	TTGTTCTGTCG	ACAACATTTT	700
	CAGATTCACC	CAAGCCGGTT	CTGAGGTGTC	TGCCTTGTTG	GGTCGTATTC	750
	CATCCGCTGT	CGGATAACCAG	CCAACCTTGG	CCACCGATAT	GGGTGCCTTG	800
	CAGGAGAGAA	TTACCACCAC	CAAGAAGGGT	TCCGTCACCT	CCGTCCAGGC	850
30	CGTCTACGTG	CCAGCCGATG	ACTTGACTGA	CCCTGCGCCA	GCCACCACTT	900
	TCGCCCCACTT	GGACGCCACC	ACTGTGTTGT	CCAGAGGTAT	CTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCTGA	CCCCTTGAGC	TCCAACCTCA	GATTGTTGGA	1000
	CGCCACCGTT	GTTGGCCAGG	AGCACTACGA	CGTCGCCACC	AACGTCCAGC	1050
	AAACTTTACA	AGCTTACAAG	TCCTTGACAG	ATATCATTCG	CATTTTGGGT	1100
35	ATGGATGAGT	TGTCCGAGAC	CCGACAAGTT	GACCCGTCGA	GAGAGCCAGA	1150
	AAGATCCAGA	AGTTCTTGTC	CCAGCCATTT	GCCGTCGCCG	AGGTTTTTAC	1200
	CGGTATTGAG	GGTAGATTGG	TTAGATTGGA	GGACACCGTT	AGATCCTTTA	1250
	AGGAGGTTTT	GGAAGGTAAG	TACGACCACT	TG		1282

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2) INFORMATION FOR SEQ ID NO: 487

(i)SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 482 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: WSA-214

55

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 487

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TTACCTTTCT	GCCTGACTGT	50
	TTACGACAAC	TAACGAAAGC	GTAGAACAAC	ATTGCCAAGG	CTCACGGTGG	100
60	TTACTCTGTC	TTCACTGGTG	TCGGTGAACG	TACTCGTGAG	GGTAACGATT	150

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TGTACCACGA AATGCAGGAA ACTGGTGTCA TTCAGCTCGA GGGTGAATCC 200
AAGGTCGCCC TCGTGTTCGG TCAGATGAAC GAGCCCCCGG GTGCCCCGTGC 250
CCGTGTCGCT CTTACTGGTT TGACCATTTGCG GAGTACTTTC CGTGACGAGG 300
AAGGTCAGGA CGTGCTTCTC TTCATTGACA ACATTTTCCG TTCACTCAG 350
5 GCCGGTTCTG AGGTGTCTGC CCTTCTGGGT CGTATCCCCT CTGCCGTCGG 400
TTACCAGCCC ACCCTTGCCG TCGACATGGG TATCATGCAG GAGCGTATTA 450
CCACCACCAC CAAGGGTTCC ATCACCTCCG TC 482

10

2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1290 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

TCGAACAAGG TAACTTACCA GCTATCTTGA ATGCTTTAGA AATCAAAACC 50
CCAAGTGGTA CTCCATTAGT TTTAGAAGTT GCTCAACATT TAGGTGAAAA 100
CACTGTCAGA ACTATTGCTA TGGATGGTAC TGAAGGTTTA GTTCGTGGTG 150
30 AACAAGTTAC TGATACTGGT TCTCCAATCA CTGTCCCAGT TGGTCGTGAA 200
ACTTTAGGTC GTATTATCAA CGTTGTTGGT GAACCAATTG ATGAACGTGG 250
TCCAATTAAC ACCAAACAAA GAAACCCAAT TCACGCTGAA CCACCTTCAT 300
TCAGTGAACA ATCAACTGCT GCTGAAGTTT TAGAACTGG TATCAAAGTT 350
GTYGATTTAT TAGCTCCATA CGCTAGAGGT GGTAAAATTG GTTTATTCGG 400
35 TGGTGCCGGT GTCGGTAAAA CTGTCTTTAT CCAAGAATTG ATTAACAACA 450
TTGCTAAAGC TCATGGTGGT TTCTCAGTTT TCACCGGTGT TGGTGAAAGA 500
ACCAGAGAAG GTAACGATTT ATACCGTGAA ATGAAAGAAA CTGGTGTTAT 550
TAACTTGGA GGTGATTCTA AGGTCGCTTT AGTTTTCGGT CAAATGAATG 600
AACCACCAGG TGCTAGAGCT CGTGTGCTT TAACTGGTTT GACCATTGCT 650
40 GAATACTCA GAGATGAAGA AGGTCAAGAT GTCTTGTTAT TCGTTGATAA 700
CAATTTTCAG TTCACCCAAG CCGGTTTCAGA AGTTTCTGCC TTATTAGGTC 750
GTATTCCATC TGCTGTCGGT TATCAACCAA CTTTAGCAAC TGATATGGGT 800
TTGTTACAAG AACGTATTAC CACCACACAA AAAGGTTTCAG TTACTTCTGT 850
CCAAGCTGTT TATGTCCCAG CTGATGATTT AACAGATCCT GCTCCAGCTA 900
45 CCACTTTCGC CCATTGATG GCTACTACTG TCTTGTCTCG TGGTATTTCA 950
GAATTAGGTA TTTACCCAGC TGTCGATCCA TTAGATTCTA AATCAAGATT 1000
ATTAGATGCT TCAGTTGTTG GTCAAGAACA TTATGATGTT GCTACCAACG 1050
TTCAACAAAC TTTACAAGCT TACAAATCTT TACAAGATAT TATTGCTATT 1100
TTAGGTATGG ATGAATTGTC TGAACAAGAT AAATTGACTG TCGAAAGAGC 1150
50 AAGAAAAATC CAAAGATTCT TATCTCAACC ATTTGCTGTT GCCGAAGTTT 1200
TCACTGGTAT YCCAGGTAGA TTGGTTAGAT TAAAAGACAC TATCAAATCA 1250
TTCAAAGATG TTTTGAAGG TAAATATGAT CACTTACCAG 1290

55

2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1291 bases
(B) TYPE: Nucleic acid

300

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 2149

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

	CCAATTCGAA	CAAGGTA	ACT	TACCAGCTAT	CTTGAATGCT	TTAGAAATCA	50
	AAACCCCAAG	TGGTACTCCA	TTAGTTT	TTAG	AAGTTGCTCA	ACATTTAGGT	100
	GAAAACACTG	TCAGAACTAT	TGCTATGGAT	GGTACTGAAG	GTTTAGTCCG		150
15	TGGTGAACAA	GTTACTGATA	CTGGTTCTCC	AATCACTGTC	CCAGTTGGTC		200
	GTGAAACTTT	AGGTCGTATT	ATCAACGTTG	TTGGTGAACC	AATTGATGAA		250
	CGTGGTCCAA	TTAACACCAA	ACAAAGAAAC	CCAATTCACG	CTGAACCACC		300
	TTCATTACAGT	GAACAATCAA	CTGCTGCTGA	AGTTTTAGAA	ACTGGAATCA		350
	AAGTTGTTGA	TTTATTAGCT	CCATACGCTA	GAGGTGGTAA	AATTGGTTTA		400
20	TTCGGTGGTG	CCGGTGT	CGG	TAAAACTGTC	TTTATCCAAG	AATTGATTAA	450
	CAACATTGCT	AAAGCTCATG	GTGGTTTCTC	AGTTTTTCACC	GGTGTGGTG		500
	AAAGAACCAG	AGAAGGTAAC	GATTTATACC	GTGAAATGAA	AGAAACTGGT		550
	GTTATTAACT	TGGAAGGTGA	TTCTAAGGTC	GCTTTAGTTT	TCGGTCAAAT		600
	GAATGAACCA	CCAGGTGCTA	GAGCTCGTGT	TGCTTTAACT	GGTTTGACCA		650
25	TTGCTGAATA	CTTCAGAGAT	GAAGAAGGTC	AAGATGTCTT	GTTATTCGTT		700
	GATAACATTT	TCAGATTCAC	CCAAGCCGGT	TCAGAAAGTTT	CTGCCTTATT		750
	AGGTCGTATT	CCATCTGCTG	TCGGTTATCA	ACCAACTTTA	GCAACTGATA		800
	TGGGTTTGTT	ACAAGAACGT	ATTACCACCA	CACAAAAAGG	TTCAGTTACT		850
	TCTGTCCAAG	CTGTTTATGT	CCCAGCTGAT	GATTTAACAG	ATCCTGCTCC		900
30	AGCTACCACT	TTCGCCCATT	TGGATGCTAC	TACTGTCTTG	TCTCGTGGTA		950
	TTTCAGAATT	AGGTATTTAC	CCAGCTGT	CG	ATCCATTAGA	TTCTAAATCA	1000
	AGATTATTAG	ATGCTTCAGT	TGTTGGTCAA	GAACATTATG	ATGTTGCTAC		1050
	CAACGTTCAA	CAAACCTTAC	AAGCTTACAA	ATCTTTACAA	GATATTATTG		1100
	CTATTTTAGG	TATGGATGAA	TTGTCTGAAC	AAGATAAATT	GACTGT	CGAA	1150
35	AGAGCAAGAA	AAATCCAAAG	ATTCTTATCT	CAACCATTTG	CTGTTGCCGA		1200
	AGTTTTTCACT	GGTATCCCAG	GTAGATTGGT	TAGATTAAAA	GACACTATCA		1250
	AATCATTCAA	AGATGTTTTG	GAAGGTAAAT	ATGATCACTT	A		1291

40

2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 508 bases
45	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*

(B) STRAIN: ATCC 10658

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

	CGTATTGATT	CGTGAGTGGC	CGTTCCCTTA	CAGCAAGCTT	ATAAAGGAGC	50	
	GAAAAAGATC	TGACATT	CGG	CTTATGTGCT	ATACAGAGGA	ACTCATCAAC	100
	AACGTCGCCA	AGGCTCATGG	TGGTTACTCT	GTCTTCACCG	GTGTCGGAGA		150
60	GCGAACACGT	GAAGGTAACG	ATCTCTACCA	CGAAATGATT	GAAACCGGTG		200

TCATTTCAGCT CAAGAACGAC AAGTCCAAGG CCGCTCTGGT CTTCGGACAG 250
ATGAACGAGC CCCCCGAGC TCGTGCCCGT GTCGCTCTGA CCGGTCTCAC 300
CATCGCCGAG TACTTCCGTG ACGTCGAAGG ACAGGATGTG CTACTCTTCA 350
TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCAGAGGT ATCTGCCCTG 400
5 CTCGGACGTA TCCCATCTGC TGTCGGATAC CAGCCCACAC TCTCAACCGA 450
TATGGGTGGT ATGCAAGAGC GAATCACAAC CACCAAGAAG GGTTCGATTA 500
CCTCCGTC 508

10

2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 686 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula mucilaginosa*
(B) STRAIN: ATCC 66034

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

TGTCCTCATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
ACTCGGTCTT CACCGGTGTC GGCGAGCGTA CCCGTGAGGG TAACGGTGAG 100
TCTCCCCCTT CAAACTTTTG GCCGGCTAGT TGGCGCAGCG CAAACTGACG 150
30 CGCGCGCCCT GTCCAGACTT GTACCACGAG ATGATCGAGA CTGGTGTCAT 200
CCAGCTCGAG AACGACAACT CGAAGTGCGC TCTCGTGTTT GGCCAGATGA 250
ACGAGCCCCC TGGTGCCCGT GCCCGTGTCG CTCTCACTGG GTTCGTCCTT 300
TCTCTCTCTC GAGCGTCTTG GCTTGATACG GAACGCTGAC ACGTCACGCA 350
GTCTCACTAT TGCTGAGTAC TTCCGTGACG AGGAGGGCCA GGACGTGCTC 400
35 CTCTTCATCG ACAACATCTT CCGTTTCACC CAGGGTGAGC CGCCTCCGCG 450
GGCATTCTCC CGTTTCTTTC GCGCTGACGT CTGTCCCGTA TAGCCGGTTC 500
GGAGGTGTCT GCCCTTCTCG GACGTATCCC GTCCGCTGTC GGATACCAGC 550
CGACTCTCTC GACCGACATG GGTCAGATGC AGGAGCGTAT CACGTAAGTT 600
TGGCCGCAGC TCCGTCCGCG GCGCCCTTTG TGTCTGACCG TGTTCACCG 650
40 CTCAGCACCA CCAAGAAGGG CTCGATCACC TGTGTC 686

45

2) INFORMATION FOR SEQ ID NO: 492

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 625 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Sporobolomyces salmonicolor*
(B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

60 TGTCTTGATT CAGGAGCTCA TCAACAACGT CGCCAAGGCG CACGGTGGTT 50

	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	CACACTTTTCG	CCGACCTGGC	CATTCCGGAA	CGTGCGGACT	GACGAGGACC	150
	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
5	CCCCCTGGCG	CCCGTGCCCG	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTA CTTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
	TCTTCCGTTT	CACCCAGGGT	ACGTTTCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTTCG	GAGGTGTCTG	450
	CCCTTCTCGG	TCGTATCCCG	TCCGCTGTGC	GATACCAGCC	CACTCTCTCG	500
10	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGCTCACGCA	TGTTTCGCCCC	ACAGCACCAC	600
	CAAGAAGGGT	TCGATCACCT	GTGTC			625

15

2) INFORMATION FOR SEQ ID NO: 493

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1211 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: WSA-148

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTCGGCCC	CGGTACCCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
35	ATCGACGAGC	GCGGTCCCCT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACCAGTCGAC	CACCGCTGAG	GTTCTCGTGA	200
	CTGGTATCAA	GGTCGTCGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGTAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCCCACG	TGGTTACTCC	GTCTTCACCG	350
40	GTGTCGGCGA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTTCAGCT	TGACGGTGAC	TCCAAGGTCG	CCCTGGTGTT	450
	CGGTCAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCCGTGC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
45	TGTCAGTGCT	TCTCTTCATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
	GCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCCGTGAC	800
	GATCTGACGG	ATCCCGCCCC	CGCCACCACC	TTCGCCCATC	TGGACGCCAC	850
50	CACTGTGCTG	TCCCGAGGTA	TCTCTGAGCT	GGGTATCTAC	CCCGCTGTGC	900
	ACCCCTCGA	CTCCAAGTCG	CGTATGCTGG	ACCCCGTAT	TGTCGGTGAC	950
	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
55	CAGCCGTTCA	CGGTCGCGCA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
	GTGACAGCCT	T				1211

60

2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1133 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
(B) STRAIN: ATCC 52550

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

TCTTGTTAGA GGCACCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC 50
CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA 100
ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC 150
20 TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA 200
CCGGTATTAA GGTTGTCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG 250
ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTGAGGA 300
GCTTATTAAC AACATTGCTA AGGCCACGG TGGTTACTCT GTCTTCACTG 350
GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG 400
25 GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTTGT 450
CGGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG 500
GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG 550
TTGTTTCATTG ACAACATTTT CCGATTACAC CAGGCCGGTT CTGAGGTCTC 600
TGCCTTGTTG GGTCTGATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG 650
30 CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAAGGGT 700
TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA 750
TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT 800
CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCGA CCCTCTTGGT 850
TCCAAGTCCC GTCTTTTGGA TGCCCTCCGTC GTCGGCCAAG AGCACTACGA 900
35 CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCTTACAAG TCTCTCCAGG 950
ATATCATTCG CATTTTGGGT ATGGACGAAT TGCTGAGGC TGATAAGCTC 1000
ACTGTGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC 1050
CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG 1100
ACACCATCCG ATCCTTCAAG GAGATCCTTG AC 1133
40

2) INFORMATION FOR SEQ ID NO: 495

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
55 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
60 GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTCC 100

	AGTATTAATT	GTTTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
	TCTGTCTTCA	CTGGTGTCCG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCCG	300
5	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATAAAAA	AAAAATTTTT	TTTTTTTTTT	400
	TTTTTTTCAA	GAAATTCATG	TTCTAACAAA	GTGTATTCTA	GTGCTTCTCT	450
	TCATCGACAA	CATTTTCCGT	TTCACTCAGG	CTGGTTCCGA	AGTGTCTGCC	500
	CTGCTTGCTC	GTATCCCATC	TGCCGTCGGT	TACCAACCCA	CTCTTGCCGT	550
10	CGACATGGGT	GGTATGCAGG	AACGTATTAC	CACCACCAAG	AAGGGATCCA	600
	TTACCTCC					608

15 2) INFORMATION FOR SEQ ID NO: 496,

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

30	GTTTATTCAA	GAATCATTG	TGGGTGGCAT	TCTCATAATG	TTTCGGCCAC	50
	AATTACTGAT	TGAAAATAGA	ACAACATTGC	AAAGGCTCAT	GGTGGTTACT	100
	CCGTGTTTAC	TGGTGTCCGC	GAGCGAACTC	GTGAGGGTAA	CGACTTGTAC	150
	CACGAAATGC	AGGAGACCTC	TGTCATTTCAG	CTCGATGGCG	AGTCCAAGGT	200
35	CGCGCTGGTG	TTTGGTCAAA	TGAACGAACC	TCCTGGTGCT	CGTGCTCGTG	250
	TTGCTCTGAC	TGGGTAAGTT	GTTCTTTCGC	TTCTTGCGCG	TATCCACATC	300
	CCCATCTTGA	GAATACGTCT	GCCACCATGT	CATGTGATGT	TGGGCTGGTT	350
	CTGGTTTTTG	GGAGGCCCTC	AAGTTCAATT	TTTGATGAC	AGCACCAGCT	400
	TTACAAGATT	ATGCTAACTT	AATGGAGTCT	TACGGTGGCT	GAGTCTTCA	450
40	GGGATGAGGA	GGGACAGGAT	GGTAAGTTTG	ATAACAATCT	CGTCGGTGTC	500
	AATATCGACG	GCGTACTCTT	CGCATCAAAA	AACCAAAGAG	GTGGTTTGTT	550
	GTGAGAAAGT	CGCCGGAAT	AATGGCAACC	ACGTGACAAT	GACCACGTGT	600
	GGGGCTCCCG	TGCTAACACG	TGACAGTCTT	GCTCTTCATC	GACAACATTT	650
	TCCGATTTCAC	TCAASCCGGT	TCTGARGTGT	CTGCCTTGCT	TGGTCGTATT	700
45	CCATCTGCCG	TCGGTTACCA	ACCCACACTC	GCCGTCGACA	TGGGTCTCAT	750
	GCAGGAACGT	ATCACCACCA	CCCGGAAGGG	ATCCATCACA	TCTG	794

50 2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*

(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

5 TCTTGTCCGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC 50
 CCGTCGGCCG AGGTACCCTT GGTCGAATCA TCAACGTCTG TGGTGAGCCC 100
 ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC 150
 TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA 200
 10 CCGGTATTAA GGTCGTCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG 250
 ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA 300
 GCTGATTAAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG 350
 GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG 400
 GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT 450
 15 CGGTCAGATG AACGAGCCTC CCGGAGCCCC TGCCCGAGTC GCCCTTACTG 500
 GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG 550
 CTCTTCGTTG ACAACATTTT CCGATTACCC CAGGCCGGTT CCGAGGTGTC 600
 CGCTCTGCTT GGTGCAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG 650
 CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT 700
 20 TCCGTCACCT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA 750
 TCCTGTCTCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCTCTG 800
 CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT 850
 TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAAGG AGCACTACGA 900
 TGTTGCTTCC AACGTCCAGC AGACCCCTCA GGCTTACAAG TCTCTCCAGG 950
 25 ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG 1000
 ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC 1050
 CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG 1100
 AACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC 1148

30

2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT 50
 CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTCG CGAATAGGCC 100
 50 CCAGACTCGT GAGCATTGTC TGCTCGCCCC CCAGGTGGT GTCCAGAAGA 150
 TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG 200
 GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA 250
 GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG 300
 GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT 350
 55 GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT 400
 GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT 450
 CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTTGAGATT 500
 GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC 550
 CTTCAAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC 600
 60 TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCAATTGCT 650

5 GTTCCCGGCA GCACCAAGGC TCACGACAAG TTCCTCGTCT CCATGTACGT 700
CCTGACCGAG GCGGAGGGTG GTCGTCGTAC TGGCTTCGGT GCCAACTACC 750
GTCCCCAAGT CTTTCATCCGT ACTGCAGGTA AGTTCCCGCA CACCGTGTCC 800
AGATCTTCCG AGAGATTAGC GATATATGCT AATGATTCAT CAGACGAGGC 850
TGCTGACCTC AGCTTCCCTG ACGGCGACCA ATCTCGCAGA GTTATGCCTG 900
GTGACAACGT CGAGATGATC CTGAAGACCC ACCACCCTGT TGCTGCTGAG 950
GCTGGTCAAC GCTTCA 966

10

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

30 TGGTGCTATT ATTGTTGTTG CTGCTTCTGA TGGTCAAATG CCCCAAACCC 50
GTGAGCACTT GCTTCTTGCT CGTCAAGTTG GTGTTAAGCA CATTGTTGTT 100
TTCGTTAACA AGATTGATAC TATTGATGAT CCTGAAATGT TGGAACCTGT 150
CGAAATGGAA ATGAGAGAAC TTCTTTCTTC TTACGGTTTT GATGGCGATA 200
ACACCCCTGT CATTATGGGT TCTGCTCTCT GTGCTCTTGA AGGTCGTGAA 250
CCAGAAATTG GTGAACAAAG AATCAACCAA CTCCTTGATG CTATCGATGA 300
ATACATTCCT ACCCCAGTTC GTGATATGGA CCAACCTTTC TTGATGCCAC 350
TTGAAGGTGT TTTCTCTATT CCAGGTCGTG GTACTGTTGC CACTGGACGT 400
35 GTCTATCGTG GTACTTTGAA GAGAGGTGAA GAAGTTGAAG TTGTTGGCTA 450
CAATGATGCT CCAATCAAGA CCACCGTTAC TGGTATTGAA ATGTTCAAGA 500
AGGAAGTTGA TCAAGCTCAA GCTGGTGACA ACGCTGGTAT TCTTTTGAGA 550
GGTGTAAAGC GTGAAGACCT TAAGCGTGGT ATGGTTGTTG CTAAACCAGG 600
TACCGTTAAG CCACACACCA AGTTCCTTGC CTCCATCTAT GTTTTGACTA 650
40 AGGAAGAAGG TGGCAGACAC TCTGGCTTTG GTCTTAACTA CAGACCTCAA 700
CTTTTCCTTG GTTCTGCTGA TGTACCACCT GTCTTGACCT TCCCAGAGGG 750
TGTTGACCAA AGCACTCAAG TCATGCCAGG TGACAACACT GAAATGGTTT 800
GCGAACTTGT TCACCCAGTT GCTGTCGAAC AAGGCCAACG TTTCOA 846

45

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

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5   GGTGCCATTA TTGTTGTTGC TGCCTCTGAT GGACAGATGC CCCAGACCCG      50
    TGAGCATCTT TTGCTTGCCC GCCAAGTCGG TATGCAAAAG GTCGTTGTGT      100
    TTGTTAACAA GATTGATACC ATTGATGACC CTGAAATGCT TGATCTTGTC      150
    GAGATGGAGA TCGTGAACT GTTGAATGAA TATGACTTCG ATGGAGATAA      200
    CTCTCCTGTC ATTATGGGCT CTGCTCTTGC TGCTCTTGAG GACAAGAACC      250
    CCGAGATTGG TAAGGACCGT ATCATGCAGC TCTTGACGCG TGTTGATGAA      300
    TGGATCCCTA CCCCCGAGCG TGACCTTGAC AAGCCTTTCA TGATGCCTAT      350
10  TGAGGCCTCT TTCTCCATTT CTGGTCGTGG TACTGTTGCC ACTGGCCGTG      400
    TCGAGCGTGG TATTCTCAAG AAGGGTGAGG AAGTCGAGAT CGTTGGTTTC      450
    AACAAGCAGC CCCTGAAATC TGTGTACTT GGTATTGAAA TGTTCAAGAA      500
    GGAAGCTGAT CAGGCCCAGG GCGGTGATAA TGCTGGTATC TTGCTTCGTG      550
    GTATTCGTCT TGAGGACTTG CAGCGTGGTA TGGTTTTGGC CAAGCCTGGA      600
15  ACTGTTAAGG CTCACACCAA GTTCCTTTCC TCCATCTACG TTCTCTCCAA      650
    GGAAGAGGGC GGCCGTCAC CTCTTTTCGG TATGAACTAT CGTCCCAGAA      700
    TGTTCGTTTC TGCAGCTGAT GTCACCGTTA CTCTTACTTT CCCTGAGGGT      750
    GTTGAACAGC AACTCAGGT CTTCCCTGGT GAGAACACCG AGATGGTTGG      800
    CGAGCTCGTT CACCCTACTG CTATTGAGGT TGGTCAACGC TTCAAC          846
20

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2) INFORMATION FOR SEQ ID NO: 501

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25  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 944 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Coccidioides immitis
35  (B) STRAIN: Silveira

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

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40  AGTTGTCGTC GTTGCTGCTT CAGACGGTCA AATGTATGCA ACCGAGAGCA      50
    CTCCCGGATC TTGGTTTAAA TGGCACTAAT ATAAGACAGG CCTCAAACCTC      100
    GAGAGCATTT ACTTCTCGCC CGTCAGATCG GTATCCAAAA AATCGTCGTC      150
    TTCGTGAACA AGGTTGATGC CATCGAGGAC AAAGAGATGT TGGAGCTTGT      200
    TGAATTGGAG ATGCGTGAAC TCCTAACCAG CTACGGTTTC GAGGGTGAAG      250
    AAAGTCCCAT CATTTTGGC TCTGCTCTCT GTGCCCTCGA AGGAAGACAA      300
45  CCCGAGATCG GTGTTACCAA GATTGATGAG CTCTTGACAG CCGTCGACAC      350
    CTGGATTCCC ACTCCTCAGC GTGAGACTGA CAAGCCCTTC TTGATGTCCA      400
    TTGAGGAAGT GTTCTCTATT TCCGGACGAG GAACCGTTGT CTCCGGCCGT      450
    GTGGAGCGTG GTATCCTCAA GAAGGACTCC GAAGTTGAAA TTGTCGGCGG      500
    TTCGCCCAGG CCAATCAAAA CCAAGTTTAC CGATATCGAA ACCTTTAAGA      550
50  AGTCTTGCGA CGAGTCTCGC GCTGGTGATA ACTCCGGCTT GCTCCTACGA      600
    GGCCTTAAGC GTGAAGATAT TAGCCGTGGC ATGGTCGTCG CTGTACCAGG      650
    AAGTGTCGAG GCCCATACTG AATTCTTAGT TTCGCTTTAC GTCCTCACCG      700
    AAGCTGAGGG TGGGCGCAAA TCTGGATTCA GCAGCAAGTA CCGCCACAG      750
    ATGTTTCATTC GCACTGCCGG TATGTAATAC TGTGATAATT TCGTTGACAT      800
55  GGTACTGATT GAATTCTATA GACGAAGCGG CTCAGCTCAG CTGGCCCGGA      850
    GAAGATCAAG ACAAGATGGC TATGCCAGGA GACAATATCG AAATGATTTG      900
    CACCACCTTG CACCCAGTTG CCGCCGAGGC TGGCCAGCGA TTCA          944
60

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2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

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GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA      50
ACACTTGCTC CTCGCTCGTC AGGTCGGTGT CCAGCGAATT GTCGTCTTCG     100
TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GTCGTCTCGAG     150
ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC      200
TCCCGTCATC ATGGGCTCTG CTCTTATGTC TCTCCAGAAC CAGCGCCCCG      250
AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG      300
ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCTGA      350
GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG      400
AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG      450
CAGGAGGTTA TCAAGACCAA GGTACCGAC ATTGAGACCT TCAAGAAGTC      500
TTGTGAGCAG TCCCAGGCTG GTGACAACTC TGGTCTCCTC ATCCGAGGTG      550
TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC      600
GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA      650
GGAGGGTGGC CGACACACCG GTTTCCAGGA GCACTACCGA CCCCAGCTCT      700
ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT      750
GAGGATGCCT CCAGTAAGAT GGTGCATGCCT GGTGACAACA CCGAGATGGT      800
TGTCACCATG GGTCAACCCA ATGCCATCGA GGTGGTTCAG CGATTCAAC      849

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2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

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TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG      50
CGAGGGACTG CTGAGGGTTT TATGCTTTT AGGCCCCCTT GTTTCTGAGA      100
GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT      150
GAGCATTTGC TCCTTGCCCG ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT      200
CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCG      250
AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG      300
ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC      350
TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT      400

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	GGATCCCCAC	ACCACAACGT	GATACCGAAA	AACCTTTCTT	GATGTCCGTT	450
	GAGGAAGTAT	TCTCTATCTC	CGGCCGTGGA	ACCGTTGCCT	CCGGTCGTGT	500
	TGAGCGCGGT	GTCCTCAAGA	AGGATTGAGA	AGTCGAGCTA	ATTGGGGGCG	550
	GCTCCACCCC	CATCAGGACG	AAGGTAAGTG	ATATCGAAAC	TTTCAAGAAA	600
5	TCCTGTGACG	AGTCTAGAGC	TGGGGACAAC	TCCGGTCTTT	TATTGCGTGG	650
	TATCAAGCGT	GAAGATATCC	GCCGTGGTAT	GGTAGTTGCC	GTTCCTGGCA	700
	GCGTCAAGGC	CCACGACAAG	TTCTTGGTGT	CGATGTATGT	CCTGACCGAA	750
	GCTGAGGGTG	GTCGCCGAAC	CGGATTTCGGC	CAGAACTATC	GTCCTCAAAT	800
	GTTTCATCCGC	ACAGCTGGTA	TGTCAAAATG	GGACCCCTTT	TCATAATCCT	850
10	TTCTTTTTTT	CCTTTTCCTC	TCTATCTCTC	TTTCTGTTTC	CTTTCAACTC	900
	GCCTGATTCA	CGAAATTAAC	TAACCCGTTT	GATTATAGAC	GAAGCCGCCC	950
	ATCTCAGCTT	CCCTAGTGGA	GCAGATGAAA	GCAAATCTCGT	TATGCCTGGT	1000
	GACAACGTCG	AGATGATCCT	CCAGACACAC	CGCCCCGTGG	CTGCTGAGGC	1050
	CGGCCAGCGA	TTCA				1064
15						

2) INFORMATION FOR SEQ ID NO: 504

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

	TGGTGCTATC	GTCGTTGTTG	CTGCCTCTGA	CGGCCAAATG	TAGGGATTTT	50
35	GCAAGACTGG	TGAAAAAATC	TAAAGAAAAT	AGAAAAGATT	GTGCTGATGT	100
	TTGGTATCAG	GCCCCAAACA	CGCGAGCATC	TGCTTCTTGC	CAGACAAGTC	150
	GGTGTTGAGA	AAATCGTTGT	TTTCGTCAAC	AAGGTCGATG	CTGTAGAGGA	200
	TAAGGAGATG	TTGGAGCTTG	TCGAATTGGA	GATGAGAGAG	CTCTTGACCA	250
	CCTATGGGTT	CGAGGGTGAG	AAGACACCTA	TCATCTTTGG	TTCTGCGCTC	300
40	TGTGCTATGG	AGGGCCGTCA	GCCCCGAGTTG	GGAGAGCAGA	AAATTGATGA	350
	ATTACTCGAG	GCTGTGATA	CTTGATCCC	TACGCCACAG	CGTGATACTG	400
	ACAAGCCCTT	CCTGATGTCC	ATTGAGGAGG	TGTTCTCTAT	CTCTGGACGA	450
	GGAACCGTTG	CCTCCGGCCG	CGTTGAGCGT	GGTATCCTCA	AGAAGGACTC	500
	CGAAGTTGAA	ATTATTGGCG	GCGGTGTTCC	CACAATCCTG	ACCAAGGTGA	550
45	CTGATATCGA	AACCTTCAAG	AAGTCTTGCG	ACGAGTCCAG	AGCCGGGGAC	600
	AACTCCGGCC	TCTTGTTGCG	CGGTGTCAAG	CGTGAGGATA	TCCGCCGTGG	650
	TATGGTCGTT	GCAGTTCCCG	GAAGCGTCAA	AGCACATGAC	AGATTCTTGG	700
	TGTCGATGTA	CGTTCTGACC	GAGGCTGAGG	GTGGTCGCCG	CACTGGCTTC	750
	GGTCAGAACT	ATCGTCCTCA	AATGTTTCATC	CGCACAGCTG	GTACGTTTAT	800
50	TCTTTTACTA	TATTCTTATA	TGCATAGCCC	GATCCTCCCA	TTAACTAATT	850
	GACACAGACG	AGGCTGCTGA	ACTCAGCTGG	CCTGATGGAG	ACGACGAAGC	900
	CAAAATGGTC	ATGCCCCGGT	ACAATGTTGA	AATGGTCCTG	AAGTCACACC	950
	GCCCCGGGCC	GCTGAGGCTG	GACAGCGATT	CA		982
55						

2) INFORMATION FOR SEQ ID NO: 505

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 58950

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
15	CACTTGCTCC	TCGCCCCGTC	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACTCTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATTT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGGCGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
20	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
25	CAAGCGTGAG	GACATTCGTC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GACTGAGGCT	700
	GAAGGTGGTC	GTCGTACTGG	ATTGCGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTACT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
30	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

35 2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
55	ACGTCCCACT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATTC	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTAACCTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
60	AAACAAAAC	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500

AAGAATTGGA CCAAGCTATG GCTGGTGATA ACTGTGGTAT CTTATTACGT 550
 GGTATCAAAA GAGATGACAT YAAAAGAGGT ATGGTTATTG CTAAAACCGG 600
 TACCATCTCW GCTCACACTA AATTCTTAGC CTCAATGTAT ATTTTGACTA 650
 AAGAAGAAGG TGGTCGTCAC TCAGGTTTTG GTGAACATTA CAGACCTCAA 700
 5 TTATTCATCA GAACTGGTGA TGTTACCGTT GTTTTAACCT TYCCAGAAGG 750
 TGGTGATTCA TCTCAACAAA TCTTACCAGG TGACAATGTC GAAATGGTTT 800
 GTGAATTGGT TCACCCAAC TCTTTAGAAG CTGGTCAAAG ATTCAA 846

10

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

GGAGCTGTTG TCGTTGTCGC AGCTTCTGAC GGTCAAATGT AATTGAATGC 50
 CCGCCCAGAC GGATGAAAGG ATTTGACGTT TCTAACATCA GTCTAGGCCT 100
 CAGACCAGAG AACATTTGCT CTTGCCCCGC CAGGTCGGTG TCCAGAAGCT 150
 30 GGTTCGTTTTT GTTAACAAGG TCGATGCCGT TGAGGACCCA GAGATGTTGG 200
 AGCTTGTCGA ACTTGAAATG CGTGAACCTC TCAGCCACTA CAGTTTTGAG 250
 GGTGAGGAGA CCCCCATCAT TTTTGGCTCT GCTCTCTGTG CCCTCGAGTC 300
 CCGTCGACCT GAGCTTGGTG TCGAGAAGAT TGACGAGCTA TTGAACGCCG 350
 TCGACACCTG GATCCCCACC CCGGAGCGCG CCACTGATAA GCCTTTCCTC 400
 35 ATGTCCATTG AGGAAGTGTT CTCTATCTCT GGTCGTGGTA CCGTCGTCTC 450
 CGGTCGTGTT GAGCGTGGTA TCCTCAAGAA GGATTCCGAC GTCGAAATTG 500
 TTGGTGGCTC TACCACCCCT ATCAAGACCA AGGTCACAGA TATCGAAACC 550
 TTCAAGAAGT CCTGCGATGA ATCTCGAGCT GGTGACAACT CTGGTCTCCT 600
 TCTCCGAGGT ATCAAGCGTG AGGACTTGAA GCGTGGAATG GTTGTGCTG 650
 40 CCCCCGGATC CACCAAGGCT CACACCGACT TCATGGTCTC CCTCTACGTC 700
 CTGACTGAGG CTGAGGGTGG TCGTTCCAAC GGCTTCACCC ACAAGTACCG 750
 CCTCAAATG TTCATCCGTA CTGCTGGTAT GTAACCAAAG TTTCCGCTAT 800
 TTACTAAGTA GATCATTGCT AACTTGTATT CCCTTCCGTA GACGAAGCCG 850
 CATCTTTCAG CTGGCCTGGA GAAGACCAAG ACAAGAAGGC TATGCCTGGT 900
 45 GACAACGTCG AGATGATTTG CAAAACCCTC CACCCCATTG CTGCCGAGGC 950
 TGGCCAACGA TTCA 964

50 2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*

(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

5
GGTGCTATCA TTGTCGTTGC TGCTGGAGAC GGTTCGAAGC CCCAGACCCG 50
AGAGCATCTG CTGCTTGCTC GACAGGTCGG TGTCCAGAAC CTGGTTGTGT 100
TTGTTAACAA GGTTGATCAG ATTGATGATA AGGAGATTCT TGAGCTCGTT 150
GACATGGAGA TGCAGATCT GCTGACCCAG TACGGTTTTG ATGGTGACAA 200
10 CACCCCCGTT GTCATGGGCT CTGCTCTGTG CGCTCTTGAG GGCAAGCAGA 250
AGGATATTGG AGAGGACGCC ATCATGGCCC TTATGGATGC CGTTGATGAG 300
CACATCCCTA CCCCTAACCG TGACCTTGAG AAGCCCTTCC TGATGCCCCG 350
TGAGGACGTT TTCTCCATCT CTGGCCGAGG AACTGTTGTT ACTGGCCGAG 400
TCGAGCGAGG AAACCTGAAG AAGGGTGAGG AAATCGAGAT TGTGCGCTAC 450
15 AACACAAGC CCATCAAGGC TGTGTTACC GGTATTGAGA TGTTCAAGAA 500
GGAGCTCGAG TCCGCCATGG CCGGTGACAA CGCCGGTATC CTGCTCCGAG 550
GTATCAAGCG AGACGAGATC AAGCGAGGTA TGGTCATGTG CAAGCCTGGC 600
ACCGTCAACG CCCACACCAA GTTCCTTGCT TCTCTTTACA TCATCCCCAC 650
CGAGGAGGGT GGTGCAACCA GCTCTTTCGG CGCCAACCTAC CGACCCAGA 700
20 TGTTTCATCCG AACTTCTTCC GTCACCCGCA CTCTCACCTT CCCCAGGGT 750
ACCGACGAGT CCCAGACCGT CAACCCCGGT GACAACACTG AGATGGTTCT 800
CGAGCTTGTT CACCCTACCG CCATTGAGGT CAACCAGCGA TTCA 844

25

2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1067 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*
(B) STRAIN: Suarez-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

CTTGACAAG CTGAAGAGCG AGCGTGAGCG TGGTATCACC ATTGACATTA 50
CCCTGTGGAA GTTCGAAACT GGCAAGTACT ACTACACCGT CATTGACGCC 100
CCCGGTCACC GTGACTTCAT TAAGAACATG ATTACGGGTA CCTCCCAGGC 150
45 CGATGTTGCT ATGCTTGTCG TGCCCGCCGA GGCTGGTGGT TTCGAAGCTG 200
CCTTCTCTAA GGAAGGTCAG ACCCGTGAGC ACGCTCTTTT GGCCTTCACC 250
CTTGGTGTCA AGCAGATCAT TTGCGCCATC AACAAAGATGG ACAAGTGCGA 300
CTACAAGGAG GACCGTTACA GCGAAATCCA GAAGGAAGTT CAGGGTTACC 350
TGAAGAAGGT CGGTTACAAC ATCGAGAAGG TGCCTTTCGT CGCCATCTCC 400
50 GGTTCATGCG GTGACAACAT GGTGAGCGC TCCACCAACA TGCCGTGGTA 450
CAAGGGCAAG ACCTTGGTCG AGGCCCTCGA CATGATGGAG CCCCCGAAGA 500
GGCCCGTCGA CAAGCCCTCG CGTCTTCCCC TCCAGGGTGT GTACAAGATC 550
GGTGGTATCG GTACCGTCCC TGTCGGTCGT GTGGAGACTG GTCAGCTCAA 600
GGCCGGTATG GTCCTCACCT TCGCCCCCAA CCCGATCACT ACTGAGTGCA 650
55 AATCCGTCGA AATGCACCAC GAAGTTATCG ATGTTGCCAG CCCTGGTGAC 700
AACGTTGGTT TCAACGTGAA GAACGTGTCC ACCTCTGACA TCCGCACTGG 750
TCACGTCGCT TCTGACTCCA AGAACGACCC CGCCAAGGCC GCCGTGTCCT 800
TCACCGCCCA GGTCATCATC TTGAACCACC CTGGTACCAT CAAGGCCGGT 850
TACTCCCCTG TGGTTGACTG CCACACTGCC CACATCTCGT GCAAATTCGA 900
60 CGAGATCACC AGCCGTATGG ACAAGCGTAC CGGTAAGGCC CTTGAGGAGA 950

ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTCGT	CCTGAAGCCG	1000
TGCAAGCCCA	TGGTCGTCGA	GGCCTTCACT	GAATACGCTC	CCCTTGGTCG	1050
TTTCGCCGTG	CGTGACG				1067

5

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA	ACGTGGTATT	ACTATTGATA	TTACCTTATG	GAAGTTCGAG	50
ACCACCAAGT	ACTACTACAC	CGTCATTGAT	GCCCCCTGGTC	ACCGTGACTT	100
25 CATCAAGAAC	ATGATTACGG	GTACTTCTCA	AGCCGATGTT	GCTATGCTTG	150
TTGTACCAGC	TGAGGCTGGT	GGTTTCGAGG	CCGCTTTCTC	CAAGGAAGGA	200
CAGACCCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTTGGTG	TCAAACAGAT	250
CATCTGTGCC	ATTAACAAGA	TGGACAAGTG	CGACTACAAG	GAGGACCGTT	300
ACAGTGAAAT	CCAGAAGGAA	GTCCAGGGTT	ACCTCAAGAA	GGTCGGTTAC	350
30 AATATTGAGA	AGGTGCCCTT	CGTTGCCATC	TCCGGTTTCA	TGGGAGACAA	400
CATGGTTGAG	CGTTCCACCA	ACATGCCCTG	GTATAAGGGA	AAGACATTGG	450
TCGAGGCCCT	TGATCAGATG	GAACCCCCAA	AGAGGCCCGT	TGACAAGCCA	500
CTTCGTCTTC	CCCTCCAGGG	TGTCTACAAG	ATCGGTGGTA	TCCGTACCGT	550
CCCCGTCGGT	CGTGTTGAAA	CTGGTATGTT	GAAGGCTGGT	ATGATTCTAA	600
35 CCTTTGCTCC	TAACCCAATC	ACCACTGAAT	GCAAATCCGT	TGAAATGCAC	650
CACGAAACCG	TTGAGGTTGC	TTACCCCGGT	GACAACGTCG	GTTTCAACGT	700
AAAGAACGTT	TCTACTTCTG	ACATTGCGAG	TGGTCACGTT	GCCTCTGATT	750
CTAAGAACGA	CCCTGCCAAG	GCTGCTGTTT	CCTTCACTGC	CCAGGTCATT	800
GTGCTCAACC	ACCCTGGTAC	CATTAAAGCC	GGTTACTGCC	CCGTCGTCGA	850
40 TTGCCACACC	GCTCACATTT	CATGTAAATT	CGAAGAGATC	ACCAGCCGTA	900
TGGACAAGCG	TACCGGTAAA	TCTCTTGAGG	AAAACCCCAA	GACCATCAAG	950
AACGGTGACG	CTGCCATGGT	TGTGCTCAAG	CCAATGAAGC	CCATGGTTGT	1000
CGAATCCTTC	ACTGAGTATG	CTCCTCTTGG	TCGTTTCGCT	GTTTCGTGAC	1049

45

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
5	CGGCCACCGC	GACTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCCG	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
10	TACCTGAAAG	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTTCGT	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TGCACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCCGTGG	CCGTGTGGAG	ACCGGCGTGA	600
15	TGAAGCCGGG	CGACGTTGTG	GTGTTTCGCG	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCCG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
20	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGAGAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCCA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
	GCCGCTTCGC	TGTCCGCGAT				1070
25						

2) INFORMATION FOR SEQ ID NO: 512

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-IMMS

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTCATTAT	GGAAATTCGA	50
45	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAACCTCAC	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTATA	CACTCTTGGA	GTTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
50	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCCTTAAGA	AGACWGGATA	350
	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTCAGT	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTTCAGGT	ATTGGAACCTG	550
55	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACATTTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
60	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850

ATTGCCATAC ATCACACATT GCATGTAAAT TCGAAGAATT ATTAAGCAAG 900
 ATTGATAGAA GAACAGGTAA ATCCATGGAA GGAGGAGAAC CAGAATATAT 950
 TAAGAATGGA GATTCAGCAC TTGTTAAGAT TGTTCCTCACT AAACCACTTT 1000
 GTGTTGAAGA ATTTGCTAAA TTCCCACCAT TGGGAAGATT TGCTGTTAGA 1050
 5 GA 1052

2) INFORMATION FOR SEQ ID NO: 513

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Giardia lamblia*
 (B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25 GACGAGCGCG AGCGCGGGAT CACGATCAAC ATCGCGCTCT GGAAGTTCGA 50
 GACGAAGAAG TACATCGTCA CGATCATCGA CGCCCCGGGC CACCGCGACT 100
 TCATCAAGAA CATGATCACG GGGACGTCCC AGGCCGACGT CGCGATCCTC 150
 GTCGTCGCGG CGGGCCAGGG CGAGTTCGAG GCCGGGATCT CGAAGGACGG 200
 CCAGACGCGC GAGCACGCGA CCCTTGCGAA CACGCTCGGG ATCAAGACGA 250
 30 TGATCATCTG CGTCAACAAG ATGGACGACG GCCAGGTCAA GTACTCGAAG 300
 GAGCGCTACG ACGAGATCAA GGGCGAGATG ATGAAGCAGC TCAAGAACAT 350
 CGGCTGGAAG AAGGCCGAGG AGTTCGACTA CATCCCGACG TCCGGCTGGA 400
 CCGGGGACAA CATCATGGAG AAGTCCGACA AGATGCCCTG GTACGAGGGC 450
 CCGTGCCTGA TCGACGCGAT CGACGGGCTC AAGGCCCCGA AGCGCCCGAC 500
 35 CGACAAGCCC CTCCGCCTCC CGATCCAGGA CGTCTACAAG ATCTCGGGCG 550
 TCGGGACCGT CCCC GCGGGC CGCGTCGAGA CGGGCGAGCT CGCGCCCGGG 600
 ATGAAGGTCG TCTTCGCCCC GACGTCCCAG GTCTCGGAGG TCAAGTCCGT 650
 CGAGATGCAC CACGAGGAGC TCAAGAAGGC CGGGCCCGGG GACAACGTCTG 700
 GCTTCAACGT CCGCGGGCTC GCCGTCAAGG ACCTCAAGAA GGGCTACGTC 750
 40 GTCGGGACG TGACGAACGA CCGGCCGTC GGCTGCAAGA GCTTCACCGC 800
 CCAGGTCAATC GTCATGAACC ACCCGAAGAA GATCCAGCCC GGCTACACGC 850
 CCGTCATCGA CTGCCACACC GCGCACATCG CGTGCCAGTT CCAGCTCTTC 900
 CTCCAGAAGC TCGACAAGCG CACGCTCAAG CCCGAGATGG AGAACCCGCC 950
 CGACGCAGGC CGCGGCGATT GCATCATCGT CAAGATGGTC CCCCAGAAGC 1000
 45 CCCTGTGCTG CGAGACGTT AACGACTACG CGCCCCTCGG CCGCTTCGCC 1050
 GTCCGCGACA TCGGCCAAAC CGTTGCCGTC GG 1082

50 2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

5
 ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG 50
 ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTCACGAT 100
 CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA 150
 CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC 200
 10 TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT 250
 TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAAGATGG 300
 ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG 350
 GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG AGAAGGTGCG 400
 CTTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG 450
 15 ACAACATGCC GTGGTACAAG GGTCCCACGC TGCTGGACGC GCTCGACATG 500
 CTGGAGCCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCTGCA 550
 GGACGTGTAC AAGATCGGCG GTATCGGGAG GGTGCCCCGTG GGGCGCGTGG 600
 AGACCGGCAT CATGAAGCCG GGCAGCTGGT TGACGTTTCG GCGCGCCAAC 650
 GTGACGACTG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA 700
 20 GGCAGAGCCC GGCAGACAAC TCGGCTTCAA CGTGAAGAAC GTGTCGGTGA 750
 AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG 800
 AAGGAGGCGG CCGACTTCAC GCGCAGGTG ATCGTGCTGA ACCACCCCGG 850
 CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC ACGAGCCACA 900
 TTGCGTGCCG CTTGCGGGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC 950
 25 AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT 1000
 CGTGAAGATG GTGCCGAGA AGCCGATGTG CGTGGAGGTG TTCAACGACT 1050
 ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCCTTG 1098

30

2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1104 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*

(B) STRAIN: ATCC 50119

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACAGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 50 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 55 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGCCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTC GCGCCGCCAA 650
 60 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700

AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGGTG -750
 AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 5 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTC 1104
 10

2) INFORMATION FOR SEQ ID NO: 516

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tropica*
 25 (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 30 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC KCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 35 GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
 40 AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCCG GGGGCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTC CGCCCGCCAA 650
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
 AGGCGCAGCT CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGTG 750
 AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 45 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 50 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTCGG 1106

55 2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*

(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

10 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 15 CTTGAGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTAC GCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC 450
 20 GACAACATGC CGTGGTACAA GGGTCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCGC CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCCTGC 550
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG 600
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
 25 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
 AAGGACATCC GCCGTGGCAA CGTGTCGGC AACTCGAAGA ACGACCCGCC 800
 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 30 CAAGGAGCTG GAGAAGAACC CCAAGCGCAT CAAGTCTGGC GATGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG 1099

35

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

55 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTGAGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTAC GCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 60 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC 450

	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCCAA	650
5	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
10	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

15

2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1071 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania enriettii*

(B) STRAIN: ATCC 50120

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCTGT	GTTCACGATC	ATCGATGCGC	100
35	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACCGGCAC	GTCGCAGGCC	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACC	CAGGGCGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTC	GCCTTCACGC	250
	TTGGTGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGCAGTACT	CGCAGGCGCG	CTACGAGGAG	ATCAGCAAGG	AGGTGGGCGC	350
40	GTACCTGAAG	CGCGTCGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	ACAAGTCGGA	CAGCATGCCG	450
	TGGTACAAGG	GGCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGGCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCCTGCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCGTGG	GCCGCGTGGA	GACCGGCATC	600
45	ATGAAGCCTG	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGGTGCCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGETAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCTGGC	CAGATCAGCA	850
50	ACGGCTACGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	CGCGTGCCGC	900
	TTCGCGGATA	TCGAGTCCAA	GATCGACCGC	CGCTCTGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCCGGCGA	TGCGGCCATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CCCGCCGCTG	1050
	GGGCGCTTCG	CTGTGCGCGA	C			1071

55

2) INFORMATION FOR SEQ ID NO: 520

60 (i) SEQUENCE CHARACTERISTICS:

320

(A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

```

15  CTCGACAAGC TGAAGGCGGA GCGCGAGCGC GGCATCACGA TCGACATTGC      50
    GCTGTGGAAG TTCGAGTCGC CCAAGTCCGT GTTCACGATC ATCGATGCGC      100
    CCGGCCACCG CGACTTCATC AAGAACATGA TCACGGGCAC GTCGCAGGCG      150
    GACGCCGCCA TCCTGATGAT CGACTCGACG CATGGTGGCT TCGAGGCTGG      200
    CATCTCGAAG GACGGCCAGA CCCGCGAGCA CGCGCTGCTT GCCTTCACTC      250
    TTGGCGTGAA GCAGATGGTG GTGTGCTGCA ACAAGATGGA CGACAAGACG      300
20  GTGACGTACG CGCAGTCGCG CTACGATGAG ATCAGCAAGG AGGTGGGCGC      350
    GTACCTGAAG CGCGTGGGCT ACAACCCGGA GAAGGTGCGC TTCATCCCGA      400
    TCTCGGGCTG GCAGGGCGAC AACATGATCG AGAAGTCGGA CAACATGCCG      450
    TGGTACAAGG GTCCACGCT GCTGGACGCG CTCGACATGC TGGAGCCGCC      500
    GGTGCGCCCG GTGGACAAGC CGCTGCGCCT GCCCCTGCAG GACGTGTACA      550
25  AGATCGGCGG TATCGGGACG GTGCCCCTGG GCCGCGTGGA GACCGGCATC      600
    ATGAAGCCGG GCGACGTGGT GACGTTTCGCG CCCGCCAACG TGACGACTGA      650
    GGTGAAGTCG ATCGAGATGC ACCACGAGCA GCTGGCGGAG GCGCAGCCCG      700
    GCGACAACGT CGGCTTCAAC GTGAAGAACG TGTCGGTGAA GGACATCCGC      750
    CGTGGTAACG TGTGCGGCAA CTCGAAGAAC GACCCGCCGA AGGAGGCGGC      800
30  CGACTTCACG GCGCAGGTGA TCGTGCTGAA CCACCCCGGC CAGATCAGCA      850
    ACGGCTATGC GCCGGTGCTG GACTGCCACA CGAGCCACAT TCGGTGCCGC      900
    TTCGCGGAAA TCGAGTCCAA GATCGACCGC CGCTCCGGCA AGGAGCTGGA      950
    GAAGAACCCC AAGGCGATCA AGTCTGGCGA TGCCGCGATC GTGAAGATGG     1000
    TGCCGCAGAA GCCGATGTGC GTGGAGGTGT TCAACGACTA CGCGCCGCTG     1050
35  GGCCGCTTTG CCGTGCGCGA C                                     1071
  
```

2) INFORMATION FOR SEQ ID NO: 521

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

```

55  TCGTTCAAGT ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG      50
    CGGTATCACG ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCGG      100
    TGTTACAGAT CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG      150
    ATCACCGGCA CGTCGCAGGC GGATGCTGCC ATTCTGATGA TCGATTGCAG      200
    GCAGGGTGGC TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACGCGCGAGC      250
60  ACGCGCTGCT GGCCTTCACG CTGGGCGTGA AGCAGATGGT TGTGTGCTGC      300
  
```

321

	AACAAGATGG	ACGACAAGAC	GGTGCAGTAC	GCGCAGGCGC	GCTACGAGGA	350
	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	400
	AGAAGGTGCG	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
5	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	550
	TGCCCCTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTTCG	650
	GCCCCCCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TGGGCTTCAA	CGTGAAGAAC	750
10	GTGTGCGGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
	CGACCCGCGG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
15	ACGCCGCCAT	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	1050
	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTCCACGA	100
	TCATCGATGC	GCCCCGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
40	ACGTCGCAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
45	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
50	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGCTGC	TGGACTGCCA	CACGAGCCAC	900
55	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCGG					1106

60

2) INFORMATION FOR SEQ ID NO: 523

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
20	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTCACGA	100
	TCATCGATGC	GCCCCGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGCTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
25	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
30	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
35	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
40	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCCG					1105

45 2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

60

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTCACGA	100
	TCATCGATGC	GCCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
5	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGCTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
10	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
15	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGGT	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAAGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGCGTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
20	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

25

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTCACGA	TCATCGATGC	GCCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
45	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGCGCTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
50	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCCG	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTC	CGCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
55	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
60	CATCGAGTCC	AAGATTGACC	GCCGCTCCGG	CAAGGAGCTG	GAGAAGAACC	950

CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGC CG CAG	1000
AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT	1050
TGCTGTGCGC	GACATGCGCC	AAACCGTTGC	C		1081

5

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT	GGGTGCTCGA	CAAGCTGAAG	GCGGAGCGCG	AGCGCGGCAT	50
CACGATCGAC	ATTGCGCTGT	GGAAGTTCGA	GTCGCCCCAAG	TCCGTGTTCA	100
25 CGATCATCGA	TGCGCCCGGC	CACCGCGACT	TCATCAAGAA	CATGATCACG	150
GGCACGTGCG	AGGCGGACGC	CGCCATCCTG	ATGATCGACT	CGACGCATGG	200
TGGCTTCGAG	GCTGGCATCT	CGAAGGACGG	CCAGACCCGC	GAGCACGCGC	250
TGCTTGCCCT	CACKCTTGGC	GTGAAGCAGA	TGGTGGTGTG	CTGCAACAAG	300
ATGGACGACA	AGACGGTGAC	GTACGCGCAG	TCGCGCTACG	ATGAGATCAG	350
30 CAAGGAGGTG	GGCGCGTACC	TGAAGCGCGT	GGGCTACAAC	CCGGAGAAGG	400
TGCGCTTCAT	CCCGATCTCG	GGCTGGCAGG	GCGACAACAT	GATCGAGAAG	450
TCGGACAACA	TGCCGTGGTA	CAAGGGTCCC	ACGCTGCTGG	ACGCGCTCGA	500
CATGCTGGAG	CCGCCGGTGC	GCCCCGTGGA	CAAGCCGCTG	CGCCTGCCCC	550
TGCAGGACGT	GTACAAGATC	GGCGGTATCG	GGACGGTGCC	CGTGGGGCGC	600
35 GTGGAGACCG	GCATCATGAA	GCCGGGCGAC	GTGGTGACGT	TCGCGCCCGC	650
CAACGTGACG	ACTGAGGTGA	AGTCGATCGA	GATGCACCAC	GAGCAGCTGG	700
CGGAGGCGCA	GCCCCGCGAC	AACGTCGGCT	TCAACGTGAA	GAACGTGTCT	750
GTGAAGGACA	TCCGCCGTGG	TAACGTGTGC	GGCAACTCGA	AGAACGACCC	800
GCCGAAGGAG	GCGGCCGACT	TCACGGCGCA	GGTGATCGTG	CTGAACCACC	850
40 CCGGCCAGAT	CAGCAACGGC	TACGCGCCGG	TGCTGGACTG	CCACACGAGC	900
CACATTGCGT	GCCGCTTCGC	GGAATCGAG	TCCAAGATCG	ACCGCCGCTC	950
CGGCAAGGAG	CTGGAGAAGA	ACCCCAAGGC	GATCAAGTCT	GGCGATGCCG	1000
CGATCGTGAA	GATGGTGCCG	CAGAAGCCGA	TGTGCGTGGA	GGTGTTCAAC	1050
GACTACGCGC	CGCTGGGCCG	CTTTGCCGTG	CGCGACATGC	GCCAAACCGT	1100
45 TG					1102

2) INFORMATION FOR SEQ ID NO: 527

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Neospora caninum*
 325

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

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5  GGACRAACTT AAAGCTGAAC GTGAGCGTGG TATCACCATT GATATCTCCC      50
   TGTGGAAATT TGAGACCAGC AAGTACTATG TTACCATCAT TGATGCCCCA      100
   GGACACAGAG ACTTCATCAA AAACATGATT ACAGGCACAT CCCAGGCTGA      150
   CTGTGCTGTC CTGATTGTTG CTGCTGGTGT TGGTGAATTT GAAGCCGGTA      200
   TCTCCAAGAA CGGGCAGACC CGTGAGCATG CCCTTNTGGC TTACACCCTG      250
10  GGTGTGAAAC AACTAATTGT TGGCGTTAAC AAAAKGGATT CCACTGAGCC      300
   ACCCTATAGC CARAAGAGAT ACGARGAAAT TGTTAAGGAA GTCAGCMCCT      350
   AYNTTAAAAA AATTGGYTAC AACCCCGACA CAGTANCATT TGKGCCAATT      400
   TNTGGCTGGA ATGGTGACAA CATGCTGGAN CCAAGTGCTA ATATGCCATG      450
   GTTCAAGGGA TGGAAAGTCM CCCGTAAGGA CGGCAATGCC AGKGAACCM      500
15  CCCTGCTTGA AGCTYTGGAT TGCATTYTGC CACCAAYTTG CCCAACTGAC      550
   AAACCCCTGC GTTTGCCTYT CCAGGATGTC TATAAAATTG GKGGTATTGG      600
   TACTGTCCCT GTGGGTCGTG TGGAGACTGG TGTTCTCAA CCTGGCATGG      650
   TGGTCACCTT TGCTCCAGTC AATGTAACAA CTGAAGTGAA GTCTGTAGAA      700
   ATGCACCATG AAGCATTGAG TGAAGCCCTT CCTGGGGACA ATGTGGGCTT      750
20  CAATGTCAAG AACGTGTCTG TCAAAGATGT CCGTCGTGGC AATGTGGCTG      800
   GTGACAGCAA AAATGATCCA CCCATGGAAG CTGCTGGCTT CACAGCTCAG      850
   GTGATTATTT TGAACCATCC AGGCCAAATC AGTGCTGGAT ATGCACCTGT      900
   GCTGGATTGT CACACAGCTC ACATTGCTTG CAAGTTTGCT GAGCTGAAGG      950
   AGAAGATTGA TCGTCGTTCT GGGAAAAAGC TGAAGATGG CCCTAAATTC     1000
25  TTGAAATCTG GTGACGCTGC CATCGTTGAT ATGGTTCCTG GCAAGCCCAT     1050
   GTGTGTCGAG AGCTTCTCTG ATTATCCTCC CCTGGGCCGT TTTGCTGTGC     1100
   GTGAC                                     1105

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30

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

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35  (A) LENGTH: 935 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

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   (A) ORGANISM: Trichomonas vaginalis
   (B) STRAIN: ATCC 30001

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45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

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   GCACATCCCA GGCTGATGCT GCTATCCTTG TCATCGACTC CACACTCGGT      50
   GGYTTCGAAG CCGGTATCGC TGAACAAGGC CAGACACGTG AACACGCTCT      100
   TCTTGCCTTC AACTCGGCA TCAAGCAGGT CATTGTCGCC GTCAACAAGA      150
50  TGGATGACAA GACAGTCAAC TACAACAAGG CYCGTTTCGA CGAAATCACA      200
   GCCGAAATGA CACGCATCCT TACAGGCATC GGCTACAAGC CAGAAATGTT      250
   CCGCTTCGTC CCAATCTCCG GCTGGGCTGG CGACAACATG ACAGAGAAGT      300
   CTCCAAACAT GCCATGGTAC AATGGCCCAT ACCTTCTTGA AGCCCTCGAT      350
   TCCCTTCAGC CACCAAAGCG CCCATTGAC AAGCCACTCC GTCTTCCACT      400
55  CCAGGATGTC TACAAGATCA ACGGTATCGG TACAGTTCCA GTCGGCCGTG      450
   TCGAATCCGG CACAATGAAG CCAGGCATGA TCGTTAACTT CGCCCCATCC      500
   ACAGTTACAG CTGAAGTTAA GTCCATCGAA ATGCACCACG AATCCCTTCC      550
   AGAGGCTCTT CCAGGTGACA ACATCGGCTT CAACGTCAAG AACGTTTCCA      600
   CAGCTGATGT CAAGCGTGGC TACGTCGTTG GTGATACAAA GCGTGACCCA      650
60  CCAGTCGAAT GCGCTTCCTT CACAGCTCAR ATGATCATCT CCAACCACCC      700

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	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTCCGCAC	800
	GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTCAGAAGG	ATGATGCCGC	850
	TATCGTCCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTCCGAG	TCCTTCCAGG	900
5	AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

2) INFORMATION FOR SEQ ID NO: 529

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

25	AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TGCACTGTG	50
	GAAATTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
	GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
30	TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTGTGAAC	300
	TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
	CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
	GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
	AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCAAGTGC	500
35	TCCGAGCGAC	AAGCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
	GTGGTATTGG	CACCGTGCCC	GTTGGTCGTG	TGGAGACCGG	CGTGATGAAG	600
	CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
	ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
	ACGTCGGCTT	TAACGTGAAG	AACTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
40	AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
	CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
	ATGCGCCCGT	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
	GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
	TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
45	AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
	TTTGCCGTGC	GTGAC				1065

50 2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

327

(A) ORGANISM: *Crithidia rasciculata*

(B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

5
 TTCGCGGAGG GCGTGCCGCC GGTGCTGACG GCGCTGGACG TGACGGAGGA 50
 CCTCGGCCGC GACGAGCCGC TGACGCTGGA GATTGTGCAG CACTTGGACG 100
 CGAACACCGG CCGCTGCATT GCCATGCAGA CGACGGATCT GCTGAAGCTG 150
 AAGTCGAAGG TTGTGTCGAC GGGCGGCAAC ATCTCCGTGC CGGTTGGCCG 200
 10 CGAGACGCTG GGCCGCATCT TCAACGTGCT CGGCGACGCG ATCGACCAGC 250
 GCGGTGTGGT GGGCGAGAAG ATGCGCATGC CGATCCACGC CGAGGCGCCG 300
 AAGCTGGCGG ACCAGGCCGC GGAGGACGCG ATTCTGACGA CCGGCATCAA 350
 GGTGATCGAC CTGATTCTGC CGTACTGCAA GGGTGGCAAG ATCGGGCTGT 400
 TCGGCGGTGC TGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC 450
 15 AACGTGGCCA AGGGCCACGG TGGTTTCTCC GTGTTCCGCC GCGTTGGCGA 500
 GCGCACCCGC GAGGGCACGG ATCTGTACCT GGAGATGATG CAGTCGAAGG 550
 TCATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTGGTGTA CGGCCAGATG 600
 AACGAGCCCC CGGGTGCGCG TGC CGCTGTT GCGCAGTCTG CGCTGACGAT 650
 GGCAGAGTAC TTCCGTGACG TGGAGGGCCA GAACGTGCTG CTGTTTCATCG 700
 20 ACAACATCTT CCGCTTACC CAGGCCAAT CCGAGGTGTC CGCCCTGCTG 750
 GGCCGCATTC CCGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT 800
 TGGTATGCTG CAGGAGCGCA TTACGTGACG GACGAAGGGC TCGATTACGT 850
 CTGTGCAGGC CGTGTACGTG CCGGCCGATG ATATCACGGA TCCGGCGCCG 900
 GCGACGACCT TCTCGCACCT GGATGCGACG ACGGTGCTGG ACCGCGCGGT 950
 25 TGCCGAGTCT GGCATCTACC CCGCCGTGAA CCCGCTGGAG TGCGCGTTCG 1000
 GTATCATGGA CCCCAGTGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG 1050
 GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC 1100
 CGTGCTGGGT ATCGACGAGC TGAGCGAGGA GGACAAGCTT GTGGTGGACC 1150
 GCGCTCGCAA GGTGACGCGC TTCCTGTCGC AGCCGTTCCA GGTGGCCGAG 1200
 30 GTGTTACCG GCATGACGGG CCACTACGTG CAGCTGGAGG ACACAGTGGA 1250
 GTCGTTCTCT GGCCTGCTGA TGGGCTCGTA CGACCAGATC CCGGAGA 1297

35 2) INFORMATION FOR SEQ ID NO: 531

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

50
 CTTCTCGGAG GCGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
 GCGAACACGG GCCGCTGCAT TCGATGCAG ACGACGGACC TGCTGAAGCT 150
 GAAGTCGAAG GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 55 GTGAGACGCT GGGCCGCATC TTCAAYGTT TGGGCGACGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 60 CAACGTCGCG AAGGGCCACG GCGGTTTCTC CGTGTGTTGCC GCGGTTGGCG 500

	AGCGCACGCG	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTGGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
5	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCAAT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
10	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
15	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTTCG	ACGACCAGAT	CCCGGAGA	1298

20 2) INFORMATION FOR SEQ ID NO: 532

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGCCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTGCGC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
40	TGAGACCGTG	GGCCGCATCT	TCAACGTTCT	GGCGACGCG	ATCGACGACG	250
	GCGGCCCCCTG	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCGGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
45	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	GCGCGCGGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
50	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
55	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTCCG	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCCTGTGCG	AGCCGTTCCA	GGTTGCGGAG	1200
60	GTGTTACGCG	GCATGACGGG	CCACTACGTG	CAGCTGGTGC	ACACGGTGGG	1250

5 2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20 CTTCTCGGAG GCGGTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG 50
ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACCTGGAT 100
GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
25 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG 250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
30 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GCGGTTGGCG 500
AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG 550
GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA 650
TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700
35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
GGGCCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC 800
TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850
TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900
CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
40 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCC 1000
CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTT 1100
CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
CGCGCGCGCA AGGTGACCCG GTTCCTGTGC CAGCCGTTCC AGGTTGCGGA 1200
45 GGTGTTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

50 2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

```

5   CTTCTCGGAG GCGTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG      50
    ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
    GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT      150
    GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
10  GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
    CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
    AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
    AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG      400
    TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
15  CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTGTTGCC GCGGTTGGCG      500
    AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG      550
    GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
    GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA      650
    TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC      700
20  GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
    GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC      800
    TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG      850
    TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC      900
    CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
25  TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG      1000
    CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
    GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
    CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
    CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA      1200
30  GGTGTTACAG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG      1250
    AGTCGTTCTC TGGCCTGCTG ATGGGGTCTG ACGACCAGAT CCCGGAGA      1298
  
```

35 2) INFORMATION FOR SEQ ID NO: 535

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 1301 bases
    (B) TYPE: Nucleic acid
40  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

```

50  GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
    AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
    GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
    GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
55  GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TGCGATCGAC      250
    CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
    CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
    TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
    CTGTTTCGCG GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT      450
60  CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG      500
  
```

	GCGAGCGCAC	GCGCGAGGGC	ACGGACCTGT	ACCTGGAGAT	GATGCAAGTCG	550
	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTACTTCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
5	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
	GCTGGGCCCG	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCGC	900
	GCCCCGCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
10	CGGTGGCGGA	GTCGGGCATC	TACCCTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCTG	TGCGAGCCGT	TCCAGGTTGC	1200
15	GGAGGTGTTT	ACGGGCATGA	CGGGCCACTA	CGTGCAGCTG	GTCGACACGG	1250
	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

20

2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGGAC	100
	GCGAACACCG	GTCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
40	GAAGTCGAAG	GTCGTGTCTGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
	CGAGAGACCT	GGGTGCGATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
45	TTCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTC	CGTGTTTGCT	GGCGTGGGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTGT	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
50	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTTATT	700
	GACAACATCT	TCCGCTTCAC	GCAGGCCAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTGCGATT	CCTGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTCGA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
55	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGTGC GG	950
	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
60	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200

GGTGTTCACT GGCATGACGG GTCACTACGT TCAGCTGGAG GACATGGTGG 1250
AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACCACCAGAT CCCGGAGA 1298

5

2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1297 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
(B) STRAIN: ATCC 50122

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GCGGCTGGAT GTGACGGAGG 50
ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
25 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG 250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
30 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
CAATGTCCGG AAGGGCCACG GTGGTTTCTC CGTGTGTGCC GCGGTTGGCG 500
AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
35 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750
GGGCCGCAAT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850
TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
40 CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950
TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
CGTATCATATG ACCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTTG 1100
CGGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
45 CGCGCGCGCA AGGTGACCCG GTTCCTGTCTG CAGCCGTTCC AGGTTGCGGA 1200
GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACCACCAGAT CCCGGAG 1297

50

2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1297 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

```

TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA      50
CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACCTGGACG      100
CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GTTGAAGCTG      150
10 AAGTCGAAGG TTGTGTCGAC CGGCGGCAAC ATCTCTGTGC CCGTGGGCCG      200
TGAGACGCTG GGCCGCATCT TCAACGTGCT GGGCGACGCG ATCGACCAGC      250
GCGGCCCCGT GGGTGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCCG      300
AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA      350
GGTGATCGAC CTGATTCTGC CCTACTGCAA GGGTGGCAAG ATCGGCCTGT      400
15 TTGGTGGCGC CCGGTGTGGG AAGACCGTGA TCATCATGGA GTTGATTAAC      450
AACGTCGCGA AGGGCCACGG TGGTTTCTCG GTGTTTGCCG GCGTTGGCGA      500
GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG      550
TGATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTTGTGTA CGGGCAGATG      600
AACGAGCCCC CGGGTGC GCGCGCGGTT GCGCAGTCTG CGCTGACGAT      650
20 GCGCGAGTAC TTCCGAGACG TGGAGGGCCA GAATGTGCTG CTGTTTCATCG      700
ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TCGCTGCTG      750
GGCCGCATTC CGGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT      800
TGGTATGCTG CAGGAGCGCA TCACGTGCGA GACGAAGGGG TCGATCACGT      850
CCGTGCAGGC CGTGACGTG CCTGCGGATG ATATCACGGA TCCGGCGCCC      900
25 GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT      950
GGCGGAGTCG GGGATCTACC CTGCCGTGAA CCCGCTGGAG TGCGCGTCGC      1000
GTATCATGGA CCCCAGATGT ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC      1100
GGTGCTTGGT ATCGACGAGC TGAGCGAGGA GGACAAGGTC GTGGTGGACC      1150
30 GCGCGCGCAA GGTGACCCGG TTCCTGTCGC AGCCGTTCCA GGTGCGGAG      1200
GTGTTACGCG GCATGACGGG CCACTACGTG CAGCTGGCCG ACACGGTGGA      1250
GTCGTTCTCT GGGCTGCTGA TGGGTCGTA CGACCAGATC CCGGAGA      1297

```

35

2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

20 GTKGAAATGT TCCGCAAGCT GCT

23

2) INFORMATION FOR SEQ ID NO: 542

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

35

CGGAARTAGA ACTGSGGACG GTAG

24

2) INFORMATION FOR SEQ ID NO: 543

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

50

ATCTTAGTAG TTTCTGCTGC TGA

23

2) INFORMATION FOR SEQ ID NO: 544

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

60

335

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

CCRCGICCGG TRATGGTGAA GAT

23

40

2) INFORMATION FOR SEQ ID NO: 547

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

GTACAGTTGC TTCAGGACGT ATC

23

55

2) INFORMATION FOR SEQ ID NO: 548

60

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548
ACGTTTCGATT TCATCACGTT G 21

15 2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549
GAACGTGATA CTGACAAACC TTTA 24

30 2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550
GAAGAAGAAC ACCAACGTTG 20

45 2) INFORMATION FOR SEQ ID NO: 551

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551
60 GAAGAAAAA TCTTCGAACT GGCTA 25

2) INFORMATION FOR SEQ ID NO: 552

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

15

TACACGGCCG GTGACTACG

19

2) INFORMATION FOR SEQ ID NO: 553

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

30

GGCCGTGTTG AACGTGGTCA AATCA

25

2) INFORMATION FOR SEQ ID NO: 554

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

45

GTTCCCTTACA TCGTTGTTTT TCTC

24

50

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

5 TCTCGAACTT TCTCTATGTA TGCA

24

2) INFORMATION FOR SEQ ID NO: 556

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

20

CGGCGCNATC YTS GTTGTG C

21

2) INFORMATION FOR SEQ ID NO: 557

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

35

CCMAGGCATR ACCATCTCGG TG

22

2) INFORMATION FOR SEQ ID NO: 558

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYG CITGGGT

20

2) INFORMATION FOR SEQ ID NO: 559

55

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

10 CCGACRGCRA YIGTYTGICK CAT 23

2) INFORMATION FOR SEQ ID NO: 560

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

25 GAYTTCATYA ARAAYATGAT YAC 23

2) INFORMATION FOR SEQ ID NO: 561

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

40 ACIGTICGGC CRCCCTCACG GAT 23

45 2) INFORMATION FOR SEQ ID NO: 562

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCIGG IGYIMGIATG 30

60

2) INFORMATION FOR SEQ ID NO: 563

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT 26

2) INFORMATION FOR SEQ ID NO: 564

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA 29

2) INFORMATION FOR SEQ ID NO: 565

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

GGYTGRTAIC CIACIGCIGA IGGDAT 26

2) INFORMATION FOR SEQ ID NO: 566

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

5 2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG

26

20.

2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT

23

35

2) INFORMATION FOR SEQ ID NO: 569

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

RTIRTIGGIS CIGTIRTIGA TAT

23

50

2) INFORMATION FOR SEQ ID NO: 570

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

5 RTIRYIGGIC CIGTIRTIGA YGT 23

2) INFORMATION FOR SEQ ID NO: 571

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

20

RTIRTIGGIC CIGTIRTIGA TGT 23

25 2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

RTIRTIGGIS CIGTIRTIGA 20

40

2) INFORMATION FOR SEQ ID NO: 573

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC 20

55

2) INFORMATION FOR SEQ ID NO: 574

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

343

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

10 ATIGCIATGG AYGGIACIGA RGG 23

2) INFORMATION FOR SEQ ID NO: 575

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

25 TIACCATTTC AGTACCTTCT GGTA 25

2) INFORMATION FOR SEQ ID NO: 576

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

40 AACTTCRTCA AGAAGGTYGG TTACAA 26

45 2) INFORMATION FOR SEQ ID NO: 577

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA 20

60

2) INFORMATION FOR SEQ ID NO: 578

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA

20

15

2) INFORMATION FOR SEQ ID NO: 579

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA

20

30

2) INFORMATION FOR SEQ ID NO: 580

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

45 GCTAAACCAG CTACAATCAC TCCAC

25

2) INFORMATION FOR SEQ ID NO: 581

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

60

5 2) INFORMATION FOR SEQ ID NO: 582

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT

28

20

2) INFORMATION FOR SEQ ID NO: 583

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG

35

35

2) INFORMATION FOR SEQ ID NO: 584

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA

20

50

2) INFORMATION FOR SEQ ID NO: 585

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

5 ACCACATACT GAATTCAAAG

20

2) INFORMATION FOR SEQ ID NO: 586

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

20

CAGAAGTATA CGTATTATCA

20

25 2) INFORMATION FOR SEQ ID NO: 587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

CGTATTATCA AAAGACGAAG

20

40

2) INFORMATION FOR SEQ ID NO: 588

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAAA CTATCGTCCA

20

55

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

10 GCACGAAACT TCTAAAACAA 20

2) INFORMATION FOR SEQ ID NO: 590

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT 20

2) INFORMATION FOR SEQ ID NO: 591

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

40 TCCTGGTTCT ATTACACCAC 20

45 2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

CAAAGCTGAA GTATACGTAT 20

60

2) INFORMATION FOR SEQ ID NO: 593

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCACTAACT ATCGCCCACA

20

15

2) INFORMATION FOR SEQ ID NO: 594

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

30 ATTGGTATCC ATGACACTTC

20

30

2) INFORMATION FOR SEQ ID NO: 595

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

45 TTAAAGCAGA CGTATACGTT

20

45

2) INFORMATION FOR SEQ ID NO: 596

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

60

5 2) INFORMATION FOR SEQ ID NO: 597

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAACTTC

20

20

2) INFORMATION FOR SEQ ID NO: 598

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT

20

35

2) INFORMATION FOR SEQ ID NO: 599

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA

50

20

2) INFORMATION FOR SEQ ID NO: 600

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

350

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

5 ATGCAAGAAG AATCAAGCAA

20

2) INFORMATION FOR SEQ ID NO: 601

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

20

GTTTCACGTG ATGATGTACA

20

25 2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTTGGTATT

20

40

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC

20

55

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 20 bases

351

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT

20

2) INFORMATION FOR SEQ ID NO: 605

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

25 GAAATGTTCC GTAAATTATT

20

2) INFORMATION FOR SEQ ID NO: 606

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

40

ATTAGACTAC GCTGAAGCTG

20

45 2) INFORMATION FOR SEQ ID NO: 607

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

60

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAAACAC	50
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
5	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCCAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
10	CGAAACATCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
15	TTCCGTACAA	CAGACGTTAC	TGGTGTGTTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTACC	800
	CAATCGCTAT	CGAAGACGGA	A			821

20

2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTCCTTA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
40	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCCCTGT	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
45	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
50	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

55

2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: ATCC 49573

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

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CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC      50
GTGAACACAT CTTGTTATCA CGTAACGTTG GCGWACCATA CATCGTTGTT      100
TTCTTGAACA AAATGGATAT GGTGAYGAC GAAGAATTGC TAGAATTAGT      150
15 TGAAATGGAA GTTCGTGACC TATTGTCTGA ATATGACTTC CCAGGCGACG      200
ATGTTCTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA AGGAGATCCT      250
TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT      300
TCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
20 CGTGGACAAG TTCGCGTTGG TGATGAAGTA GAAATCGTTG GTATTGCTGA      450
CGAAACTGCT AAAACAACCTG TAACAGGTGT TGAAATGTTC CGTAAATTGT      500
TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGGGTT      550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACRAT      600
CACACCTCAT ACAAATTTCA AAGCTGAAGT TTATGTTTTG ACAAAGAAG      650
25 AAGGTGGRCG TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC      700
TTCCGTACAA CTGACGTAAC TGGTGTGTT GAATTACCAG AAGGAACCTGA      750
A                                                                751

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30

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

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35 (A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae* Rd

(B) STRAIN: KW20

(C) ACCESSION NUMBER: extracted from U32739

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

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AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC      50
AGCAACAGAT GGTCTATATG CACAACTCG TGAACACATC TTATTAGGTC      100
50 GCCAAGTAGG TGTTCCATAC ATCATCGTAT TCTTAAACAA ATGCGACATG      150
GTAGATGACG AAGAGTTATT AGAATTAGTC GAAATGGAAG TTCGTGAAC      200
TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC GTACGTGGTT      250
CAGCATTACA AGCGTTAAAC GCGGTAGCAG AATGGGAAGA AAAAATCCTT      300
GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT      350
55 TGACCAACCG TTCCTTCTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC      400
GTGGTACTGT AGTAACAGGT CGTGTAGAAC GAGGTATTAT CCGTACAGGT      450
GATGAAGTAG AAATCGTCGG TATCAAAGAT ACAGCGAAAA CTACTGTAAC      500
GGGTGTTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT GCAGGTGAAA      550
ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT      600
60 CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC      650

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	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCATCT	700
	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	GTACAACAGA	CGTGACTGGT	750
	ACAATCGAAT	TACCAGAAGG	CGTGGAATG	GTAATGCCAG	GCGATAACAT	800
	CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
5	GTTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 611

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

25	CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
30	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
	AACTTCTAAA	ACAACCTGTTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
35	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCA	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
	ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCATAACT	ATCGCCCACA	ATTCTATTTC	700
	CGTACTACTG	ACGTAACTGG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
40	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TCGCTATCGA	AGACGGAA				818

45 2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi A
- (B) STRAIN: ATCC 9150

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

355

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
5	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
10	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAACT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTGCAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	650
15	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20

2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 778 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*

(B) STRAIN: ATCC 33105

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTTGG	CGTTCCTTTC	ATCATCGTGT	100
40	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTGCGGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
50	CCGCACACCC	AGTTGATTC	AGAAGTGATC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55

2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 653 bases

356

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

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GTGCGATCTT AGTAGTATCA GCTACTGATG GTCCAATGCC TCAAACTCGT      50
GAACACATTT TGTATCACG TCAAGTTGGT GTTAAGCACT TGATCGTTTT      100
15 CTTGAACAAA GTAGATTTAG TTGATGACGA AGAATTGATC GACTTAGTTG      150
AAATGGAAGT ACGTGAATTA CTTTCTGAAT ATGGTTTCCC AGGTGATGAT      200
ATTCCAGTGC TTAAAGGTTT TGCTTTGAAA GCATTAGAAG GCGATCCAGA      250
ACAAGAACAA GTTATTCTTG ATTTGATGGA TACCGTTGAT GAATATATCC      300
CAACACCTGA ACGTGACAAT GACAAACCGT TCTTGTTACC AGTTGAGGAT      350
20 GTTTTCTCGA TCACAGGACG TGGTACTGTA GCTTCTGGTC GTATCGACCG      400
TGGCGAAGTT AAAGTCGGCG ATGAAATTGA AATCATCGGG ATCAAACCTG      450
AAGTTCAAAA AGCAATCGTT ACTGGACTTG AAATGTTCCG TAAAACATTG      500
GATTATGGTG AAGCTGGCGA TAACGTTGGG GTTCTATTAC GTGGGATTAC      550
ACGTGATGAA ATCGAACGTG GCCAAGTATT AGCTAAACCA GGTTCATCA      600
25 CACCACATAC TAAGTTCAAA GCCGAAGTAT ATGTGTTGAC GAAAGAAGAA      650
GGT                                                                653
  
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30 2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

45

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CCATTCTAGT TGTATCTGCA ACAGATGGAC CAATGCCACA AACACGTGAA      50
CATATTTTAT TGTCACGTCA AGTAGGTGTT AAATATTTGA TCGTCTTCTT      100
GAACAAAATC GACTTAGTAG ATGATGAAGA ATTGATTGAT CTTGTGCGAA      150
TGGAAGTTCG TGAATTATTA AGCGAATATG GTTTCCCAGG TGACGATACA      200
50 CCAGTCATCA AAGGTCAGC ATTAAAAGCT TTACAAGGAG ATCCTGATGC      250
AGAAGCAGCT ATCATGGAAT TGATGGATAC TGTTGATGAA TATATCCCAA      300
CACCAGAACG TGATACAGAC AAACCATTAT TGTTACCAGT GGAAGATGTC      350
TTCTCAATCA CAGGTCGTGG GACTGTTGCT TCAGGTCGTA TCGATCGTGG      400
TGCAGTTCGT GTAGGTGATG AAATCGAAAT CGTCGGTATC AAACCTGAAA      450
55 CACAAAAAGC TGTTGTAAC TGGGTCGAAA TGTTCCGCAA GACATTAGAC      500
TATGGTGAAG CAGGAGATAA CGTTGGGGTA TTGTTACGTG GTATCCAACG      550
TGAAGATATC GAACGTGGAC AAGTAATCGC AAAACCAGGT TCAATCACAC      600
CACATACAAA ATTCAAAGCA GAAGTGACG TATTGACAAA AGAAGAAGGT      650
GGACGTCATA CACCATTCTT CAATAACTAT CGTCCACAA TCTACTTCCG      700
60 TACAACTGAC GTAAC TGAA CAATCGTTTT ACCTGGAGGC ACTGAAATGG      750
  
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TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCAGTT 890
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

5

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

GGTGCAATTT TAGTAGTATC TGCTACTGAT GGCCCAATGC CACAAACACG 50
TGAACATATC TTGTTATCAC GTCAAGTAGG GGTAAACAC TTAATCGTCT 100
TCTTGAACAA AGTTGATTTA GTTGATGATG AAGAATTGAT CGATTTAGTT 150
25 GAAATGGAAG TTCGGGAATT GCTTTCTGAA TATGGTTTCC CAGGCGATGA 200
TATTCCAGTA CTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG 250
AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC 300
CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA 350
TGTCTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC 400
30 GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT 450
GAAGTGCAA AAGCTGTCTG AACTGGACTA GAAATGTTCC GTAAGACATT 500
GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTTCTATTA CGTGGGATTA 550
CTCGTGATGA AATCGAACGT GGACAAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CGAAATTCAG TGCAGAAAGTT TATGTATTGA CGAAAGAAGA 650
35 AGGTGGCCGT CATACGCCA 669

2) INFORMATION FOR SEQ ID NO: 617

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

CGGGGCAATT TTAGTTGTAT CTGCAACTGA TGGCCCAATG CCACAAACAC 50
GTGAACACAT TTTGTTAGCT CGTCAAGTAG GGGTTAAATA TTTAATCGTC 100
TTCTTGAACA AAACAGATTT AGTTGATGAT GAAGAATTAT TGGAACTAGT 150
TGAAATGGAA GTTCGTGAAT TATTAAATGA ATACAATTTC CCTGGCGATG 200
ATATTCCTGT TATTCGCGGA TCTGCTTTAA AAGCATTAGA AGGCGATCCA 250
60 GAACAAGAAG AAGTAATTAT GAACTTGATG GATACTGTGG ATGAATATAT 300

	CCCAACTCCA	GAACGTGACA	ATGATAAACC	ATTCTTGTTA	CCAGTGGGAAG	350
	ATGTCTTCAC	AATTACTGGT	CGTGGTACTG	TTGCTTCAGG	TCGTATCGAC	400
	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTT	CGTAAACTT	500
5	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
	TACACCGCAT	ACCAAATTTA	AAGGTGAAGT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACTGA	750
10	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTTCATC	800
	CAATCGCCGT	TGAAAAAGGG	ACTACTTTCT	CAATT		835

15 2) INFORMATION FOR SEQ ID NO: 618

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

30	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAATTGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
35	TATTCCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
	CCAACCTCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
40	GAAATTCAAA	AAGCAGTCGT	AACTGGACTT	GAAATGTTCC	GTAAAACTTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
45	AGGTGGACGT	CATACACCAT	CTT			673

2) INFORMATION FOR SEQ ID NO: 619

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 60 (C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

	TTTCATATTT	TTAAGGATTT	TGTTTTAGCA	CCCATCCGAC	CTCAGTCAAT	50
5	ATATCCTTTC	GCGACCAGGC	TTTCCTCCCT	TTTGCTGCTA	ACTGGTTACA	100
	GATTTTCCCTA	TTTTTGGTCA	TTTTTATCTT	TGAAACTGAT	TAAGCTGAAA	150
	AAATTTGAGC	TTCTTTGTTG	TAAACTATTT	TGTGCTTTCA	GTTTTATTCT	200
	AGCTCGACAA	AGGTAACAGA	CAAAAATGTC	AGCTTTATTA	CCAAGATTAC	250
	TCACAAGAAC	AGCTTTTAAA	GCTTCTGGA	AACCTTCTGAG	GCTCTCTTCA	300
10	GTAATTTCTA	GGACCTTTTC	TCAAACACT	ACTTCCTATG	CAGCTGCTTT	350
	TGATCGTTCC	AAACCGCATG	TAAATATAGG	TACGATCGGC	CATGTTGATC	400
	ATGGGAAGAC	AACTTTAACC	GCAGCCATTA	CGAAAACGTT	AGCCGCAAAA	450
	GGTGGTGCCA	ACTTCTTGGA	CTATGCTGCC	ATCGATAAGG	CTCCGGAAGA	500
	AAGAGCTCGT	GGTATTACAA	TTTCTACTGC	ACACGTGGAA	TACGAAACGG	550
15	CCAAGAGACA	TTATTCTCAC	GTCGACTGTC	CAGGCCACGC	TGATTACATC	600
	AAGAATATGA	TTACCGGTGC	TGCTCAAATG	GATGGTGCTA	TCATTGTTGT	650
	AGCTGCTACC	GATGGACAAA	TGCCCCAAAC	TAGAGAACAT	TTACTTTTGG	700
	CCAGACAAGT	TGGTGTCCAA	CATATTGTCG	TTTTTGTAA	CAAGGTTGAT	750
	ACCATTGATG	ATCCAGAAAT	GTTAGAGTTA	GTCGAAATGG	AAATGAGAGA	800
20	ACTTTTAAAC	GAATATGGGT	TTGACGGTGA	TAATGCTCCA	ATTATCATGG	850
	GTTCTGCCCT	TTGCGCTTTG	GAAGGTCGCC	AACCTGAAAT	TGGGGAGCAG	900
	GCCATCATGA	AACTTTTGGA	TGCAGTGAT	GAGTATATTC	CTACACCTGA	950
	AAGAGATTTG	AACAAGCCTT	TCTTGATGCC	CGTTGAAGAT	ATCTTCTCTA	1000
	TCTCCGGTAG	AGGTACTGTG	GTCACTGGTC	GTGTGGAAAG	GGGTAATTTA	1050
25	AAGAAAGGTG	AGGAATTGGA	AATTGTTGGT	CACAACTCCA	CCCCATTGAA	1100
	AACAACAGTT	ACTGGTATTG	AAATGTTTAG	AAAGGAATTG	GACTCTGCTA	1150
	TGGCAGGTGA	CAATGCCGGT	GTTTTACTTA	GAGGTATCAG	GAGAGATCAA	1200
	TTGAAGAGAG	GTATGGTCTT	AGCTAAGCCA	GGTACCGTTA	AAGCCCATAC	1250
	AAAGATTCTA	GCCTCTTTGT	ACATTTTATC	CAAAGAGGAA	GGTGGTAGAC	1300
30	ATTCTGGGTT	TGGTGAAAAC	TACAGACCAC	AAATGTTTAT	AAGAACAGCT	1350
	GATGTTACAG	TTGTGATGAG	ATTTCTAAG	GAGGTTGAAG	ATCATTCTAT	1400
	GCAAGTTATG	CCAGGTGACA	ATGTTGAAAT	GGAATGTGAT	TTGATCCATC	1450
	CTACCCCAT	AGAAGTTGGT	CAACGTTTCA	ATATCAGAGA	GGGTGGAAGA	1500
	ACTGTTGGTA	CCGGTCTAAT	CACACGTATT	ATTGAATAGA	CTTATTGATG	1550
35	CAACTGGAGT	ATATTTCTAT	ATATTCTGTT	CATTTCCCCT	CTCATAATAT	1600
	ATACTTGTTT	CGTTAAAT	TTATACGTGT	AAATAAAGTG	CCATAAATTT	1650
	TTCAGCTTTA	CTTTTGGTAG	AGTCCTGCTA	GCACTAGATT	TTACAATTTT	1700
	ATGTGCACAC	ACC				1713

40

2) INFORMATION FOR SEQ ID NO: 620

(i) SEQUENCE CHARACTERISTICS:

45	(A)	LENGTH: 18 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Single
	(D)	TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

55 ATTGGTGCAT TGCTACGT

18

55

2) INFORMATION FOR SEQ ID NO: 621

60 (i) SEQUENCE CHARACTERISTICS:

360

(A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

15	TGGTGCAATC	TTAGTTGTTT	CTGCAACTGA	CGGTCCGATG	CCTCAAACAC	50
	GTGAACACAT	TTTATTGTCA	CGCCAAGTTG	GTGTAAAATA	CCTGATTGTT	100
	TTCTTGAACA	AAGTTGATTT	AGTCGATGAT	GAAGAATTGA	TCGATTTGGT	150
	AGAAATGGAA	GTTGCGGAGT	TATTGAGCGA	ATATGGTTTC	CCAGGCGATG	200
	ACACTCCTGT	GATCAAAGGT	TCCGCATTAA	AAGCATTGCA	AGGCGATCCA	250
	GATGCTGAAG	CTGCTATTAT	GGAAATTGATG	GATACAGTAG	ATGAATATAT	300
20	CCCAACACCA	GAACGTGATA	CAGATAAACC	ATTACTATTG	CCAGTGGAAG	350
	ACGTCTTCTC	AATTACAGGT	CGAGGAACTG	TTGCCTCAGG	TCGTATTGAT	400
	CGTGGTGCTG	TTCGTGTCGG	TGATGAGGTA	GAGATCGTAG	GGATCAAACC	450
	TGAAACACAA	AAAGCAGTTG	TAACAGGTGT	AGAAATGTTC	CGTAAAACGT	500
	TAGATTACGG	GGAAGCTGGG	GATAACGTAG	GCGTGTTGTT	ACGGGGGATC	550
25	CAACGTGACG	ATATCGAACG	TGGACAAGTA	CTTGCTAAAC	CAGGTTCCAT	600
	TACTCCACAT	ACAAAATTCA	AAGCAGAAGT	GTACGTGTTG	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTATCGTCC	ACAGTTCTAC	700
	TTCCGCACAA	CTGATGTTAC	AGGAACAATC	ACATTGCCAG	AAGATACAGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 622

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: ATCC 13264

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

50	GTCAAATGGG	ACGAATCCAG	ATTCCAAGAA	ATTGTCAAGG	AAACCTCCAA	50
	CTTTATCAAG	AAGGTTGGTT	ACAACCCAAA	GACTGTTCCA	TTCGTCCCAA	100
	TCTCTGGTTG	GAACGGTGAC	AACATGATTG	AAGCTACCAC	CAACGCTCCA	150
	TGGTACAAGG	GTTGGGAAAA	GGAAACCAAG	GCCGGTGTCT	TCAAGGGTAA	200
	GACTTTGTTG	GAAGCCATTG	ACGCCATTGA	ACAACCATCT	AGACCAACTG	250
	ACAAGCCATT	GAGATTGCCA	TTGCAAGATG	TTTACAAGAT	TGGTGGTATT	300
55	GGTACTGTGC	CAGTCGGTAG	AGTTGAAACC	GGTGTCATCA	AGCCAGGTAT	350
	GGTTGTTACT	TTCGCCCCAG	CTGGTGTTAC	CACTGAAGTC	AAGTCCGTTG	400
	AAATGCATCA	CGAACAATTG	GAACAAGGTG	TTCCAGGTGA	CAACGTTGGT	450
	TTCAACGTCA	AGAACGTTTC	CGTTAAGGAA	ATCAGAAGAG	GTAACGTCTG	500
	TGGTGACGCT	AAGAACGATC	CACCAAAGGG	TTGCGCTTCT	TTCAACGCTA	550
60	CCGTCATTGT	TTTGAACCAT	CCAGGTCAAA	TCTCTGCTGG	TTACTCTCCA	600

361

GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTTCG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAATC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

5

2) INFORMATION FOR SEQ ID NO:623

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTCGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
25 CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150
GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
TATCTCCAAG	GACGGTCAGA	CCCGAGAGCA	CGCCCTCCTC	GCCTTCACCC	250
TCGGTGTCAG	GCAGCTCATT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
30 CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCCTCGTC	CCCATCTCTG	400
GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGGT	500
ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
35 GCCCCTCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
TCTCATCTCT	CTTGTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCCGAGGG	TCTTCCCGGA	850
40 GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCCTATG	GAGGCTGCTT	950
CTTTCAACGC	CCAGGTTATC	GTCCTTAACC	ACCCCTGGTCA	GATCGGTGCC	1000
GGTTACACCC	CCGTTCTCGA	CTGTCACACT	GCCCGTAAGC	CTGACCCAAT	1050
ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
45 TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
GTCGATTTCG	CGTCCGAGA				1269

50

2) INFORMATION FOR SEQ ID NO: 624

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 753
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

362

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 36801

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

```

TCTGTCAAAT GGGACAAAAA CAGATTTGAA GAAATCATCA AGGAAACCTC      50
CAACTTCGTC AAGAAGGTTG GTTACAACCC AAAGACTGTT CCATTCGTTT      100
10 CAATCTCTGG TTGGAATGGT GACAACATGA TTGAACCATC CACCAACTGT      150
CCATGGTACA AGGGTTGGGA AAAGGAAACC AAATCCGGTA AAGTTACTGG      200
TAAGACCTTG TTAGAAGCTA TTGACGCTAT TGAACCACCA ACCAGACCAA      250
CCGACAAACC ATTGAGATTG CCATTGCAAG ATGTTTACAA GATCGGTGGT      300
ATTGGTACTG TGCCAGTCGG TAGAGTTGAA ACTGGTATCA TCAAAGCCGG      350
15 TATGGTTGTT ACTTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAATCCG      400
TTGAAATGCA TCACGAACAA TTGCTGAAG GTGTTCCAGG TGACAATGTT      450
GGTTTCAACG TTAAGAACGT TTCCGTTAAA GAAATTAGAA GAGGTAACGT      500
TTGTGGTGAC TCCAAGAACG ATCCACCAA GGGTTGTGAC TCTTTCAATG      550
CCCAAGTCAT TGTTTTGAAC CATCCAGGTC AAATCTCTGC TGGTTACTCT      600
20 CCAGTCTTGG ATTGTCACCC TGCCCACATT GCTTGTAAT TCGACACTTT      650
GGTTGAAAAG ATTGACAGAA GAACTGGTAA GAAATTGGAA GAAAATCCAA      700
AATTCGTCAA ATCCGGTGAT GCTGCTATCG TCAAGATGGT CCAACCAA      750
CCA                                                                753
  
```

25

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

```

CGTTGAAGAC ACGACCCAAA GTATCC      26
40
  
```

2) INFORMATION FOR SEQ ID NO: 626

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

```

55 TACCACCTTT TAAGTAAGGT GCTAAT      26
  
```

2) INFORMATION FOR SEQ ID NO: 627

60

2) INFORMATION FOR SEQ ID NO: 631

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631
15 CAGACCAACY GAIAARCCAT TRAGAT 26

2) INFORMATION FOR SEQ ID NO: 632

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632
30 CCCTTTGGTG GRTCSTKCTT GGA 23

35 2) INFORMATION FOR SEQ ID NO: 633

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633
45 CAGACCAACY GAIAARCCIT TRAGAT 26

50 2) INFORMATION FOR SEQ ID NO: 634

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA 26

5

2) INFORMATION FOR SEQ ID NO: 635

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

20 AAACCRGTIA RRGCRCTCT IGCTCT 26

2) INFORMATION FOR SEQ ID NO: 636

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

35 ACTGGYGTTG AIATGTTCCG YAA 23

2) INFORMATION FOR SEQ ID NO: 637

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

50 ACGTCAGTIG TACGGAARTA GAA 23

55 2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Single

366

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT 26

10

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTCWACAC CWGTIACA 28

25

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA 23

40

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

55 TGATAACCWA CIGCIGAIGG CATACG 26

2) INFORMATION FOR SEQ ID NO: 642

60

23

23

23

23

2) INFORMATION FOR SEQ ID NO: 646

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646
15 ATCGACAAGC CITTCTIAT GSC 23

2) INFORMATION FOR SEQ ID NO: 647

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647
30 ACGTCCGTSG TRCGGAAGTA GAACTG 26

35 2) INFORMATION FOR SEQ ID NO: 648

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648
ACGTCSGTSG TRCGGAAGTA GAACTG 26

50 2) INFORMATION FOR SEQ ID NO: 649

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC 26

5

2) INFORMATION FOR SEQ ID NO: 650

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

20 TTACGGAACA TYTCAACACC IGT 23

2) INFORMATION FOR SEQ ID NO: 651

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

35 TGACGACCAC CITCYTCYTT YTTCA 25

2) INFORMATION FOR SEQ ID NO: 652

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

50 CCWAYAGTIY KICCICCYTC YCTIATA 27

2) INFORMATION FOR SEQ ID NO: 653

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Single

370

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT

20

10

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG

20

25

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA

20

40

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

55 AATTAATGGC TGCAGTTGAY GA

22

60

2) INFORMATION FOR SEQ ID NO: 657

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA 22

15 2) INFORMATION FOR SEQ ID NO: 658

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT 23

30 2) INFORMATION FOR SEQ ID NO: 659

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTGGIG TTTCWGGTTT RAT 23

45

2) INFORMATION FOR SEQ ID NO: 660

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

GTAGAATTGA GGACGGTAGT TAG 23

2) INFORMATION FOR SEQ ID NO: 661

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661
- 15 GTAGAAATGT GGWCGATART TRT 23

2) INFORMATION FOR SEQ ID NO: 662

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

35	CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC	50
	GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT	100
	GCTCTGAACA AGTGCGACAT GGTTGATGAT GAGGAAATCA TCGAGCTCGT	150
	CGAGATGGAG ATCCRTGAGC TGCTCGCTGA GCAGGATTAC GACGAAGAGG	200
	CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG CGACGAGAAG	250
40	TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
	AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA	350
	TCTTACCAT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT	400
	GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA	450
	KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG	500
45	ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG	550
	CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
	CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG	650
	GTGGCCGCCA CACCCCATTC TTCGACAACT ACCGCCACA GTTCTACTTC	700
	CGCACCACCG ACGTTACCGG TGTTGTGAAG CTTCTGAGG GCACCGAGAT	750
50	GGTCATGCCT GGCGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG	800
	TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC	832

55 2) INFORMATION FOR SEQ ID NO: 663

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1192 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*

(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

10 AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA 50
 CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA 100
 CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT 150
 ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG 200
 15 TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT 250
 TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT 300
 GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG 350
 TGGTGCCGGT GTCGGTAAGA CCGTGTTTCAT CCAGGAGTTG ATTAACAACA 400
 TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CGGTGAGCGT 450
 20 ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT 500
 CAACTTGAGG GGCGACTCCA AGGTGGCCTT GGTGTTTCGGT CAGATGAACG 550
 AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC 600
 GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA 650
 CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC 700
 25 GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT 750
 TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT 800
 GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCGCCA 850
 CCACTTTCGC TCACTTGGAC GCCACCACCG TGTGTCGCG TGGTATCTCC 900
 GAGTTGGGTA TCTACCCCGC CGTCGACCC TTGGACTCCA AGTCGAGATT 950
 30 GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG 1000
 TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT 1050
 TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC 1100
 CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTGCTGTG GCGGAGGTTT 1150
 TCACTGGTAT CCCCCGTAGA TTGGTGAGAT TGCAGGACAC CG 1192

35

2) INFORMATION FOR SEQ ID NO: 664

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

50 AAYATGATIA CIGGIGCIGC ICARATGGA

29

2) INFORMATION FOR SEQ ID NO: 665

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

374

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

```

10 ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA      50
   TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
   TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
   AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
   AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
15 AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG      300
   AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
   TGGTGGTGTC GGTGAATTTC AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
   GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
   GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
20 AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
   AGACTGTTCC ATTCTGTTCC ATCTCTGGTT GGAACGGTGA CAACATGATT      600
   GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTTGGGAAA AGGAAACCAA      650
   GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
   AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
25 GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
   CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTTA      850
   CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
   GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
   AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG     1000
30 GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA     1050
   ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACTACT CTCACATTGC     1100
   TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA     1150
   AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC     1200
   AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC     1250
35 ACCATTAGGT AGATTGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCTG     1300
   GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG     1350
   GCTGCTCAAA AGGCTGCTAA GAAATAA      1377

```

40

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1536 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from M12082

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

```

ATGGTTTTGC CAAGACTATA TACTGCTACA TCCCGTGCTG CTTTTAAAGC      50
AGCCAAACAA TCCGCTCCGC TTCTATCCAC TTCGTGGAAG AGATGTATGG      100
CCTCAGCTGC TCAATCTACT CCAATCACCG GTAAAGTTAC CGCTGTCATT      150
60 GGTGCCATTG TTGACGTTCA TTTTGAACAA TCAGAGTTGC CCGCTATTTT      200

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	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
5	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTTCATT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
10	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACCTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGT	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCA	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTTGTT	TATCGACAAT	ATCTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
15	GTCTCTGCCC	TTTTGGGTCG	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCGAAGA	GGTATTTTCA	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
20	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCT	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
25	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

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2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
50	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCTGGGAG	200
	ACACTTGCCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTC	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTTTG	400
55	TGGTGCTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAACCT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGAATCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
60	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700

	CATTTTCCGC	TTTACGCAGG	CAAACCTCTGA	GGTGTCTAGCG	CTGTTGGGTC	750
	GTATTCCC	TGCCGTCGGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
5	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCCGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
10	GCGTAAGGTG	ACAAAGTTTC	TCTCCCAGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCCGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCCG	AGA	1293

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2) INFORMATION FOR SEQ ID NO: 668

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1191 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Corynebacterium glutamicum*
 - (C) ACCESSION NUMBER: X77034

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTCGAC	150
35	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCACGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGGCCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
40	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTTCGAGA	TGGAAGTTCG	TGAACTTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCTCTCA	TGCCTATCGA	650
45	GGACATCTTC	ACCATCACCG	GTCGTGGCAC	CGTTGTTACC	GGTCGTGTTG	700
	AGCGCGGTAC	CCTGAACGTG	AACGATGATG	TTGACATCAT	CGGCATCAAG	750
	GAGAAGTCCA	CCTCCACCAC	CGTTACCGGT	ATCGAGATGT	TCCGTAAGCT	800
	TCTTGACTCC	GCTGAGGCTG	GCGACAACCTG	TGGTCTGCTT	CTCCGTGGTA	850
	TCAAGCGCGA	AGATGTTGAG	CGTGGCCAGG	TTATCGTTAA	GCCAGGCGCT	900
50	TACACCCCTC	ACACCGAGTT	CGAGGGCTCT	GTCTACGTTT	TGTCCAAGGA	950
	TGAAGGTGGC	CGCCACACCC	CATTCTTCGA	CAACTACCGT	CCTCAGTTCT	1000
	ACTTCCGCAC	CACCGACGTT	ACCGGTGTTG	TGAAGCTTCC	AGAGGGCACC	1050
	GAGATGGTCA	TGCCTGGCGA	CAACGTCGAC	ATGTCCGTCA	CCCTGATCCA	1100
	GCCTGTGCTG	ATGGACGAGG	GCCTGCGTTT	CGCTATCCGC	GAAGGCTCCC	1150
55	GCACCGTTGG	CGCTGGTCTG	GTCACCAAGA	TCATCAAGTA	A	1191

60

2) INFORMATION FOR SEQ ID NO: 669

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

15 ATGGCTACTG GAAAGATTGT CCAGGTAATC GGCGCCGTAG TTGACGTCGA 50
ATTCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA 100
ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT 150
ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT 200
GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAAGCGA 250
20 CTCTGGGCCG TATCATGAAC GTACTGGGTG AACC GGTCGA CATGAAAGGC 300
GAGATCGGTG AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA 350
CGAAGAGCTG TCAAACCTCTC AGGAAC TGCT GGAACCGGT ATCAAAGTTA 400
TCGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCCGT 450
GGTGCGGGTG TAGGTAAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT 500
25 CGCGATCGAG CACTCCGGTT ACTCTGTGTT TCGGGGCGTA GGTGAACGTA 550
CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC 600
GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG 650
TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG 700
AAGGTCGTGA CGTTCTGCTG TTCGTTGACA ACATCTATCG TTACACCCTG 750
30 GCCGGTACGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG 800
TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA 850
CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT 900
GCGGATGACT TGACTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA 950
CGCAACCGTG GTACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG 1000
35 CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT 1050
GGTCAGGAAC ACTACGACAC CGCGCGTGCC GTTCAGTCCA TCCTGCAACG 1100
TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT 1150
CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC 1200
CTGTCCCGAG CGTTCTTCGT GGCAGAAGTA TTCACCGGTT CTCCGGGTAA 1250
40 ATACGTCTCC CTGAAAGACA CCATCCGTGG CTTTAAAGGC ATCATGGAAG 1300
GCCAATACGA TCACCTGCCG GACGAGCGGT TCTACATGGT CGGTTCCATC 1350
GAAGAAGCTG TGGAAAAAGC CAAAAA ACTT TAA 1383

2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*
(B) STRAIN: NCTC 11638
(C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

	ATGAAAGCGA	TGGAAGGTAA	AATCATTCAG	GTTTTAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
5	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAAGG	200
	CTTAGTGCGT	AACCAAGCCG	TCAAAGCTCG	TGGCAAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGGC	CCATTCACAG	350
10	AAAAGCCCCT	AGTTTGTAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTTCG	GTGTTTGCAG	550
	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
15	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCATT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
	TATCCCTTCA	GCGGTGGGGT	ATCAGCCCAC	GCTAGCCGGG	GAAATGGGGA	850
20	AACTTCAAGA	GCGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
25	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCCTGA	AAACGCGTTT	1350
30	TACATGGTGG	GCAGCATTCA	AGAGGTTTTA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

35 2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1401 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*
(B) STRAIN: DSM 792
(C) ACCESSION NUMBER: extracted from AF101055

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

	ATGCCAGAAC	ATGTAGGTAA	AATTGTTCAG	GTAATAGGAC	CTGTTGTGGA	50
	TATTAAATTT	GATGCAGAGA	ACCTTCCTGA	CATCTATAAT	TCCATAGAAA	100
	TAGATATGGG	AGATAATAAA	AAACTCATTG	CTGAAGTTGA	ACAACATGTA	150
55	GGAGATGACA	TAGTAAGAAC	AATAGCAATG	GAAGGTACTG	ACGGATTAAA	200
	AAGAGGAATG	GAAGCAGTTA	ACACTGGTAA	ACCAATATCT	GTACCAGTTG	250
	GAGAAAATGT	TTTAGGACGT	CTTTTAAATG	TTTTAGGTCA	GACAATAGAT	300
	GAAGCAGGAG	ACATGAATGC	TGATAAGTAT	TATCCAATTC	ATAGACCAGC	350
	TCCAACCTTT	GAAGAACAAT	CAGTTCAACC	AGAAATGTTT	GAAACAGGTA	400
60	TTAAGGTTAT	AGATTTACTT	GCTCCATATC	AAAAGGTTGG	AAAAATCGGT	450

	TTGTTCCGGTG	GTGCCGGTGT	TGGTAAAACA	GTTCTTATTC	AGGAACTTAT	500
	AAATAATATA	GCAAAAAGAAC	ACGGTGGATT	ATCAGTATTC	ACAGGTGTTG	550
	GAGAAAGAAC	AAGAGAAGGT	AATGACCTTT	ATTATGAAAT	GAAAGATTCA	600
	GGAGTTATAA	ATAAAACAGC	TCTAGTATTT	GGTCAGATGA	ATGAACCACC	650
5	TGGCGCTAGA	ATGAGAGTTG	CTTTAACAGG	ACTTACAATG	GCTGAATATT	700
	TTAGAGACAA	AGGTCAAGAT	GTGCTTCTAT	TTATAGATAA	TATATTTCAGA	750
	TTTACACAAG	CTGGTTCAGA	GGTTTCAGCT	TTACTTGGTA	GAATACCTAG	800
	TGCCGTTGGT	TATCAGCCAA	CACTTGCAAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
10	TATGTTCTTG	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACCAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTG	1150
15	ATGAACCTTC	AGATGAGGAT	AGATTGTTAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAAATGA	TGGAAAGCTA	1400
20	A					1401

2) INFORMATION FOR SEQ ID NO: 672

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cytophaga lytica*
 (B) STRAIN: DSM 2039
 (C) ACCESSION NUMBER: M22535

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

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	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTTGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATGGATTCTT	CTGATGGTTT	200
45	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
50	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
55	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
60	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000

	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCA A CTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
5	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
10	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

15 2) INFORMATION FOR SEQ ID NO: 673.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*
 (B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

30	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTG GTT	TAGAAGTAGT	TTGTTTCAGGA	150
	AATCCAATTC	AGGTTCCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
35	TGTTGTTGGT	AAAACAATTG	ACAACTTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
40	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAAGTC	GTGAAGGTAA	500
	TGACTTGAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTGTTG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTC	CGTGATGTTT	AAAACCAAGA	650
	TGTTTTGTTA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
45	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
	AAGTGGTTCT	ATAACATCT				819

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2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

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AGAGCGAAGT ACCAAGTGTT TACGATGCTC TGAATGTTGT GGATTCCAAA      50
GAACGTCTGG TTCTGGAAGT TCAACAGCAG CTAGGCGGTG GCGTGATTCTG      100
CGCTATCGTT ATGGGTAGCT CGGATGGTTT ACGTCGTGGA ATGACAGTAC      150
10 AAAACACTGG CGCTCCAATT TCAGTACCAG TAGGTACTAA AACCCTAGGT      200
CGTATCATGA ACGTGCTTGG TGATGCGATT GACGAACGTG GCGACATTGG      250
CGCAGAAGAG GTGTACTCGA TTCACCGTCC TGCTCCAAGC TACGAAGAAC      300
AGTCTAGTGC AACTGAACTT TTGGAAACGG GTGTTAAGGT TATCGACCTG      350
ATCTGTCCGT TTGCGAAAGG CCGTAAAATC GGTCTGTTTC GTGGTGCGGG      400
15 TGTAGGTAAG ACCGTTAACA TGATGGAAC TATCAACAAC ATCGCGCTAC      450
AGCACTCAGG TTTGTCAGTA TTTGCTGGGG TAGGTGAGCG TACTCGTGAG      500
GGTAACGACT TCTACCACGA AATGCAGGAA GCGGGCGTTG TAAACGTTGA      550
ACAACCAGAA CTGTCGAAAG TAGCGATGGT TTACGGTCAG ATGAACGAGC      600
CACCAGGCAA CCGTCTGCGT GTAGCACTGA CTGGTCTGAC TATGGCGGAA      650
20 AAGTTCCGTG ATGAAGGCCG TGACGTACTG CTGTTTATCG ACAACATCTA      700
CCGTTACACC CTAGCGGGA CCGAAGTATC TGCTCTGCTT GGCCGTATGC      750
CTTCAGCGGT AGGTTACCAA CCAACACTGG CTGAAGAGAT GGGTGTCTG      800
CAAGAACGTA TCACGTCAAC CAAAAAAGGT TCTATCACCT      840

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2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

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CGGCGGTATC CTAGTTGTAG CGGCAACTGA CCGTCCAATG CCACAAACTC      50
GTGAGCACAT CCTGCTGGGT CGCCAAGTAG GTATTCCCTTA CATCATCGTA      100
45 TTCATGAACA AGTGTGACAT GGTGACGAT GAAGAGCTTC TAGAGCTGGT      150
AGAGATGGAA GTTCGTGAGC TGCTGTCTGA GTACGATTTT CCAGGTGATG      200
ACCTGCCAGT AATCCAAGGT TCAGCACTAG GCGCGCTAAA CGGCGAAGCA      250
CAGTGGAAG CGAAGATTGT TGAGCTAGCA GAAGCACTGG ATACTTAYAT      300
TCCAGAGCCA GAGCGTGCAG TAGACATGGC ATTCCTGATG CCAATCGAAG      350
50 ACGTATTCTC AATCCAAGGT CGTGGTACAG TAGTAACTGG CCGTATCGAG      400
CGCGGCATCC TGAAAGTGGG TGACGAAGTA GCGATCGTTG GTATCAAAGA      450
GACAGTAAAA ACGACCTGTA CAGGTGTAGA GATGTTCCGT AAGCTGCTTG      500
ACGAAGGTCG TGCAGGTGAG AACGTAGGTG CACTRCTACG TGGTACTAAG      550
CGTGAAGAAG TAGAGCGTGG TCAAGTACTG GCGAAGCCAG GTTCAATCAC      600
55 ACCACACACT AAGTTCGAAT CAGAAGTATA CGTACTGTCA AAAGATGAAG      650
GTGGCCGTC TACTCCATT TTTCAAAGGT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTAACAGG CAGCATTGAG CTACCAGARG GCGTAGAAAT      750
GGTAATGCCA GGCGACAACG TGAAGATGGT TGTAGACCTG ATTGCACCAA      800
TCGCGATGGA CGAAGGTCTA CGCTTCGC      828

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60.

2) INFORMATION FOR SEQ ID NO: 676

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania enriettii*
 15 (B) STRAIN: ATCC 50120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

	CTTCTCGGAT	GGCGTGCCGC	CGGTGCTGAC	GGCGCTGGAC	GTGACGGAGG	50
20	AACTCGGGCG	CGACGAGCCG	CTGACGCTAG	AGATCGTGCA	ACACTTGGAC	100
	GCGCACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TACTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGGAA	CATCTCTGTG	CCTGTGGGCC	200
	GCGAGACGCT	TGGCCGCATC	TTCAACGTAC	TGGGCGACGC	GATTGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CGGAGGCGCC	300
25	GAAGCTGGCG	GACCAGGCGG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AAGTGATCGA	TCTGATCCTG	CCGTACTGCA	AGGGCGGCAA	GATCGGTCTG	400
	TTCGGCGGTG	CCGGTGTGGG	GAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTGCGC	GGCGTTGGGG	500
	AGCGCACCCG	CGAGGGGACG	GATCTGTACC	TGGAGATGAT	GCAATCGAAG	550
30	GTGATCGACC	TGAAAGGTGA	GTCGAAGTGT	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CAGCGCTGCT	750
	GGGCCGCGATC	CCCGCCGCTG	TGGGCTACCA	ACCGACGCTT	GCGGAGGATC	800
35	TCGGCATGTT	GCAGGAGCGC	ATCACGTCGA	CGACGAAGGG	GTCGATCACG	850
	TCTGTGCAGG	CGGTGTACGT	GCCTGCGGAT	GATATCACGG	ATCCCGCGCC	900
	GGCGACGACA	TTCTCGCACC	TGGACGCGAC	GACGGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	TGGCATCTAC	CCCGCGGTCA	ACCCACTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCTGATGT	GATCGACGTG	GATCACTACA	ACGTTGCGCA	1050
40	GGACATTGTT	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGTGCGCGCA	AGGTGACCCG	GTTCTGTGTA	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACT	GGCATGACAG	GCCATTACGT	ACAGCTGAGC	GACACGGTGG	1250
45	AGTCGTTCTC	CGGTTTGCTG	ATGGGGTCGT	ACGACCAGAT	TCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 677

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia microtti*
 60 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

	CAAGCTCAAG	TCTGAGCGTG	AGAGAGGTAT	TACTATTGAC	ATTACTCTCT	50
5	GGAAATTTGA	GACCCAGAAA	TACGAGTACA	CTGTCATAGA	CGCACCTGGT	100
	CATCGTGACT	TTATCAAAAA	TATGATTACT	GGGACTTCAC	AAGCCGACGT	150
	TGCTATGCTT	GTCGTTCCCTG	CTGAATCTGG	CGGATTTCGAG	GCTGCTTTTT	200
	CCAAAGAAGG	TCAGACCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
10	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
	CACGGTGACA	ACATGGTTGA	AAAACTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCAGT	CAGTCTATAA	AATTGGAGGT	550
15	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTT	GACCACTGAA	TGTAAATCTG	650
	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
20	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCCCACAT	GCTTGCAAAT	TCGAATCTCT	900
	AGACACTAGG	ATTGACAAGC	GTACTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGAAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
25	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

2) INFORMATION FOR SEQ ID NO: 678

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: Lev-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

45	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGCCCTG	ACTAAAACTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
50	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTAATTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
	TTTTCCGATT	CACCCAGGCC	GGTTCCGAGG	TGTCTGCCTT	GCTCGGTCGT	400
	ATCCCCTCTG	CCGTCCGGTA	CCAGCCCACT	CTTTCCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
55	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

60 2) INFORMATION FOR SEQ ID NO: 679

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

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15  TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT      50
    ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG      100
    TACCACGAAA TGAGGGAGAC TGGTGTTATC AACCTTGAGG GTGACTCCAA      150
    GGTCGCTCTT GGTGAGTTCT TTTTTTTGGG AGCTAATTAG TCGATGACGT      200
20  GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC      250
    CCCTGGAGCC CGTGCCCGAG TTGCTCTTAC TGGTTTGACC ATTGCCGAGT      300
    ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT      350
    TTCCGATTCA CCCAGGCCGG TTCCGAGGTG TCTGCCTTGC TCGGTCGTAT      400
    CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA      450
25  TGCAAGAGCG AATGTAAGTT GCATTTTTTG TGATTTTACG GCAAGTCTTG      500
    ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG      550
    TC                                                                552
  
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30 2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

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    TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC      50
    GTCTTGTTCT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT      100
    ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTTtagAT GATCATAAAT      150
50  AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT      200
    AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT      250
    TTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC      300
    CTTTTTTATA AAATTAATCA GGTCTTGTC GTGGTCAAAA GGTGTTGAT      350
    ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT      400
55  CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA      450
    AGTCTCACCG TGCTATTCAC GCTGAAGCTC CAGAATTCGT TGATCAATCT      500
    CCTACTCCCG AAATTCTTGA AACTGGTATT AAGGTTGTCG ATTTATTAGC      550
    TCCTTATGCT CGTGGTGGTA AGATTGGTCT TTTCCGGTGGT GCTGGTGTAG      600
    GTAAACTGT CTTGATTCAA GAACTTATTA ACAACATTGC TAAAGCCCAT      650
60  GGTGGTTACT CTATTTTCTG TGGTGTGTTG GAACGTACTC GTGAAGGTAA      700
  
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	CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
	ACTCCAAGTG	TGCTCTTGTA	TTCGGTCAAA	TGAACGAACC	TCCTGGTGCT	800
	CGTGCCCGTG	TTGCTTTAAC	TGGTTTAACC	ATTGCTGAAT	ACTTCCGTGA	850
	TGAAGAAGGT	CAAGATGTGT	TACTTTTCAT	TGATAACATT	TTCCGTTTCA	900
5	CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
	GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
	TATTACTACT	ACCAAGAA				1018

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2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

15 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC

23

25

2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC

26

40

2) INFORMATION FOR SEQ ID NO: 683

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

55 GTIACIGGIT CISWIAWRTC ICCICC

26

2) INFORMATION FOR SEQ ID NO: 684

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

15	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGTTTGTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
20	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCCCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTGGT	TCTATTTATG	AAAACCTCTT	500
25	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTGGGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCCATG	TGTTCAAGGT	750
30	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACTCTGA	TGTTATTATC	TATGTTGGTT	850
	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTT	1000
35	GTCAACTTTC	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCACTGTTT	CTGCTGATCA	TAAACTTATC	TTGAAAACTA	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTACTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
40	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCAATTGAAG	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500
45	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACATA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAACATA	1600
	ATGTCGCTGA	AAACGAAGAA	GAATTTTTC	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTTTAC	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTTCATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
50	TGTGGAATGC	TTTGAAATCT	CTTGTTTTC	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCCTCAACA	TATTGCTGTT	GATGATATTG	TTGTCAGAGA	1850
	ATCTTTGATT	GCCGGTTTAG	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCATTCTTTG	GGTATTGAAT	CATCTATTAA	2000
55	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTC	TTCTAAATGT	2100
	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTTGA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
60	TTGGTGCACA	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTGTAT	2300

	GGAATTCCCA	GAATTGTTTA	CTGAAATTTT	TGGTAGAAAA	GAACCAATTA	2350
	TGAAACGTAC	CACTTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTTTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
5	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
	CGGTAAAGCC	ACTGCTTTGG	GTTCAACCAGA	TAGAGTTGGT	TCAGTTTCTA	2650
	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTT	TGGGGGTTGG	ATAAGAAATT	2750
10	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGTT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAACATA	TCCAGAATTC	2850
	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATTT	CTTGCAACAA	3000
15	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTTGGAG	ATTTATTAAC	CACATATCTCC	GAAAGATTTG	3250
20	CTGAAGCTTC	AGAATAA				3267

2) INFORMATION FOR SEQ ID NO: 685

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Enterococcus hirae*
- (B) STRAIN: ATCC 9790
- (C) ACCESSION NUMBER: D17462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

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	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GAGTCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AAACTTCAGG	AATTGGTCCC	GGAGAACCCTG	TTCGTTCCAC	200
45	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGTTT	GAAGCGACAA	TCGAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTTG	GTACGTGGAT	GAAACGAAGA	TCATTTCAGCA	CAAAATCATG	450
50	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAG	550
	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTCC	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
55	TTGGTGCAAG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCTGC	AATGAATTTT	CTGAACCTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACTGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCACGATTG	CCGAGTACTT	950
60	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000

	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCCTGGT	1050
	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTTCAGGA	CGTGTTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
5	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAAGTGG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCGGATCT	TGCAAGAAGA	1400
	AGAACAATTA	AATGAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
10	ATAACGATCG	CTTGACCCCTT	GAAGTAGCAA	AATCGATTTCG	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
15	AGCCAAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

20 2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1781 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029
 (C) ACCESSION NUMBER: Genome project

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTCAACGTA	GATAATACCT	100
	GGTTAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCAG	150
40	GTATTTGAAG	ATACACAAGG	CGCGTGTGCA	GGAGCTCTTG	TTACGTTTTTC	200
	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATTT	250
	TCGATGGACT	TCAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTTAAGACGA	GGAGATCTTC	400
45	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTTCTG	AAGGAACCTA	500
	TAATGCTCAT	ACTGTGGTCG	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCCTTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCTT	650
50	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACTTTCTGT	ACCCCAGGAC	700
	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	GTGTGCGTGC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
55	GTGGCTGCCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTCCG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCTCTG	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
60	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAAACTTTGA	AGAACCAGTC	1200

	ACTCAATCTA	CATTAGCTGT	AGTCGGAGCG	TTCTGTGGTC	TTTCAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCTTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTTCAGA	1400
5	AATCGGCAAG	CGTATGGAAG	TTGTCAGTGA	AGAAGGGGTT	TCTATGGAAG	1450
	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTTG	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TGATGCTAAA	TTTGTTTTTG	1600
	ATAGTCCTGA	TGATGCAAGA	AGCTTTTTTC	TTGAGCTGCA	GAGCAAGATT	1650
10	AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

15

2) INFORMATION FOR SEQ ID NO: 687

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Halobacterium salinarum*
 (C) ACCESSION NUMBER: S56356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTGC	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
35	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCGGG	200
	CCAGCCCGTC	GACAACACGG	GCGAACCCTG	CACCGTGGAC	CTGGGCCCGG	250
	GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCCT	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
40	AGGTCGCGGC	CGGCGATGTC	GTCGGCACCG	TGCAGGAAAC	GGTCAGCATC	450
	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGGC	AAGTCGTCGC	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
45	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
	CGGGGCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
	TTCGCCGACG	CGGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCCAGA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
50	ATGCCGGTTG	CCGGGCCGTA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCGGCG	AGGAGGGGTA	TCCCCGCTAC	CTGGCCGCCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
55	CCATCTCGGT	CATCGGTGCG	GTGTCGCCGC	CCGGCGGGGA	CTTCTCCGAG	1200
	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTCAC	GGACAACGTC	1350
	GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTGACAA	TCCTCGACGA	1400
60	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450

	CCGAGGACCA	GCAGCTCACG	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1800
	TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCGCCCGA	1550
	GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
	TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
5	GCCGCGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCCGACG	ACGAGCACGA	1700
	GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
	TCTACTGA					1758

10

2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 3118 bases
15	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human
(C) ACCESSION NUMBER: L09234

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

	GAATTCCGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
	TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
	GTCCAAATTC	GGCTTTGTTT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
30	AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
	GAACTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
	AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
	CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
	TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
35	TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
	AGTGGGACTT	CAGTCCCGTC	AGTGTCAAGG	TTGGAAGCCA	CATTACTGGT	500
	GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
	GCTGCTGCCG	CCCCGTGCCA	AGGGAACGTG	CACGTACATT	GCAGAACCTG	600
	GAAACTACAC	AGTTGATGAT	GTTGTCTTGG	AGACAGAATT	TGACGGCGAG	650
40	CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCCAGGCC	700
	TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
	TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCTT	800
	GGGGCCTTCG	GATGTGGCAA	GACTGTAATA	TCACAGTCTT	TGTCAAATAA	850
	CTCAAACCTC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
45	AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCGTT	GGAGATTGAT	950
	GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCG	CAAACACATC	1000
	AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
	TGTCAGAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
	TCAACTTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
50	TGAAATGCCT	GCCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
	CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAC	1250
	AGGGAGGGCT	CCGTGAGTAT	AGTGGGCGCC	GTGTCGCCGC	CCGTTGGAGA	1300
	CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
	GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
55	TGGCTCATCT	CGTACAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
	CAAGAATTTC	CCAGAGTTTG	TCCCACTGCG	TACAAAGGTG	AAGGAGATTT	1500
	TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
	TCATTGGCAG	AAACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
	GGATGATTTT	CTGCAACAGA	ACAGCTATTC	ACCATATGAC	CGTTTCTGCC	1650
60	CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700

	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAATATCAC	1750
	TTGGAAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTCAG	CAAGCCTTCA	GGAACCTGGA	1900
5	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCA	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAATTTACT	TCCAGTTTTT	TTCCATTTTC	CTCCTCATTT	2150
10	TAAGTGTCCG	TACAGAGGCA	ATAATCTGAT	AACTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTGTT	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
15	AACTGCCATC	CATTGTCCTA	TTTATTCACA	TAAGTAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCGA	2500
	ACCTCACATT	GTAAGTCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
20	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTTCC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
25	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCCTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTAT	TAGCATTTCA	CTGTTGTCAC	3100
	ATAAATTATG	CCCGGAAT				3118
30						

2) INFORMATION FOR SEQ ID NO: 689

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1836 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Plasmodium falciparum*
 - 45 (B) STRAIN: 3D7
 - (C) ACCESSION NUMBER: L08200
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

50	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAAC	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
55	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
60	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550

	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTTCGTGA	TCCTAGACCT	GTTTTAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTTCG	TTATTTCCAA	700
	CAGTTCAAGG	AGGTACTTGT	GCTATTCCTG	GTGCATTTGG	TTGTGGAAAA	750
5	ACTTGTGTTT	CTCAGGCCTT	ATCAAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCCTGA	ATTAACACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
10	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTCAGG	ACGTTTAGCT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAECTAC	1250
15	AGCAACCATG	TCTATTGTTC	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
20	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
25	AAAATTCAGA	TGAATATTTT	AAAAAGTATT	TTAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

30 2) INFORMATION FOR SEQ ID NO: 690

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3216 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: X2180-1A
 (C) ACCESSION NUMBER: J05409

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
50	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAA	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
55	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTCGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGATTGC	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTT	ACTCTTTACC	ATACTTGGCC	650
60	TGTTTCGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700

	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTAAATGG	CGGATGGGTC	TATTGAATGT	900
5	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCACAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAG	GGTGTCGAAT	1150
10	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTTG	AGCTTGTCAA	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
15	TGAGAATGAC	CACTTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGGTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAACGTG	TAATTTGTAC	1650
20	TCTAAAGTTG	TCAGAGGTAA	TGGTATTTCG	AATAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
25	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
30	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCTG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
35	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCACG	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGCTGCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
40	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTATGA	TTCCAATTAC	CCTGAATTTT	2800
	CTGTTTTTAA	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGTCTG	ATAGTGATAA	2900
45	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACCTATGAT	GCTTTCTGTC	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
50	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTGC	3200
	TGAATCTACC	GATTAA				3216

55 2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1860 bases

(B) TYPE: Nucleic acid

60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(B) STRAIN: 972 h-

(C) ACCESSION NUMBER: S47814

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGTA	CGAACTCGTT	150
15 CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTTAA	AGCAAATTTT	350
CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
20 TTAATCGTGA	GCATAAGTGG	GATTTACAC	CAAATAAGGA	TTTACGCATT	450
GGCGATCATG	TATCCGGTGG	TGATGTTTTC	GGTTCGTGAT	TTGAAAACCTC	500
TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
TCACATATAT	TGCTGAAGCT	GGATCATACC	ATGTTGATGA	AAAACCTTCTT	600
GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
25 GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
GGTGGCACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
TTCACAATCT	CTTTCTAAGT	ACTCTAATTC	TGATTTGATT	GTTTACGTCG	850
GTTGTGGTGA	ACGTGGAAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
30 GAACTAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
TACATTGGTA	GCCAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCCG	1150
35 CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
TGTTTCTCCT	CCGGGTGGTG	ATTTTCTGTA	TCCTGTACT	AGTGCAACCT	1300
TGGGAATTGT	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
40 TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
GTGATCAAAT	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
ATTCAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
45 AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750
TAACCTCGAT	GAAATTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
50 GACTGAGTAA					1860

2) INFORMATION FOR SEQ ID NO: 692

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1833 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trypanosoma congolense*
 (B) STRAIN: IL3000
 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

```

10 ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT      50
   GAAGGCCGTC TCCGGGCCAG TTGTCATTGC TGAAAACATG GGCGGTAGCG      100
   CTATGTATGA GCTTGTGCAG GTAGGTTCTT TCCGGTTAGT GGGCGAGATC      150
   ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG      200
   TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTTCGC      250
15 TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG      300
   CCTCTTGACA CCATCTACCG CATGGTGGAA AACGTGTTTA TCCCCAGGGG      350
   CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTAAAGCCAT      400
   GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG      450
   GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCCAATGT      500
20 GCGGGGCCGT GTTACTTCCA TTGTTCTTTC AGGAAATTAC ACCCTCCAAG      550
   ATGACATTAT TGAATTGGAA TATAATGGGA CAGTGAAATC ACTAAACTT      600
   ATGCATCGCT GGCCAGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC      650
   CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC      700
   CATCCGTCCA GGGTGGAAACA TGCGCCATCC CTGGCGCGTT TGGATGCGGA      750
25 AAGACGGTTA TCAGTCAGGC TCTTTCGAAG TTCTCCAACA GCGACGCTGT      800
   TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA      850
   TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC      900
   ATGAAGCGTA CCTGCCTGGT GGCAAACACC TCAAATATGC CTGTCGCTGC      950
   TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCGTG      1000
30 ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT      1050
   GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG      1100
   TGGTTACCCT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG      1150
   CGGGGCGCGT GACATGCATC GGTGGGCCAA AACGCGAGGG CTCAGTAACC      1200
   ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC      1250
35 GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC      1300
   TTGCGCAACG TAAACACTTT CCTTCTGTTA ATTGGCTCAT TTCCTATTCA      1350
   AAATACCTTA ATGCTTTGGA GCCCTTCTTC AACACGCTTG ACCCTGACTA      1400
   CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CCTTCAGCGT GAGGAAGAGT      1450
   TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC      1500
40 AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA      1550
   GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT      1600
   GGATGCCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA      1650
   GCTGAGTCCG CTGGGGAAC TAAGATTACG TGGAAC TACA TTCGTGAAAT      1700
   GATTCCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC      1750
45 AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA      1800
   ATTGTCAGCG CATTGCTCTC GCTGCTGCAA TAA      1833

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50 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*
 (B) STRAIN: HB8
 (C) ACCESSION NUMBER: D63799

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

	ATGATCCAAG	GGGTGATCCA	GAAGATCGCG	GGCCCGGCGG	TGATCGCCAA	50
	GGGCATGCTC	GGGGCCCCGA	TGTACGACAT	CTGCAAGGTG	GGCGAAGAGG	100
	GCCTCGTGGG	CGAGATCATC	CGCCTGGACG	GGGACACGGC	CTTCGTCCAG	150
10	GTCTACGAGG	ACACCTCGGG	CCTAAAGGTG	GGGGAGCCCG	TGGTCTCCAC	200
	GGGCCTTCCC	TTGGCGGTGG	AGCTCGGCC	CGGGATGCTG	AACGGCATCT	250
	ACGACGGCAT	CCAGCGCCCC	CTGGAGCGCA	TCCGGGAGAA	GACGGGGATC	300
	TACATCACCC	GGGGCGTGGT	GGTCCACGCC	CTGGACCGGG	AGAAGAAGTG	350
	GGCCTGGACG	CCCATGGTCA	AGCCCGGGGA	CGAGGTGCGG	GGGGGTATGG	400
15	TCCTGGGCAC	GGTGCCCGAG	TTCGGCTTCA	CCCACAAGAT	CCTGGTACCC	450
	CCGGACGTGC	GGGGCCGGGT	CAAGGAGGTG	AAGCCCGCCG	GGGAGTACAC	500
	CGTGAGGAGG	CCGGTGGTGG	TCCTCGAGGA	CGGCACCGAG	CTCAAGATGT	550
	ACCACACCTG	CCCCGTTCGC	CGGGCGAGGC	CCGTGCAAAG	GAAGCTTGAC	600
	CCCAACACCC	CCTTCCTCAC	GGGGATGCGC	ATCCTGGACG	TCCTCTTCCC	650
20	CGTGGCCATG	GGGGGCACCG	CCGCCATCCC	TGGGCCCTTC	GGCAGCGGCA	700
	AGACCGTGAC	CCAGCAGTCC	CTGGCCAAGT	GGTCCAACGC	CGACGTGGTG	750
	GTCTACGTGG	GCTGCGGGGA	GCGGGGGAAC	GAGATGACCG	ACGTGCTCGT	800
	GGAGTTCCCC	GAGCTCACCG	ACCCCAAGAC	GGGTGGGCCC	TTGATGCACC	850
	GCACCGTCCT	CATCGCCAAC	ACCTCCAACA	TGCCCCGTGGC	CGCCCGCGAG	900
25	GCCAGCATCT	ACGTGGGCGT	GACCATCGCC	GAGTACTTCC	GCGACCAGGG	950
	CTTCTCCGTG	GCCCTCATGG	CCGACTCCAC	GAGCCGCTGG	GCCGAGGCTT	1000
	TGCGCGAGAT	CTCTAGCCGC	CTCGAGGAGA	TGCCCCGCCA	GGAGGGCTAC	1050
	CCGCCCTACC	TCGCCGCCAG	GCTCGCCGCC	TTCTACGAGC	GGGCGGGCAA	1100
	GGTCATCACC	CTGGGCGGCG	AGGAGGGGGC	GGTGACCATC	GTGGGGGCCC	1150
30	TCTCCCCGCC	GGGCGGCGAC	ATGTCCGAGC	CCGTGACCCA	GTCCACCTTG	1200
	AGGATCGTGG	GGGCCTTCTG	GCGGCTTGAC	GCCTCCCTGG	CCTTCCGCCG	1250
	CCACTTCCCC	GCCATCAACT	GGAACGGCTC	CTACAGCCTC	TTCACCTCCG	1300
	CCCTTGACCC	CTGGTACCGG	GAGAACGTGG	CCGAGGACTA	CCCCGAGCTC	1350
	CGCGACGCCA	TCTCCGAGCT	TTTGACGCGG	GAGGCGGGCC	TCCAGGAGAT	1400
35	CGTCCAGCTC	GTGGGGCCCG	ACGCCCTCCA	GGACGCCGAG	CGCCTCGTCA	1450
	TTGAGGTGGG	CCGGATCATC	CGCGAGGACT	TCCTGCAGCA	GAACGCCTAC	1500
	CACGAGGTGG	ACGCCTACTG	CTCCATGAAG	AAGGCCTACG	GGATCATGAA	1550
	GATGATCCTC	GCCTTCTACA	AGGAGGCGGA	GGCGGCCATC	AAGCGGGGGG	1600
	TTTCCATAGA	CGAGATCCTG	GAGCTCCCCG	TTCTGGAGCG	CATCGGCCCG	1650
40	GCCCCGTACG	TGAGCGAGGA	GGAGTTCCCC	GCCTACTTTG	AGGAGGCCAT	1700
	GAAGGAGATC	CAGGGGGCCT	TCAAGGCTGG	CCTAAAGGGG	GAGAGATGGA	1750
	CCTTCTGA					1758

45

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTT GTTG C

21

60

2) INFORMATION FOR SEQ ID NO: 695

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

15 GTTTCACGTG ATGACGTACA 20

2) INFORMATION FOR SEQ ID NO: 696

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

30 ATIGGICAYR TIGAYCAYGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 697

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

45 CCIACIGTIC KICCRCCYTC RCG 23

50 2) INFORMATION FOR SEQ ID NO: 698

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

5 GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTTA ACGTTGGTAC 50
TATCGGCCAC GTTGACCACG GTAAACTACT TCTGACCGCT GCAATCACCA 100
CCGTACTGGC TAAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC 150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACTTCTCA 200
10 CGTTGAATAC GACACCCCGA CCCGTCACCTA CGCACACGTA GACTGCCCGG 250
GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC 300
GGCGCGATCC TGGTAGTTGC TGCAGCTGAC GGCCCGATGC CGCAGACTCG 350
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 400
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 450
15 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 500
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 550
AGTGGGAAGC GAAAATCCTG GAACGGCTG GCTTCCTGGA TTCTTATATT 600
CCGGAACGAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 650
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC 700
20 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG 750
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 800
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 850
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 900
CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG 950
25 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 1000
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 1050
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 1100
CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG 1150
TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA 1185
30

2) INFORMATION FOR SEQ ID NO: 699

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

45 GTIACIGGYT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 700

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

60

5 2) INFORMATION FOR SEQ ID NO: 701

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G

21

20 2) INFORMATION FOR SEQ ID NO: 702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

35 2) INFORMATION FOR SEQ ID NO: 703

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

50

2) INFORMATION FOR SEQ ID NO: 704

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

5 AGTGCTCCAA TTAATGTTGG 20

2) INFORMATION FOR SEQ ID NO: 705

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

20

GTACAGTTCC AATACCTGAA 20

2) INFORMATION FOR SEQ ID NO: 706

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

35

TGAAATCTTC ACATCCAACA 20

2) INFORMATION FOR SEQ ID NO: 707

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GGTA 25

2) INFORMATION FOR SEQ ID NO: 708

55

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

401

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

10 TCRTCCATIC CIARIATIGC IATIAT

26

2) INFORMATION FOR SEQ ID NO: 709

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Borrelia burgdorferi*
 (C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

	ATGAATGAAG	TTTTATTTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
30	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAGATA	AAAAGTGGAA	TTTTAAAAAA	300
35	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTTGT	350
	AATTGAGGGA	ACTGTTCAAC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
40	GCCTTATTC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAT	TATAGATACA	600
	TTTTTCCCAG	TTGCCAAAGG	TGGAACTTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTTCTTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAAATCTTT	800
45	AATGGACAGG	ACTTGATTA	TTTGTAATAC	ATCTTCAATG	CCAGTTGCAG	850
	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900
	CAAATGGGCC	TTGATATTCT	TCTTTTGGCA	GATTCAACTT	CAAGATGGGC	950
	TCAAGCAATG	AGAGAAATGT	CTGGACGCCT	TGAGGAAATT	CCTGGCGAGG	1000
	AGGCTTTTCC	GGCATATCTT	GAGTCTGTTA	TTGCTTCCTT	TTATGAAAGG	1050
50	GCAGGTATTG	TAGTTCTTAA	TAATGGGGAT	ATTGGATCTG	TAACAGTTGG	1100
	TGGCTCTGTA	AGTCCTGCTG	GTGGTAATTT	TGAAGAGCCA	GTTACTCAAG	1150
	CAACTTTAAA	AGTTGTAGGA	GCATTTACAG	GGCTTACAAG	AGAAAGGTCT	1200
	GATGCTAGGA	AATTTCCAGC	TATTAGTCCT	CTTGAATCTT	GGAGTAAATA	1250
	TAAAGGCGTT	ATTGATCAAA	AAAAGACTGA	ATATGCAAGA	TCTTTTTTGG	1300
55	TGAAAGGTAA	TGAAATTAAT	CAAATGATGA	AAGTTGTTGG	AGAAGAAGGC	1350
	ATAAGTAACG	ATGATTTTTT	AATTTATTTA	AAATCCGAGC	TACTTGATTC	1400
	GTGCTATTTG	CAGCAAAATT	CATTTGATTC	TATTGATGCT	GCTGTTAGTT	1450
	CAGAGCGTCA	AAATTATATG	TTTGATATAG	TTTATAACAT	TCTTAAAACT	1500
	AACTTTGAGT	TTTCTGATAA	ACTTCAAGCA	AGAGATTTTA	TAAATGAGTT	1550
60	AAGGCAAAAT	CTTTTAGACA	TGAATCTTTC	TTCTTTTAAG	GATCATAAGT	1600

TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA 1650
ATTTAG 1656

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2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*
(B) STRAIN: Nichols
(C) ACCESSION NUMBER: extracted from AE000520

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

GTGATCAAAG ACGATGTGGT TACAGGCCGT GTAGTGAGGG TGTCTGGTCC 50
CATTGTGTAT GCCGAGGGCC TCTCTGCGTG CAGCGTATAC GATGTTGTCTG 100
25 ACGTAGGGGA AGCATCGCTC ATCGGAGAAA TTATCCGGTT GGATGAGAGC 150
AAGGCGGTCTG TGCAAGTATA CGAGGATGAC ACAGGTATGC GAGTCGGGGA 200
GAAGGTGACA AGCTTGCGTC GACCACTCTC AGTCCGCTTA GGGCCTGGAT 250
TAATCGGCAC CATTTATGAC GGTATTCAGC GCCCACTTGA GCGCCTCTTC 300
CAAGAAGACG GCGCCTTCTT GCGTCCTGGT GCGCGTTCAC AACCCTTGA 350
30 TGGCTCCGTA CGCTGGGATT TTCGTCCTCA TTGTAACGAG CGCGGTGAGG 400
CCCTGTGCGC GGGGATTCCG ATTGCACCTG GGTCAGTGTT AGGGACCGTG 450
CAGGAGACTC CTTCTGTTGT GCACACTATC ATGGTTCCTC CTGACATCCG 500
GGGGAGCGTG CTATCTTCGT TCAAGGGCGC AGGTGCTTAC ACAATAGATG 550
AAGAAATTGG ACGCACTGAT CTTGGTGAGC CGCTTTTCTT ATCCAGTAC 600
35 TGGCCAGTGC GTCGTGCGCG TCCTTTCAGC AAAAACTTG CAGTGTGTGA 650
GCCACTAGTT ACTGGACAGC GGGCGATTGA TGTTTCTTC CCCCTATCAA 700
AGGGAGGAAC GGCGGCTATT CCAGGGGGAT TTGGAAGTGG GAAGACAATG 750
ACGCAGCATG CCGTTGCCAA GTGGTGTGAT GCAGATATTA TCGTGATCAT 800
CGGTGCGGA GAGCGGGGCA ACGAGATGAC AGACGTGCTC TCTGAATTTT 850
40 CCAAACTCAT GATCCCGCGC ACAGGACGCT CTCTTATGGA GCGGACGATT 900
TTGATCGCAA ATACGTCCAA TATGCCGTGTG TCCGCACGCG AGGTGTCGCT 950
GTATTCAGGG ATTACCCTTG CGGAATACTA CCGTGATATG GGTATGCATG 1000
TGGCCATCAT GGCTGATTCT ACCAGCCGCT GGGCGGAGGC GCTGCGTGAA 1050
TTGTCTGGGC GCATGGAAGA AATGCCTGCG GAGGAGGGAT TCCCTGCGTA 1100
45 CCTTCCGACG CGTCTTGCA G AATTTTATGA GCGCGCAGGA CGCGTGGA 1150
CCTGTGTGGC GCGCGAGGGC TCTGTGAGCA TCATTGGTGC TGTTTCTCCC 1200
CTGGGTGGAG ATTTCTCTGA GCCGGTGACG CAGCACACAA AGCGCTTCAT 1250
CCGTTGCTTT TGGGCCTTGG ATCGTGAAC TGCACACGCG CGTCATTACC 1300
CTGCCATTGG GTGGATAGAT TCATACTCTG AATATGCGCA GGAAGTAAGT 1350
50 GCATGGTGGA GTAAGTATGA CCCGCGCGCA GCGCGGTTGC GCGCCGCAGC 1400
CTTGGATTGT CTGAGAAAGG AACAGCGGTT ACAGCAAATT GTCAGGCTTG 1450
TCGGTCCTGA TGCCTGCCTT GGAGAAGATC GTCTGGTGCT AATGGTGTGT 1500
GAAATGATCA AAGGTGGCTT TCTGCAGCAG AACGCTTTTG ATCCGACGGA 1550
TGTGTTCTCC TGTCCCGAAA AGCAGGTGCA GATCTTGCGT ACCATAGTGG 1600
55 ATTTTCACGA ACGTGCCGTG GTGCTGCTGC GTGCAGGTAT TTCGCTTTCT 1650
GCGCTGTCCC AGCTTTCGTG CCGGGAGCTC ATCGTACGTA TGAAACTAC 1700
GTACGGGAAT GAGGATGTAC ACAAGATGCA GAAAGTGTAC GACACGATGT 1750
GCACTGAGTT TGACCAACTG AGTGTGTGTG CTGCCGCGCG CACACAAGGG 1800
GGGGAGAAAAG TCGAATGA 1818

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2) INFORMATION FOR SEQ ID NO: 711

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1779 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia trachomatis*
 15 (B) STRAIN: MoPn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

	CAGGGCTATG	TCGTAGAAGC	TTACGGAAAT	TTATTGCGGG	TGCATTTTGA	50
20	TGGGCATGTG	CGTCAAGGAG	AAGTGGCCTA	TGTCAGCGTG	GATGATACTT	100
	GGTTGAAAGC	GGAAATTATA	GAAGTTGTGG	GAGATGAGGT	TAAAGTCCAA	150
	GTTTTTGAGG	AAACTCAAGG	AATTTCTCGA	GGCGCTTTGG	TAACTTTTTC	200
	CGGGCATTTA	TTAGAAGCGG	AACTTGGGCC	CGGTCTATTG	CAAGGTATTT	250
	TTGACGGACT	TCAGAATCGC	TTAGAGGTAT	TGGCAGATAC	AAGCTTGTTT	300
25	TTGAAAAGAG	GGGAGTATGT	TAATGCCATT	TGTCGGGAAA	CTGTATGGGC	350
	TTATACGCAA	AAGGCTTCTG	TCGGGGATGT	TCTATCTCGG	GGAGATGTGC	400
	TTGGTACAGT	AAAGGAAGGG	CGGTTTGATC	ATAAAATCAT	GGTTCCTTTC	450
	TCTTGTTTTG	AGGAAGTGAC	TATCACTTGG	GTCATTTCTT	CAGGAGATTA	500
	CACTGTTGAT	ACCGTTATTG	CTAAAGGACG	TACTGCTTCA	GGAGCCGAGC	550
30	TTGAATTTAC	AATGGTTCAG	AAATGGCCCA	TTAAACAGGC	TTTTTTTAGAA	600
	GGGGAAAAGG	TACCGTCTCA	TGAAATTATG	GATGTTGGGT	TACGAGTATT	650
	AGATACTCAG	ATCCCCGTCT	TAAAGGGAGG	AACTTTTTGT	ACTCCAGGGC	700
	CTTTTGGTGC	AGGAAAGACC	GTTTACAGC	ACCATTTATC	TAAGTATGCA	750
	GCTGTAGATA	TCGTAGTTTT	GTGTGCTTGT	GGAGAGCGAG	CTGGAGAGGT	800
35	TGTAGAAATT	CTTCAGGAGT	TCCCGCATTT	GACAGATCCT	CATACGGGGC	850
	AGTCTTTGAT	GCATAGGACC	TGTATTATTT	GTAATACATC	TTCCATGCCT	900
	GTAGCAGCTA	GAGAGTCCTC	CATTTATTTG	GGTATTACTA	TAGCAGAATA	950
	TTACCGTCAA	ATGGGGTTGC	ATGTTTTGTT	ATTGGCTGAC	TCGACATCTA	1000
	GATGGGCTCA	AGCTTTAAGG	GAAATTTTCA	GGCGATTAGA	AGAAATCCCT	1050
40	GGAGAAGAAG	CTTTCCACAG	CTATTTGGCG	TCTCGAATAG	CAGCTTTTTA	1100
	TGAGCGAGGC	GGGGCTGTGA	AAATGAAAGA	TGGATCGGAA	GGCTCCTTGA	1150
	CTATCTGTGG	AGCGGTTTCT	CCCGCAGGAG	GAAATTTTGA	AGAGCCTGTT	1200
	ACACAAGCAA	CTTTATCTGT	TGTTGGGGCT	TTCTGTGGGC	TTTCTAAGGC	1250
	TAGACAGAT	GCTAGACGGT	ATCCTTCTAT	TGATCCGATG	ATTTTCATGGT	1300
45	CTAAGTACTT	GGATTCTGTG	GCGGAGATTT	TAGAGAAAAA	AGTTCCAGGA	1350
	TGGGGAGATT	CCGTTAAAAA	AGCTTCTCGT	TTCTTAGAAG	AAGGAGCAGA	1400
	AATTGGTAAG	CGAATAGAAG	TTGTTGGGGA	AGAAGGGATT	TCTATGGAAG	1450
	ATATAGAAAT	CTTTTTGAAA	TCAGAGTTGT	ATGATTTCTG	TTACTTACAG	1500
	CAAAACGCTT	TCGATGCAGA	GGACTGTTAT	TGTCCTTTTG	ATCGTCAAAT	1550
50	AGAGCTTTTT	TCTTTAATGA	GTCATATTTT	TAGCTCTAGA	TTCTGTTTTG	1600
	ATTGTCCAGA	TAATGCTCGG	AGTTTCTTTT	TAGAGCTTCA	AAGTAAAATT	1650
	AAAACGCTGA	ATGGTCAAAA	ATTCCTTTCT	GAAGACTATC	AGAAGGGGCT	1700
	AGAAGTGATC	TATAAACTAT	TAGAAAGCAA	AATGGTGCAG	ACGGCGTAGG	1750
55	TATGCAAACA	ATATATACAA	GAATTACGG			1779

2) INFORMATION FOR SEQ ID NO: 712

- 60 (i) SEQUENCE CHARACTERISTICS:

404

(A) LENGTH: 965 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

	GTGCAAATTG	GAAAAATTGT	CAAAGTTTCA	GGTCCTTTGA	TTTtagCTGA	50
15	AAACATGTCA	GATGCTAGTA	TCCAAGACAT	TTGTCATGTA	GGAGATTTAG	100
	GCGTTATCGG	AGAGATTATT	GAAATGCGAG	GCGACGTCGC	TTCGATTCAA	150
	GTATATGAAG	AAACAACAGG	CATTGGACCA	GGAGAACCAG	TTATTTCAAC	200
	AGGAGAACCA	TTATCTGTTG	AATTAGCCCC	AGGTTTAATT	GCCGAAATGT	250
	TTGATGGTAT	TCAACGACCA	TTGGATACAT	TTCAAGAAGT	AACCCACAGT	300
20	AACTTTTTAG	GCCGTGGCGT	TAAAATTGAT	GCGTTAGATC	GTGAGAAAAA	350
	ATGGACGTTT	GAACCAACTG	TGGCAGTTGG	TGAAGAAGTG	TCGGCAGGTG	400
	ACATCGTCGG	TGTGGTTCAA	GAAACACCGA	TTATTCAACA	TAAAATTATG	450
	GTGCCTTTTCG	GCGTTTCAGG	AACGATTGCC	GAAATTAAAG	CAGGTGACTT	500
	TGCCATTGAT	GAAACAGTTT	ACTCAGTGGA	AACGGCTAAA	GGAACGGAAA	550
25	GTTTTAGCAT	GATGCAAAAA	TGGCCCGTTC	GGCGGGGACG	TCCCATTTTA	600
	GAAAAACTAA	GTCCCAAAGT	ACCGATGGTG	ACCGGACAAC	GCGTAATTGA	650
	TACCTTTTTTC	CCAATTACGA	AAGGCGGAGC	GGCAGCAGTT	CCAGGACCAT	700
	TTGGCGCTGG	AAAAACAGTC	GTTCAGCACC	AAATTGCTAA	GTGGGCCGAT	750
	GTCGACTTAG	TCGTTTACGT	TGTTTGTGGG	GAACGCGGGA	ATGAAATGAC	800
30	AGATGTTTTA	AATGAATTTC	CAGAATTAAT	TGACCCAACA	ACTGGTGAGT	850
	CTTTGATGAA	TCGGACGATT	TTAATTGCGA	ATACGTCAA	TATGCCGGTA	900
	GCGGCACGGG	AAGCCTCGAT	TTATACAGGG	ATTACCATTG	CAGAATATTT	950
	CCGTGATATG	GGTTA				965

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2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Methanosarcina barkeri*
 (C) ACCESSION NUMBER: extracted from J04836

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
55	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AACTTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTAGC	300
	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
60	GGATTTCAAA	CCCATTGTCA	AGAAGGGCGA	TTCCGTAAAA	GGTGAGACG	400

	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTCTGA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
5	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGAAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCCT	GAATCGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
10	GTA CTGTTCT	TATCGCTAAC	ACTTCAAACA	TGCCTGTGGC	CGCAAGAGAA	900
	GCATCTGTGT	ATACCGGAAT	CACCATTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TCCCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCGT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
15	TGCGGAGAGT	CTTTGCGGCG	AAACAGGTTC	CATTACTGTT	ATTGGAGCAG	1150
	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTCTCT	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTGCA	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
20	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTC	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
25	TTCCCGTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

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2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina jannaschii*
 (C) ACCESSION NUMBER: extracted from U67477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTCAAGTTG	150
50	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
	ACCAGGAGAG	CCAGTTGTTG	GTACTGGAGC	TCCATTGTCT	GTTGAATTAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
55	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAAGTGT	TGATGAAACT	450
	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTTA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAAGAG	AACTACCTC	CAGAAATTCC	650
60	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700

	GAGGAACAGC	AGCAATTCCA	GGTCCATTCTG	GTTTCAGGAAA	AACGGTTACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCAC	850
	ACTTAGAAGA	TATTAGAACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
5	ATAGCCAACA	CATCAAACAT	GCCTGTGCGT	GCAAGGGAAG	CATCTGTCTA	950
	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAG	AGCTGGAAGA	GTTATAACCT	1150
10	TAGGGAAAGA	TAACAGACAA	GGATTTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
15	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCTC	CAATGAAACA	GTACTTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
20	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

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2) INFORMATION FOR SEQ ID NO: 715

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: W83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

	TGAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
45	GTCTGCAACA	CGACTTGGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCGT	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
50	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
	TGGTGCAGAA	ATGGCCGGTG	AAACGTGCTA	TCACCTGCTA	TCGCGAGAAG	500
	CCGCGTCTTT	TCAAACCTGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAGAGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
55	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
60	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950

GCTTTCCCGA TGGACTTGTC AGCTATCGTA GCCAACTTCT ACGCTCGTGC 1000
 AGGATACGTT TACCTGAACA ACGGTTTCGGC CGGTTTCGGTA ACGTTCATCG 1050
 GTACGGTATC TCCC GCCGGT GGTAACCTCA AAGAGCCTGT GACGGAAC 1100
 ACCAAGAAAG TGGCTCGCTG CTTCTATGCT TTGGAGCAGA ATCGTGCCGA 1150
 5 CCGCAAACGT TATCCGGCTG TAAACCCCAT CGATAGTTAC TCGAAGTACA 1200
 TCGAATATCC CGAATTCGAG AGCTATATAT CGAACCACAT CAGTTTACTC 1250
 ATTATATTCA ACAGAAGTTG GCAGATATAT GGATCAAATC TTACAGCAGA 1300
 CTGGACTACT AAGGTGAATG AGCTGAAGAT GCGCTTGCAT CAGGGTAAAG 1350
 AAAT 1354
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2) INFORMATION FOR SEQ ID NO: 716

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1788 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 25 (B) STRAIN: Type 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

TTTGACTCAA GGGAAGATTA TAAAAGTATC GGGACCTCTA GTTATTGCAT 50
 30 CAGGTATGCA GGAGGCTAAT ATTCAAGATA TTTGCCGTGT AGGTAAGCTA 100
 GGGTTAATCG GTGAAATTAT TGAAATGAGA AGAGATCAGG CATCTATCCA 150
 AGTCTATGAA GAAACATCTG GTCTTGGTCC GGGAGAACCT GTTGTTACAA 200
 CTGGAGAACC TCTCTCGGTT GAATTAGGGC CAGGATTGAT TTCTCAAATG 250
 TTTGATGGCA TACAACGCCC ATTAGATCGA TTAAATTGG CTACTCATAA 300
 35 TGATTTTCTA GTTCGTGGGG TAGAAGTTC AAGTTTGGAT AGAGATATTA 350
 AGTGGCATT TGAATCCACT ATAGCAATTG GTCAAAAAGT GAGTACGGGT 400
 GATATTCTTG GAACTGTCAA GGAAACCGAG GTAGTTAATC ATAAATTAT 450
 GGTTCCTTAT GGAGTATCTG GAGAAGTCGT TTCTATTGCA TCTGGCGATT 500
 TTACAATTGA TGAAGTTGTA TATGAAATAA AAAAATTGGA CGGTAGTTTC 550
 40 TATAAAGGAA CGCTTATGCA AAAATGGCCT GTCCGCAAGG CGCGTCTGT 600
 TTCTAAACGT TTAATTCCAG AAGAACCATT AATCACAGGT CAACGAGTTA 650
 TTGATGCATT CTTTCCAGTA ACCAAAGGGG GAGCTGCAGC AGTTCCTGGA 700
 CCGTTTGGAG CAGGAAAGAC AGTTGTACAA CACCAAGTAG CTAAATTTGC 750
 CAATGTTGAT ATTGTTATTT ATGTCGGTTG TGGAGAACGT GGAAATGAAA 800
 45 TGACGGATGT ACTGAATGAG TTTCTGAGT TGATTGACCC TAATACCGGA 850
 CAATCAATTA TGCAACGGAC AGTTCTGATT GCTAATACTT CAAATATGCC 900
 TGTGCTGCT CGTGAGGCTT CAATTTATAC AGGAATTACC ATGGCTGAGT 950
 ATTTTCGTGA TATGGGCTAC TCTGTCGCCA TTATGGCTGA TTCAACTTCA 1000
 CGTTGGGCAG AAGCGCTACG TGAAATGTCA GGACGTCTAG AAGAAATGCC 1050
 50 TGGTGATGAG GGTATCCTG CTTATCTGGG AAGTCGTATC GCTGAATATT 1100
 ATGAAAGAGC AGGACGTTCT CAGGTTCTAG GGCTTCCAGA ACGTGAAGGA 1150
 ACGATTACTG CTATTGGAGC TGTATCGCCA CCTGGTGGAG ATATTTTCTAGA 1200
 ACCAGTTACT CAAAACACTT TACGGATTGT GAAAGTTTTT TGGGGGCTTG 1250
 ATGCTCCGTT GGCACAGCGA CGTCATTTTC CTGCAATTAA CTGGCTTACA 1300
 55 TCTTATTAC TATATAAAGA CAGTGTGGGC ACTTATATAG ATGGTAAAGA 1350
 GAAGACAGAT TGGAATAGTA AAATAACTCG TGCGATGAAC TACTTACAAC 1400
 GGAATCTAG TTTAGAGGAA ATTGTTCTGTC TTGTTGGAAT TGATTCTCTG 1450
 TCTGATAATG AACGACTAAC GATGGAAATT GCTAAACAAA TTCGAGAAGA 1500
 TTATTTGCAA CAGAACGCTT TTGATTCGGT AGATACATTC ACTTCGTTTG 1550
 60 CAAAACAAGA AGCAATGCTA AGTAATATTC TCACTTTTGC TGATCAGGCA 1600

AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAGGTAC	1650
CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTTAT		1788

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2) INFORMATION FOR SEQ ID NO: 717

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear.

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT	GTGCTCGGCC	GCTGACGGCC	CGATGCCGCA	AACGCGTGAG	50
25 CACATCCTGC	TGGCGCGTCA	GGTCGGTGTG	CCGTACATCA	TCGTGTTCTT	100
GAACAAGTGC	GACATGGTGG	ACGACGCGGA	GCTGCTCGAG	CTGGTCGAAA	150
TGGAAGTGCG	CGAACTGCTG	TCGAAGTACG	ACTTCCCGGG	CGACGACACG	200
CCGATCATCA	AGGGTTCGGC	GAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
GCTGGGCGAA	GTGGCGATCA	TGAACCTGGC	CGACGCGCTG	GACACGTACA	300
30 TCCCCGACGCC	GGAGCGTGCG	GTCGACGGCG	CGTTCCTGAT	GCCGGTGGA	350
GACGTGTTCT	CGATCTCGGG	CCGTGGTACG	GTGGTGACGG	GTCGTGTCCA	400
GCGCGGCGTG	ATCAAGGTTG	GCGAGGAAAT	CGAAATCGTC	GGTATCAAGG	450
CGACGGCGAA	GACGACCTGC	ACGGGCGTGG	AAATGTTCCG	CAAGCTGCTG	500
GACCAGGGTC	AGGCGGGCGA	CAACGTCGGT	ATCCTGCTGC	GCGGCACAAA	550
35 GCGTGAAGAC	GTGGAGCGCG	GCCAGGTTCT	GGCGAAGCCG	GGTTCGATCA	600
CGCCGCACAC	GCACTTCACG	GCAGAAGTGT	ACGTGCTGAG	CAAGGACGAA	650
GGCGGCCGCC	ACACGCCGTT	CTTCAACAAC	TACCGTCCGC	AGTTCTACTT	700
CCGTACGACG	GACGTGACGG	GCTCGATCGA	GCTGCCGAAG	GACAAGGAAA	750
TGGTGATGCC	GGGCGACAAC	GTGTCGATCA	CGGTGAAGCT	GATCGCGCCG	800
40 ATCGCGATGG	AAGAAGGTCT	GCG			823

2) INFORMATION FOR SEQ ID NO: 718

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

60 GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
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	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	ATGGTGTTCC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTTCG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
5	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
	ATCCCGACGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGA	350
	AGACGTGTTC	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
10	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
15	ATGGTGATGC	CGGGCGACAA	CGTGTCTGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

20 2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
40	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAAAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
45	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAAGTGGAA	TCGAAATGTT	CAGAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAACT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCTCA	600
	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
50	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

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2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium innocuum*

(B) STRAIN: ATCC 14501

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

	GGTGCTATCC	TGGTTGTTGC	TGCATCTGAT	GGTCCTATGC	CTCAGACTCG	50
	TGAGCACATC	CTGCTTGCTC	GTCAGGTAGG	TGTTCCCTTAC	ATCGTTGTAT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAACTGAT	CGACCTTGTT	150
15	GAAATGGAAG	TACGTGAGCT	GTAAAGCGAG	TACGGATTTCG	ACGGAGATAA	200
	CGCTCCGGTT	ATCCGTGGTT	CTGCACTGAA	GGCTCTGGAA	GGTGACGACA	250
	AATACGTTGG	CGCTATCAAA	GAACGTATGG	ATGCAGTTGA	TGAATTCATC	300
	CCAGATCCAA	CTCGTGAAAC	TGACAAACCA	TTCCTGATGT	CTGTAGAAGA	350
	CGTTATGACA	ATCACAGGAC	GTGGTACAGT	TGCTACAGGA	CGTGTTGAGC	400
20	GTGGGGTAGT	AAAACCTGCGA	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAT	450
	ACTCAGAAAA	CTGTTGTTC	CGGACTGGAA	ATGTTCCGTA	AGCAGCTGGA	500
	CTTCGCAGAA	TCCGGAGACA	ACATCGGTGC	TCTGCTGCGT	GGTATCAACC	550
	GTGACCAGAT	TCAGCGTGGA	CAGGTTCTTG	CTAAACCAGG	ATCCGTACAT	600
	CCACACACAA	AGTTCAAGGC	TCAGGTTTAT	GTATTAACAA	AAGAAGAAGG	650
25	TGGACGTCAC	ACTCCATTCG	TTTCTAACTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	GTTATTACAT	TACCGGAAGG	AACTGAAATG	750
	GTTATGCCTG	GTGACAACGT	TGAAATGAAC	GTTGAGCTGA	TTGCTCCAA	799

30

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 789 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*

(B) STRAIN: ATCC 19402

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

	TTGTATCAGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATCCTA	50
	TTAGCATCAA	GAGTAGGAGT	TAACCACATA	GTAGTATTCT	TAAACAAAGC	100
	AGACCAAGTA	GATGATCCAG	AATTACTAGA	ATTAGTAGAA	ATGGAAGTAA	150
50	GAGAATTATT	AAGCGAATAC	GGATTTGACG	GAGACGAATG	TCCAGTAGTA	200
	GTAGGATCAG	CATTAAAAGC	AATCGAAGAA	GGGGATGACC	AATGCATCCT	250
	AGACTTAATG	AAAGCTGTAG	ATGAATATAT	CCCAACTCCA	GAAAGAGCAA	300
	CAGATCAACC	ATTCTTAATG	CCTGTAGAAG	ATGTATTTAC	AATTACAGGA	350
	AGAGGAACAG	TTGCAACAGG	AAGAGTTGAA	AGAGGAGTAC	TACACGTAGG	400
55	AGATGAAGTA	CAAATCGTAG	GAATGAAAGA	AGAAATCGGA	AAGACAACAA	450
	TCACAGGAGT	AGAAATGTTC	AGAAAGATGT	TAGATGAAGC	AATGGCTGGA	500
	GATAACATCG	GAGCATTATT	AAGAGGAGTA	CAAAGAGACG	AAATCGAAAG	550
	AGGTCAAGTA	CTAGCAAAAC	CAGGTTTCAGT	AACACCTCAC	AAAAAATTCG	600
	TAGGTCAAGT	TTACGTATTA	AAGAAAGAAG	AAGGTGGAAG	ACACACTCCA	650
60	TTCTTTAACG	GATACAGACC	ACAATTCTAC	TTCAGAACAA	CAGACGTAAC	700

AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC 750
 ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA 789

5

2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

GTTCAGCAGC AGACGGTCCA ATGCCACAAA CAAGAGAACA TATACTACTA 50
 GCATCAAGAG TTGGTGTTGA CTATATCGTA GTATTCTTAA ACAAGGCAGA 100
 TATGGTAGAT GACGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTAGAG 150
 25 AATTATTATC AGAATACAAC TTCCAGGAG ATGATATTCC AGTAATCAAG 200
 GGATCAGCTT TAGTAGCATT AGAAAACCCA ACAGATGAAA AATCAATCGC 250
 TCCAATCTTA GAATTAATGG AAGCAGTAGA TAGCTACATT CCAACACCAG 300
 AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTACACA 350
 ATAAGTGGTA GAGGAACAGT TGCAACAGGA AGAGTTGAAA GAGGAGTTCT 400
 30 TCATGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GAAAGCAGAA 450
 AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCA 500
 CAAGCTGGAG ATAATGTTGG AGTACTTTTA AGAGGTGTTC AAAGAACAGA 550
 TATCGAAAGA GGTCAAGTAT TAGCAAAGAC TGGATCAGTT AAGCCACACA 600
 GCAAGTTCGT AGGTCAAGTA TACGTAATTA AGAAAGAAGA AGGTGGAAGA 650
 35 CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAAC 700
 AGACGTTACT GGATCAATCA AATTACCAGA CGGAATGGAA ATGGTTATGC 750
 CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCAA 798

40

2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

GTTCAGCAGC AGATGGTCCA ATGCCTCAAA CAAGAGAACA CATACTACTA 50
 GCTTCAAGAG TTGGTGTTGA CTACATAGTT GTTTTCTTAA ACAAGGCAGA 100
 TATGGTAGAT GACGAAGAAT TATTAGAATT AGTTGAAATG GAAGTAAGAG 150
 60 AATTATTATC AGAATACAAC TTCCAGGAG ATGATATTCC AGTAATAAAG 200

	GGTTCAGCTT	TACAAGCATT	AGAAAACCCA	ACAGATGAAA	AAGCAATCGC	250
	TCCAATCCTT	GAGTTAATGG	AAGCTGTAGA	TAGCTACATT	CCAACTCCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTACACA	350
	ATCACTGGTA	GAGGAACAGT	TGCTACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
5	TCACGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GACAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCG	500
	CAAGCTGGAG	ACAACGTAGG	AGTTCTTTTA	AGAGGAGTTC	AAAGAACTGA	550
	CATCGAAAGA	GGTCAAGTTT	TAGCAAAAAGT	TGGATCAGTT	AAGCCACACA	600
	AGAAATTTGT	AGGTCAAGTA	TACGTACTTA	AAAAAGAAGA	AGGTGGAAGA	650
10	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAAC	700
	AGAYGTTACT	GGTTCAATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

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2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium tetani*

(B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
35	GGGAATTAAT	GAACGAATAC	GGATTCCCAG	GAGATGACGC	ACCAAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
	ACAATCACAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
40	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAAC	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATT	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACCAC	600
	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
45	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
	A					801

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2) INFORMATION FOR SEQ ID NO: 725

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 633 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

413

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTT	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100
10	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATACGA	150
	CTTCCCAGGC	GACGACACTC	CAGTTATCGC	TGGTTCAGCT	TTGAAAGCTT	200
	TAGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCT	250
	GTTGATGAAT	ATATCCCAAC	ACCAGTTCGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGATGTAT	TCTCAATCAC	TGGTCGTGGA	ACTGTTGCAA	350
15	CTGGTCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGCAAC	TGCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAT	TTGTTAGATT	ACGCTGAAGC	AGGCGATAAC	ATTGGTGCAT	500
	TGTTACGTGG	TGTTGCACGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	550
	AAACCAGCTT	CAATCACTCC	ACATACAAAA	TTCTCTGCAG	AAGTTTACGT	600
20	TTTAACTAAA	GAAGAAGGCG	GACGTCATAC	TCC		633

2) INFORMATION FOR SEQ ID NO: 726

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Enterococcus sulfureus*
 (B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

40	CACGTGAACA	CATCTTGTTA	TCTCGTAACG	TAGGTGTTCC	TTACATCGTT	50
	GTATTCTTAA	ACAAAATGGA	TATGGTTGAT	GACGAAGAAT	TATTAGAATT	100
	AGTAGAAATG	GAAGTTCGTG	ACTTATTATC	AGAATACGAT	TTCCCAGGCG	150
	ATGACACTCC	AGTTGTTGCA	GGTTCTGCTT	TGAAAGCTTT	AGAAGGCGAC	200
	GCTTCTTACG	AAGAAAAAAT	CATGGAATTA	ATGGCTGCAG	TTGACGAGTA	250
45	CATCCCAACT	CCAACCTCGTG	ACACTGACAA	ACCATTTCATG	ATGCCAGTTG	300
	AGGATGTATT	CTCAATCACT	GGACGTGGTA	CTGTTGCTAC	AGGTCGTGTT	350
	GAACGTGGAC	AAGTTCGCGT	TGGTGACGTT	GTAGATATCG	TTGGTATCGC	400
	TGACGAAACT	GCTCAAACAA	CTGTAACAGG	TGTTGAAATG	TTCCGTAAAT	450
	TATTAGACTA	CGCTGAAGCA	GGCGATAACA	TCGGTGCTTT	ATTACGTGGT	500
50	GTTGCTCGTG	AAGACATCCA	ACGTGGACAA	GTTTTAGCTA	AACCAGCTTC	550
	AATCACTCCA	CATACAAAAT	TCTCTGCTGA	AGTATACGTA	TTAAGCAAAG	600
	AAGAAGGTGG	ACGTCATACT	CCA			623

55

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus garvieae*

(B) STRAIN: ATCC 49156

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

CGGTCCTATG CCTCAAACCTC GTGAACACAT CTTGTTATCA CGTAACGTTG 50
 GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT GGTGATGAC 100
 GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA 150
 15 ATATGACTTC CCAGGCGACG ATGTTCTGT AATCGCTGGT TCTGCTTTGA 200
 AAGCTCTTGA AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG 250
 GCTGCAGTTG ACGAATACGT TCCAACCTCCA GAACGTGATA CTGACAAACC 300
 ATTCTATGAT CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG 350
 TTGCTACAGG CCGTGTTGAA CGTGACAAG TTCGCGTTGG TGATGAAGTA 400
 20 GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACCTG TAACAGGTGT 450
 TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG 500
 GTGCATTGCT ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA 550
 TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTTCA AAGCTGAAGT 600
 TTATGTTTTG ACAAAGAAG AAGGTGGACG TCACACTCCA TTCTTC 646

25

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma pirum*

(B) STRAIN: ATCC 25960D

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

GAGCAATTTT AGTTGTTTCT GCAACTGATG GTCCAATGCC TCAAACCTCGT 50
 GAACATATCT TATTAGCAGC CCAAGTTGGT GTTCCTAAAA TGGTTGTTTT 100
 45 CTTAAACAAA TGTGATGTTG CTTCTGATCC AGAAATGCAA GAATTAGTTG 150
 CTGAAGAAGT AAAAGACTTA TTAATATCTT ATGGTTTTGA TGGTGACAAT 200
 ACTCCAATTA TTCGTGGTTC AGCATTAGAA GCATTAAATG GTAAACCTGA 250
 ATGAGAAGAA AAAATTAAAG AATTAATGAA GGCAGTGGAT GACACTATTC 300
 CTGATCCAGT TCGTGATACT GAAAAGCCAT TCTTGTTACC AATTGAAGAC 350
 50 GTAATGACAA TTACAGGTCG TGGTACTGTT GTTACAGGTC GTGTAGAACG 400
 TGGTACTCTA AAATTAAATG ATGAAGTTGA AATTGTTGGT TTAGGTGAAA 450
 CATTTAAATC TGTTGTAACA GGTATTGAAA TGTTCCGTAA AGAATTAGAT 500
 GAAGCTCGTG CTGGTGACAA TGCTGGTATT TTAATTCGTG GTGTTGACCG 550
 TGGTCAAGTA CAACGTGGTC AAGTTCTTGC TAAACCAGGT TCTATTACTC 600
 55 CTCATACTAA ATTTAAAGCT GAAATTTATG CTTTGAAAAA AGAAGAAGGT 650
 GGTGCTCATA CTGCTTTCTT AAACGGTTAT CGTCCTCAAT TCTATTTTCA 700
 AACAACTGAT GTTACAGGTT CTATTAAATT AAAAGATGGA ACTGAAATGG 750
 TTATGCCTGG TGACAATACT GAAATCACTG TAGAATTAAT TTCACCAATT 800
 GCTTGTAATA AGGAAGTAAG TTT 823

60

2) INFORMATION FOR SEQ ID NO: 729

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycoplasma salivarium*
 15 (B) STRAIN: ATCC 23064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

	GGAGCAATCT	TAGTTGTTGC	TGCAACTGAT	GGTGCGATGC	CTCAAACCTCG	50
20	TGAACACGTT	TTACTTGCAA	AACAAGTTGG	TGTTCTTAAA	ATCGTTGTTT	100
	TCTTAAACAA	AATCGATATG	TTCAAGCCAG	AAGAAAGAGC	CGAAATGGTT	150
	GAAATGGTTG	AAATGGACAT	TCGTGACTTA	TTAAACAAAT	ACGACTTTGA	200
	TGGTGACAAT	ACTCCTATTA	TTGCTGGTTC	AGCATTAAAA	GCATTACAAG	250
	GTGATCCAGA	ATATGAAAAG	AATATTCTAG	AACTTATGGA	TGCAGTAGAC	300
25	ACATACATTG	ATGAACCTAC	TCGTGATAAA	GATAAACCAT	TCTTAATGGC	350
	TGTAGAAGAC	GTATTTACAA	TTACTGGTCG	TGGAAGTGT	GCTACTGGTA	400
	GAGTAGAACG	TGGTACATTA	CATCTAAATG	ATGAAGTTGA	AATCGTTGGT	450
	CTACGTCCAA	CAATTAAAAC	TGTTGTTACT	GGAATTGAAA	TGTTCCGTAA	500
	AAATTTAAAA	GAAGCTCAAG	CTGGAGATAA	TGCAGGACTT	TTACTACGTG	550
30	GAATTGATAG	AGATCAAGTA	GAACGTGGAC	AAGTTTGGC	CAAACCAAAA	600
	AGTATTATTC	CTCACACAGA	ATTTGAAGCT	GCTGTGTATG	TTCTAAAAGC	650
	TGAAGAAGGT	GGACGTCACA	CTCCATTCTT	TGAACACTAT	AAACCACAAT	700
	TTTACTTTTCG	TACAACCGAC	GTTACTGGTG	GAATTAAATT	CAAACCTGGA	750
	CGTGAAATGG	TTATGCCTGG	CGAAAATGTT	GAATTTACAG	TTACTTTAAT	800
35	TGCTCCTATT	GCAGTTGAAG	AAGGAA			826

2) INFORMATION FOR SEQ ID NO: 730

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

55	TGGTATGTTC	CGCAGCYGAY	GGYCCTATGC	CTCAAACCTCG	CGAACACATC	50
	CTGYTGGCTC	GCCAAGTAGG	YGTAACCTTAC	ATCATCGTRT	TCATGAACAA	100
	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	GAAATGGAAA	150
	TCCGYGACCT	GYTGTCMAGC	TACGACTTCC	CMGGCGACGA	CTGCCCAATC	200
	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGYGAYGCTG	GTTACGAAGA	250
60	GAAATCTTTC	GAAYTGGCTG	CTGCTTTGGA	CAGCTACATC	CCAACCTCCTG	300

	AGCGTGCTGT	GGACAAACCK	TTCYTGYTGC	CTATCGAAGA	CGTRTTCTCT	350	
	ATCTCTGGYC	GYGGTACMGT	AGTAACYGGY	CGTGTAGAGC	GCGGTRTCAT	400	
	CCACGTTGGT	GACGAGATYG	AAATCGTAGG	TCTGAAAGAA	ACCCAAAAAA	450	
	CCACTTGTA	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAA	500	
5	GCWGGTGACA	ACGTAGGCGT	ATTGYTGCCT	GGTACCAARC	GTGAAGACGT	550	
	AGAGCGTGGT	CAAGTATTGG	CYAAACCAGG	YACCATYACT	CCSCACACCA	600	
	AATTCAAAGC	AGAAGTATAC	GTA	CTGAGCA	AAGAAGAGGG	TGGTCGYCAC	650
	ACTCCATTCT	TCGCYAACTA	CCGYCCMCAA	TTCTACTTCC	GTACYACTGA	700	
	CGTAACYGGT	GCAGTTACTT	TGGAAGAAGG	TGTAGAAATG	GTAATGCCAG	750	
10	GTGAGAACGT	AACCATTACY	GTAGAACTGA	TTGCGCCTAT	CGCTAGGAAG	800	
	AAGGTCTGCG					810	

15 2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Enteritidis
(B) STRAIN: ATCC 13076

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50	
	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGTA	CATCATCGTG	TTCCTGAACA	100	
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGA	AACTGGT	TGAAATGGAA	150
35	GTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	AACTCCGAT	200	
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250	
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300	
	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	ACGTATTCTC	350	
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	T	CGTGTAGAA	CGCGGTATCA	400
40	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GACTCAGAAG	450	
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500	
	TGCCCGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAA	CGTGAAGAAA	550	
	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600	
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650	
45	CACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700	
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750	
	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800	
	CGACGGTCTG	CGT				813	

50

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

417

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
5 (B) STRAIN: ATCC 9184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

```

10 CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC GTGAGCACAT      50
   CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG TTCCTGAACA      100
   AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT TGAAATGGAA      150
   GTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG ACACTCCGAT      200
   CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG      250
   CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT CCCGGAACCA      300
15 GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC      350
   CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA CGCGGTATCA      400
   TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG      450
   TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGGTGG ACGAAGGCCG      500
   TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA CGTGAAGAAA      550
20 TCGAAGCTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC      600
   AAGTTCGAAT CTGAAGTGA CATTCTGTCC AAAGATGAAG GCGGCCGTCA      650
   CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG      700
   ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAATGCCG      750
   GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA TCGCAATGGA      800
25 CGACGGTCTG CG                                     812

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2) INFORMATION FOR SEQ ID NO: 733

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

```

45 TGGTTGTTGC TGCGACTGAC GGYCCGATGC CGCAGACCCG TGAGCACATC      50
   CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA      100
   ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG      150
   TTCGYGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC      200
50 GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC      250
   GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG      300
   AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC      350
   ATCTCTGGTC GTGGTACCGT TGTACCCTG CCGTGTAGAAC GCGGTATCAT      400
   CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT      450
55 CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT      500
   GCYGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT      550
   CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA      600
   AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG CCGCCGTCAT      650
   ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA      700
60 CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG      750

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GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 806
 GACGGTCTGC GTTT 814

5

2) INFORMATION FOR SEQ ID NO: 734

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 10 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
 15
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955
 20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 25 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 30 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAG 400
 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTAAGTG CTAAGCCGGG CACCATCAAG 600
 35 CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGAAGTGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCAATGGAC GACGGTCTGC GTTTCGCA 828
 40

2) INFORMATION FOR SEQ ID NO: 735

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 50
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia grimesii*
 55 (B) STRAIN: ATCC 14460
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG 50
 60 TGAGCACATC CTGCTGGGTC GTCAGGTGCG CGTTCCTTTC ATCATCGTAT 100

	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAC T GGTA	150,
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTTCGTGGT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
5	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
10	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
	CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCCTGA	TTCAACCCAAT	800
15	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

35	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
	ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAGAGATGG	150
	AAGTAAGAGA	TTTATTAAAC	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	GTTTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
40	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
	CTCCAGATAG	AGATACAGAT	AAACCATCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
45	CAAGCACAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
	CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
	GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAT	TCTATTTCAG	700
	AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
50	TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

2) INFORMATION FOR SEQ ID NO: 737

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

```

10 GTCAACATGA TGGAGCTCAT CAACAACATC GCGAAGGAGC ACGGCGGTTA      50
   CTCCGTGTTC GCGGGCGTGG GCGAGCGTAC CCGTGAAGGG AACGACTTCT      100
   ACCACGAAAT GAAGGACTCG AACGTTCTCG ACAAGGTCGC GCTGGTGTAC      150
   GGCCAGATGA ACGAGCCGCC GGGCAACCGT CTGCGCGTGG CGCTGACGGG      200
   CCTCACGATG GCCGAGCACT TCCGTGACGA AGGCCTCGAC GTGCTGTTCT      250
15 TCGTCGACAA CATCTACCGT TTCACGCTGG CCGGTACCGA AGTGTCGGCG      300
   CTGCTCGGCC GTATGCCGTC GGCAGTGGGC TATCAGCCGA CGCTGGCTGA      350
   AGAAATGGGC AAGCTGCAAG AGCGCATCAC GTCGACGAAG AAGGGCTCGA      400
   TCACGTCGGT T                                     411

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20

2) INFORMATION FOR SEQ ID NO: 738

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium bifermentans*
35 (B) STRAIN: ATCC 638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

```

TACAAGAGCT TATTAACAAT ATAGCTACTC AACACGGTGG TATATCAGTA      50
TTCGCAGGTG TTGGAGAGAG AACAAAGAGAA GGTAACGACT TATTCCATGA      100
40 GATGAGCGAT ACAGGAGTTA TAAATAAAAC AGCTCTAGTA TTCGGACAAA      150
TGAATGAGCC ACCTGGAGCA AGAATGAGAG TTGCTTTAAC TGGTCTTACA      200
ATGGCTGAAT ACTTCAGAGA TCAACAAGGG CAAGACGTTT TATTATTCGT      250
AGATAATATA TTCCGTTTCA CTCAAGCAGG ATCTGAGGTT TCTGCACTTC      300
TTGGACGTAC TCCATCAGCA GTTGATACC AACCAACATT AGCAACAGAG      350
45 ATGGGTAGAT TACAAGAGAG AATAACATCT ACAAATAAAG GGTC          394

```

2) INFORMATION FOR SEQ ID NO: 739

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as *Clostridium butyricum*)

(B) STRAIN: ATCC 8260

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

```

TTAATAAACA ACATAGCTAA ACAACATGGT GGTTTATCAG TATTTACTGG      50
AGTTGGTGAA AGATCAAGAG AAGGTAATGA CTTATATCAT GAAATGAGAG      100
AGTCAGGAGT TATTGATAAG ACAGCATTAG TATTTGGACA AATGAATGAG      150
10 CCACCGGGTG CCAGAAATGAG AGTTGCATTA ACAGGTCTTA CTATGGCAGA      200
GTATTTTAGA GATAAAGGTC AAGATGTGTT ACTATTCATA GATAACATAT      250
TCAGATATAC TCAAGCAGGT TCAGAGGTTT CAGCATTACT TGGAAGAACA      300
CCTTCAGCGG TTGGATATCA GCCAACACTT GCAACTGAAA TGGGTGCACT      350
TCAGGAAAGA ATTACATCAA CAGTTAATGG TTCTATTACG TCAG              394

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15

2) INFORMATION FOR SEQ ID NO: 740

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- 30 (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

```

TTATAAACAA TATTGCTAAG CAACATGGTG GTATTTCTGT ATTTTCAGGA      50
35 GTAGGAGAAA GAACAAGAGA AGGTAACGAC CTTTATGGCG AAATGAGTGA      100
GTCTGGAGTT ATAAATAAAA CAGCTCTAGT ATTTGGTCAA ATGAATGAAC      150
CACCTGGAGC GAGAATGAGA GTTGCTTTAA CTGGACTTAC AATGGCAGAA      200
CATTTTAGAG ATGAGCAAGG ACAAGACGTT TTACTTTTCG TTGATAATAT      250
ATTCCGTTTC ACACAAGCTG GTTCAGAAGT TTCAGCACTT CTAGGACGTA      300
40 TGCCATCAGC TGTGTTGTTAT CAGCCAACAT TAGCTACTGA AATGGGTGCA      350
CTTCAAGAGA GAATAACATC AACTAAGAAA GGTTCATAAA CAT              393

```

45 2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium ramosum*
- (B) STRAIN: ATCC 25582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

60

TTGATTCAAG AATTCATTAA TAACATTGCT ACAGAACATG GTGGTTTATC 50
 AGTTTTTGCT GGAGTTGGTG AACGTAGCCG TGAAGGTAAT GATTTATATT 100
 ATGAAATGAA GGAAAGTGGT GTTTTATCTA AAACAACACT AGTATTTGGA 150
 CAGATGAATG AACCCCCAGG AGCTCGTTTA AGAGTTGCTT TAACGGGTCT 200
 5 TACTATGGCA GAAGAATTCC GTGATGAACA AGGTCAGGAT GTCTTATTAT 250
 TCATCGATAA TATTTTCCGT TTTACTCAAG CTGGATCTGA AGTATCTGCC 300
 TTAATTGGAC GGGTACCATC ACAAGCTGGG TATCAGCCAA CTTTAGCAAC 350
 CGAAATGGGT GCTTTACAAG AACGGATTAC ATCAACTAAA AAAGGATC 398

10

2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12964

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

TAGCTAAGGA ACACGGTGGA CTTTCAGTAT TCACAGGTGT TGGAGAAAGA 50
 TCAAGAGAAG GTAATGATTT ATATTACGAA ATGAAAGAAT CAGGAGTTAT 100
 30 AGACAAGACA GCTCTAGTGT TTGGACAAAT GAATGAATCT CCAGGAGCTA 150
 GAATGAGAGT ATCTTTAACA GGATTAACATA TGGCTGAATA TTTCAGAGAT 200
 CAAGGTCAAG ATGTGCTTTT ATTCATAGAT AACATATTTA GATTTACTCA 250
 AGCTGGATCA GAAGTATCGG CTTTACTTGG AAGAATACCA TCAGCAGTTG 300
 GTTATCAACC AACACTAGCA ACTGAAATGG GTGCACTTCA AGAAAGAATT 350
 35 ACTTCAACTA AAAATGGATC AATAACTTCA 380

2) INFORMATION FOR SEQ ID NO: 743

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

55 TTAATAAATA ATATAGCAAA AGAGCATGGT GGTCTTCTG TATTTACAGG 50
 AGTTGGAGAA AGGTCAAGAG AAGGTAACGA CTTATATTAT GAAATGAAAG 100
 AGTCAGGGGT TATAGATAAG ACAGCTTTAG TATTTGGACA AATGAATGAA 150
 TCACCAGGAG CAAGAATGAG AGTTTCATTA ACTGGATTAA CTATGGCTGA 200
 ATATTTTAGA GATCAAGGTC AAGACGTTCT TTTATTTATA GATAATATAT 250
 60 TTAGATTTAC TCAAGCGGGA TCAGAAGTTT CTGCGTTATT AGGAAGAATT 300

CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGAGCACT 350
TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

5

2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

TTCCCCCGCA CGCATGCCCA AGGTGTTCGA TGCCCTGAAG CTCGACGGCT 50
CGGCCCTGAC GCTGGAAGTG CAGCAACTGC TGGGTGACGG CGTTGTGCGT 100
ACCATCGCCC TGGGTTCGTC CGACGGTCTG CGTCGCGGCC TGATGGTGTGTC 150
25 CAACACCGGC AACCCCATCA CCGTGCCCGT GGGCAAGGCG ACGCTGGGTC 200
GCATCATGGA CGTGCTGGGC AATCCCATCG ACGAACGTGG TCCCGTGGAT 250
CAGGCGCTGA CGGCTCCCAT CCACCGCAAG GCACCGGCTT ATGACGAGCT 300
GTCGCCTTCG CAGGAACTGC TGGAAACCGG CATCAAGGTG ATCGACCTGA 350
TCTCGCCCTT CGCCAAGGGC GGCAAGGTGG GTCTGTTCGG TGGCGCCGGT 400
30 GTGGGCAAGA CCGTGAACAT GATGGAATC ATCAACAACA TCGCCAAGGG 450
CCACGGTGGT CTGTGCGTGT TCGCCGGTGT GGGTGAACGT ACCCGCGAAG 500
GCAATGACTT CTATCACGAA ATGTCCGACG CCGGCGTGGT CAACCAGGAG 550
TCGCTGAACG ACTCCAAGGT GGCCATGGTC TACGGCCAGA TGAACGAACC 600
CCCGGGCAAC CGTCTGCGCG TGGCGCTGAC CGGCCTGACC ATGGCCGAAG 650
35 CCTTCCGTGA CGAAGGCAAG GACGTGCTGT TCTTCGTGGA CAACATCTAC 700
CGCTACACGC TGGCCGGTAC CGAAGTGTCC GCTCTGCTGG GTCGCATGCC 750
TTCCGCCGTG GGCTACCAGC CCACGCTGGC CGAGGAAATG GGCCGCCTGC 800
AAGAGCGCAT CACCTCGACC AAGGTCGGTT CGATCACTTC CAC 843

40

2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
(B) STRAIN: ATCC 13884

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

GCCGTACCAC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT 50
60 TCTGGTGTCTG GAAGTTCAGC AGCAGCTGGG CGGCGGTATC GTACGTACCA 100

	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTTGACAT	GAAAGGCGAC	ATCGGCCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTCGGCGGT	GCGGGTGTAG	400
	GTAATACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
15	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Neisseria canis*
- (B) STRAIN: ATCC 14687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

35	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCT	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGGCG	GTAAGTAAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
40	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCCGA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
45	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCCG	TAACCGTTTG	CGCGTTGCGC	600
	TAACTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
50	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

55 2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cinerea*

(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

10 CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG 50
 TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA 100
 TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT 150
 ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCGTAT 200
 15 TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATACCG 250
 ACAAAGCCG TGCCATTAC CAAACTGCTC CGAAATTCGA CGAGTTGTCT 300
 TCAGCTACCG AATTGTTGGA AACCGGTATT AAAGTGATCG ACTTGCTGTG 350
 TCCGTTTGCT AAAGGCGGTA AAGTAGGTCT GTTCGGTGGT GCCGGTGTGG 400
 GCAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC 450
 20 AGCGGTCTGT CCGTGTTCGC AGGTGTGGGT GAGCGTACCC GTGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA 550
 TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT 600
 TTGACCGGTT TGA CTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
 CGGTAAAGGC CGCGACGTAT TGTTCTTCGT TGACAACATC TACCGTTACA 700
 25 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
 GTGGGTTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
 TATTACCTCT ACCCAAACCG GTTCCATTAC T 831

30

2) INFORMATION FOR SEQ ID NO: 748

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cuniculi*

(B) STRAIN: ATCC 14688

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG 50
 AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 50 CTCTGGTGCA CCGATTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAACCTCACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTCCGGTGG TGCAGGTGTG 400
 55 GGTAACACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 ACGATTTTTA TCACGAAATG CAAGAAGCAG GCGTTGTAA TACCGAAGAC 550
 TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTGACATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTG CATTGACAGG CTTGACGATG GCAGAAATATT 650
 60 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG 700

TTCGTTGATA	ACATCTATCG	TTACACACTG	GCTGGTACGG	AAGTGT ^Δ AGC	750
ACTTCTAGGT	CGTATGCCAT	CAGCAGTAGG	TTATCAACCG	ACTCTGGCTG	800
AAGAAATGGG	TGCGTTGCAA	GAGCGTATTA	CCTCAACGCA	ATCGGGTTCCG	850
ATCACTTCGG	GG				862

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2) INFORMATION FOR SEQ ID NO: 749

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

	GGA	ACT	CCCA	CGT	GAC	GCTA	TCC	CGC	ATGT	TTT	TGAT	GCA	TTA	AAATTAG	50	
25	TTG	AAA	ATGA	CCT	AAC	CTTA	GA	AGT	TCAAC	AA	CTTT	TGGG	GG	ATGGTGTA	100	
	GTG	CGT	ACCA	TTG	CGA	TGGG	TAG	TT	CAGAT	GG	ATTAA	AGC	GT	GGTATGGC	150	
	TGT	GA	ATAAT	ACC	GG	AGCTC	CG	ATT	ACTGT	TC	CTGT	TGGC	CG	TGAAACTT	200	
	TGG	GT	CGTAT	CAT	GG	ATGTA	TT	GGG	TAATC	CG	GT	GATGA	GG	CAGGTCCG	250	
	GT	AA	TGCAT	CCA	ATA	CACG	TG	CGA	TCCAT	CA	AG	AGGCTC	CT	AAGTTTGA	300	
30	TG	AG	CTTTCT	TCA	ACA	ACGG	A	ATT	ATTAGA	AA	CT	GGCATT	A	AGGTTATCG	350	
	ACT	TG	TTATG	TCC	G	TTTGCC	AA	AG	TGGTA	A	AG	TAGGTCT	GT	TTGGTGTT	400	
	GCG	GGT	GTAG	GT	AAA	ACCGT	AA	AT	TGATG	G	AG	TTAATTA	ACA	ACATTGC	450	
	CA	AGG	CACAT	AG	CGG	TTTGT	CT	GT	GTTTGC	AG	GCG	TGGGT	GA	ACGTACTC	500	
	GT	GA	AGGTAA	TG	ACT	TCTAT	C	AC	GAGATGA	A	AG	ATTCCAA	CG	TATTGGAC	550	
35	AA	AGT	GGCAA	TG	G	TTTACGG	TC	AG	ATGAAC	GA	AC	CTCCAG	G	CAACCGTCT	600	
	GCG	CGT	TGCT	TT	G	ACCGTT	TG	ACT	ATGGC	CG	AA	TACTTC	CG	TGACGAAA	650	
	AAG	AC	GAAAA	CG	G	TAAAGGT	CG	C	GACGTAT	TG	TT	CTTCGT	GG	ACAACATT	700	
	TAC	CG	TTACA	CT	TT	GGCCGG	T	AC	GGAAGTA	T	CC	G	CATTGC	TGG	GTCTAT	750
	GC	CT	TACGA	GT	AG	GTTACC	A	AC	CGACATT	GG	CT	GAAGAA	AT	GGGTCGTT	800	
40	TG	CA	AAGAGCG	T	ATT	ACCTCT	A	CC	CAGACAG	G	CT	CTATTAC	TT	CC	844	

2) INFORMATION FOR SEQ ID NO: 750

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

60	CG	C	G	A	C	G	C	T	A	TT	C	C	G	C	A	T	G	T	TT	A	C	G	A	T	T	G	G	A	C	G	A	A	C	G	G	50
----	----	---	---	---	---	---	---	---	---	----	---	---	---	---	---	---	---	---	----	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	----

	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
5	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
10	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
15	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

20 2) INFORMATION FOR SEQ ID NO: 751

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 31426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

35	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTTCG	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
40	TGTCGATGTA	TTGGGAATC	CTGTTGACGA	GGCAGGTCCA	ATTGATACCG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGTCT	GTTCCGCGGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCAAACCG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(B) STRAIN: ATCC 27628

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCGG	CATGACTGTG	AGCAATACTG	150
15	GTTCGCCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGCTTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTC	GGCGGTGCCG	GTGTGGGTAA	400
20	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCCGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCAA	CCGTCTGCGC	GTTGCTTTGA	600
	CCGGTTTGAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
25	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTC	CATTA			825

30

2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*

(B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

	GATGCGATTC	CGCATGTTTA	CGATGCCCTG	AAATTGGACG	AGAACGGTCT	50
	GACCCTGGAA	GTCCAACAGC	TTTTGGGTGA	CGGCGTTGTC	CGTACTATTG	100
50	CAATGGGTAG	TTCAGACGGC	CTGAAACGCG	GCATGTCTGT	CAGCAATACC	150
	GGTGCGCCAA	TCACTGTGCC	GGTAGGTAAA	GGTACGTTGG	GCCGTATTGT	200
	CGACGTATTG	GGTACACCTG	TTGACGAAGC	AGGTCCGATC	GATACCGACA	250
	AGAGCCGCGC	CATCCACCAA	ACCGCCCCGA	AATTCGACGA	GTTGTCTTCA	300
	ACTACCGAAT	TGTTGGAAAC	CGGCATTAAA	GTGATCGATT	TGCTGTGTCC	350
55	GTTTGCTAAG	GGCGGTAAAG	TAGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	400
	AAACCGTGAA	CATGATGGAA	TTGATCAACA	ACATCGCCAA	AGCGCACAGC	450
	GGTCTGTCCG	TGTTTGACAG	CGTGGGCGAG	CGTACCCGCG	AAGGTAACGA	500
	CTTCTACCAC	GAGATGAAAG	ATTCCAACGT	ATTGGATAAA	GTAGCCATGG	550
	TGTATGGTCA	GATGAACGAA	CCTCCGGGCA	ACCGTCTGCG	CGTTGCTTTG	600
60	ACCGGTTTGA	CGATGGCCGA	ATACTTCCGC	GACGAAAAAG	ACGAAAACGG	650

CAAAGGCCGC	GACGTATTGT	TCTTCGTGGA	CAACATCTAC	CGTTACACCC	700
TGGCCGGTAC	CGAAGTATCC	GCACTGTTGG	GCCGTATGCC	TTCCGCAGTG	750
GGTTACCAAC	CGACATTGGC	TGAAGAAATG	GGTCGTTTGC	AAGAGCGTAT	800
TACCTCTACC	CAAACCGGTT	CCATTACTTC	C		831

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2) INFORMATION FOR SEQ ID NO: 754

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear.

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 2241C

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
25 CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	GTAGTCCGTA	100
CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	GA CTGTGAGC	150
AATACCGGTG	CGCCATTAC	TGTGCCGGTA	GGTAAAGGTA	CGTTGGGACG	200
CATTGTGCGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	CCAATCGATA	250
CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	TGACGAACTG	300
30 TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	TTGACTTGCT	350
GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGC	GGTGCCGGTG	400
TGGGTAAAAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	CGCCAAAGCG	450
CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	CCCGCGAAGG	500
TAACGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GATAAAGTGG	550
35 CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	TTTGCGCGTC	600
GCATTGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	AAAAAGACGA	650
AAACGGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGACAAC	ATCTACCGTT	700
ACACTCTAGC	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	TATGCCGTCT	750
GCAGTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	GTTTGCAGGA	800
40 GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC		836

2) INFORMATION FOR SEQ ID NO: 755

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

60 CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
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430

	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	G TAGTTCGTA	100
	CTATTGCAAT	GGGTAGTTCG	GATGGTTTGA	AACGCGGCAT	GACTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTGCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
5	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
10	TAATGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCTG	TATGCCTTCA	750
15	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

20 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

35	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
40	TGTTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

	CCCGTGATGC	TATTCCCATG	TATACGATGC	CCTGAAATTG	GTAGATAACG	50
	ATCTGACCCT	GGAAGTGCAA	CAACTTTTAG	GTGATGGTGT	GGTTCGTACC	100
	ATTGCAATGG	GTAGTTCAGA	CGGCCTAAAA	CGTGGTATGG	CTGTTAACAA	150
15	TACCGGCGCT	CCGATTACTG	TTCCGGTGGG	GAAAGCCACC	TTGGGACGTA	200
	TTATGGATGT	GTTGGGTAAT	CCGTTTGATG	AAGCAGGTCC	TGTTGTATCA	250
	GAAGAACTC	GCGCTATTCA	TCAAGCTGCC	CCTAAATTTG	ACGAACTGTC	300
	TTCAGCAACT	GAGTTGTTGG	AAACAGGCAT	TAAAGTAATT	GACTTGCTGT	350
	GCCCGTTTGC	CAAAGGTGGT	AAAGTAGGTT	TGTTTGGTGG	TGCCGGCGTG	400
20	GGTAAAACCG	TAAATATGAT	GGAGTTGATC	AACAACATCG	CGAAGGCACA	450
	TAGTGGTTTG	TCTGTATTTC	CCGGTGTAGG	TGAGCGTACC	CGTGAAGGTA	500
	ACGACTTCTA	CCATGAAATG	AAAGACTCTA	ACGTATTGGA	TAAAGTAGCC	550
	ATGGTTTATG	GCCAGATGAA	TGAACCTCCG	GGTAACCGTT	TGCGCGTTGC	600
	TTTGACTGGT	TTGACTATGG	CCGAATATTT	CCGTGACGAG	AAAGATGAAA	650
25	ACGGCAAAGG	TCGTGACGTC	TTGTTCTTTG	TGGATAATAT	CTATCGCTAT	700
	ACTCTGGCCG	GTACTGAAGT	GTCTGCACTG	TTAGGTCGTA	TGCCGTCTGC	750
	AGTAGGTTAT	CAGCCTACAT	TGGCAGAAGA	AATGGGTCGC	TTGCAGGAGC	800
	GTATTACTTC	TACTCAAACA	GGTTCGATTA	CTT		833

30

2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria animalis*
(B) STRAIN: ATCC 19573

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

	CGCGATGCCA	TTCCTCACGT	TTACGATGCC	CTGAAATTGG	ACGACACCGG	50
	TCTGACTTTG	GAAGTACAAC	AACTTCTGGG	CGACGGTGTG	GTACGTACCA	100
50	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GGGGTTTGTC	TGTGAGCAAT	150
	ACCGGTTCTC	CGATTGCCGT	TCCTGTCCGT	AAAGCGACTT	TGGGTCGTAT	200
	TATGGACGTA	TTGGGCAATC	CGGTTGATGA	AGCCGGTCCG	GTTGCTACCG	250
	AAGAGAAACG	TGCTATTAC	CAAGCCGCAC	CGAAGTTTGA	TGAATTGTCA	300
	TCAGCTACCG	AGTTGTTGGA	AACCGGTATT	AAAGTAATCG	ACTTGCTGTG	350
55	TCCGTTTGCA	AAAGGCCGTA	AAGTAGGTCT	GTTCCGGCGGT	GCCGGTGTGG	400
	GCAAAACCGT	AAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCACAC	450
	AGCGGTCTGT	CTGTGTTTGC	CGGTGTAGGT	GAACGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTGTTGGAT	AAAGTAGCCA	550
	TGGTGTACGG	TCAGATGAAT	GAGCCGCCGG	GCAACCGCTT	GCGCGTGGCT	600
60	TTGACCGGCC	TGACTATGGC	CGAATACTTC	GTGACGAAAA	AGACGAAAAC	650

GGCAAAGGTC	GTGACGTATT	GTTCTTCGTG	GACAACATTT	ACCGCTACAC	700
ACTGGCCGGT	ACCGAAGTAT	CAGCATTGTT	GGGCCGTATG	CCGTCTGCAG	750
TAGGTTATCA	GCCGACATTG	GCAGAGGAAA	TGGGTCGCTT	GCAAGAGCGT	800
ATTACCTCTA	CCCAAACCGG	TTCGATTACC	TCT		833

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2) INFORMATION FOR SEQ ID NO: 759

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
- (B) STRAIN: ATCC 33519

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
25 ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTTCGTTGTA	100
TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
AAGAACGTTG	GTCTATTAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
30 AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
TCCGTTTGCT	AAAGGTGGTA	AAGTAGGTCT	GTTCCGTGGT	GCGGCTGTGG	400
GTAAAACAGT	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
TCAGGTTACT	CTGTATTTGC	TGGTGTTGGT	GAGCGTACTC	GTGAGGGTAA	500
CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCCTTGAC	AAAGTATCGT	550
35 TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCAACA	750
TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAC	800
40 AGGTTCAATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Enteritidis
- (B) STRAIN: ATCC 13076

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAGAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CAGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

20

2) INFORMATION FOR SEQ ID NO: 761

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
40	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGCC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTCG	GTGGTGCGGG	TGTAGGTAAA	400
45	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGGTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTACTGC	650
50	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

55

2) INFORMATION FOR SEQ ID NO: 762

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 \ (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

	CGACGTGATC	GAGCCCTTCT	TCGTCGACGT	GATGCGCTCT	TGCAGCTTGC	50
	CCATTTCTTC	AGCCAGCGTC	GGCTGATAGC	CCACTGCCGA	CGGCATACGG	100
15	CCGAGCAGCG	CCGACACTTC	GGTACCGGCC	AGCGTGAAAC	GGTAGATGTT	150
	GTCGACGAAG	AACAGCACGT	CGAGGCCTTC	GTCACGGAAG	TGCTCGGCCA	200
	TCGTGAGGCC	CGTCAGCGCC	ACGCGCAGAC	GGTTGCCCGG	CGGCTCGTTC	250
	ATCTGGCCGT	ACACCAGCGC	GACCTTGTCG	AGAACGTTTCG	AGTCCTTCAT	300
	TTCGTGGTAG	AAGTCGTTCC	CTTCACGGGT	ACGCTCGCCC	ACGCCCCGCGA	350
20	ACACGGAGTA	ACCGCCGTGC	TCCTTCGCGA	TGTTGTTGAT	GAGCTCCATC	400
	ATGTTGAC					408

25 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium sordellii*
 (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

40

	GAACTTATAA	ACAACATAGC	TACTCAACAT	GGTGGTATAT	CAGTATTTCGC	50
	AGGTGTTGGA	GAGAGAACAA	GAGAAGGTAA	CGACCTTTAC	GGAGAAATGA	100
	GTGAGTCTGG	AGTTATAAAC	AAGACAGCTC	TAGTATTTCGG	ACAAATGAAT	150
	GAGCCACCTG	GAGCAAGAAT	GAGAGTTGCT	TTAACTGGTC	TTACAATGGC	200
45	TGAATATTTT	AGAGATCAAG	AAGGACAAGA	CGTTTTATTA	TTCGTAGATA	250
	ATATATTCCG	TTTCACTCAA	GCAGGATCTG	AGGTTTCTGC	ACTTCTTGGA	300
	CGTACTCCAT	CAGCAGTTGG	ATACCAACCA	ACATTAGCTA	CAGAGATGGG	350
	TAGATTACAA	GAGAGAATAA	CATCTACAAA	TAAAGGGTCT	ATAACATCAG	400

50

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

435

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*

(B) STRAIN: ATCC 19402

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

	TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
	TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
10	ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
	TAGACAACAT	ATTTAGATTC	ACTCAAGCAG	G TTCAGAGGT	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
15	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCCTATAA	400
	CATCA					405

20 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium botulinum*

(B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

35	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
40	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATT	CTTGGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCCTATAA	CAT	393

45

2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 399 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium histolyticum*

(B) STRAIN: ATCC 19401

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
5	GAAAGATTCT	GGGGTTATAG	AGAAAACTGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACT	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	GTA CTTTAT	TTATAGATAA	250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
10	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

30	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTCCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTTCGTC	250
35	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

40

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

55	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAACGTC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
60	GCTGATGCTC	CCGAGTTCGT	TGATCAATCC	CCCCTCCCG	AGATTCTCGA	200

	GACTGGTATC	AAGGTTGTCT	ATTTGCTTGC	TCCCTATGCT	CGTGGTGGTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTCT	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTTACT	CTATCTTCTG	350
	TGGTGTCTGGT	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
5	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCGTG	TTGCCTTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAGTG	600
	TCCGCTTTGC	TTGGTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
10	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700
	GTTCCATTAC	CTCCGTGCAA	GCTGTCTACG	TCCCTGCTGA	CGATTTGACT	750
	GATCCTGCTC	CTGCTACTAC	TTTTGCTCAC	TTGGACGCCA	CCACTGTGTT	800
	GTCTCGTTCC	ATTGCTGAGT	TGGGTATCTA	CCCTGCTGTC	GATCCCCTTG	850
	ACTCCAAGTC	CCGTATCTTG	GATCCCCGTA	TCGTTGGTGA	TGAGCACTAC	900
15	TCTGTTGCCA	CTGGTGTCCA	ACAAATCCTT	CAAAACTACA	AGTCGCTTCA	950
	AGA					953

20 2) INFORMATION FOR SEQ ID NO: 769

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

35	CGCGGTTCCA	AGGCCACCGA	CACCGGTGCC	CCCATCAAGA	TTCCCGTTGG	50
	TCACGGTACC	CTTGGTCGTA	TCATGAACGT	CACTGGTGAC	CCCATTGACG	100
	AGCGTGGTCC	CATCAAGGCC	ACCAAGTAGC	CTCCCATCCA	CGCCGACCCC	150
	CCGGAGTTCA	CCGAGCAATC	CACCTCCGCT	GAGGTCCTCG	TTACCGGTAT	200
40	CAAGGTTGTC	GACCTGTTGG	CTCCTTACGC	TCGTGGTGGA	AAGATTGGTC	250
	TCTTCGGAGG	TGCTGGTGTC	GGAAAGACTG	TCTTCATTCA	GGAGCTGATT	300
	GTAAGGAGAC	ACACTGTCTA	CTGGCTGAGC	ATTAGCTAAC	GGCAGGCAGA	350
	ACAACATCGC	CAAGGCCCCA	GGTGGTTTCT	CTGTCTTCAC	TGGTGTCTGGT	400
	GAGCGTACCC	GTGAGGGTAA	CGATCTGTAC	CACGAGATGC	AGGAGACTTC	450
45	CGTCATTGAG	CTTGACGGTG	ACTCCAAGGT	CGCCCTCGTC	TTCGGTCAGA	500
	TGAACGAGCC	CCCGGGTGCC	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACT	550
	GTTGCTGAGT	AAGTCTTGAA	TTCATGTGT	TGACAACGTC	GTGGCTAATG	600
	GGAAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGTA	GAAGTGCCTG	TGAGACATAC	ACTGACTTCG	700
50	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTTCCGAGG	TGTCCGCTCT	750
	TCTTGGTCTG	ATCCCCCTCT	CCGTCGGTTA	CCAGCCCACC	CTCGCCATTG	800
	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGTTCCATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTTGA	CTGACCCTGC	900
	CCCCGCCACC	ACCTTCGCCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
55	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCGG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
	CACCCGCGTT	CAGCAGATTC	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTCGG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTCTG	1200
60	CCAGGTCTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250

TCCGATCATT	CAAGGCTATC	TTGACTGGTG	AGGGTGACGA	CCTTCCCAG	1300
GGTGAGTCTC	GACTATCTCC	GCATTCATAG	CGTATAACTG	ACA	1343

5

2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
(B) STRAIN: ATCC 26947

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

TTCAGGAGTT	GATTGTATGT	TCACCTGCAA	CATAAGACTT	CCCATTCTCC	50
ACTCTTTTCT	AACCTCTCAC	AGAACAACAT	TGCCAAGGCT	CACGGTGGTT	100
ACTCTGTCTT	CACTGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGATCTG	150
25 TACCACGAAA	TGCAGGAGAC	TGGTGTCAAT	CAGCTCGAGG	GTGAATCTAA	200
GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCCAGGT	GCCCCGTGCC	250
GTGTCGCCCT	TACCGGTCTG	ACCATCGCCG	AGTACTTCCG	TGACGAGGAA	300
GGTCAGGATG	TGCTGCTCTT	CATTGACAAC	ATTTTCCGTT	TCACCCAGGC	350
CGGTTCTGAG	GTGTCTGCCC	TTCTTGGTCG	TATCCCCTCC	GCTGTCGGTT	400
30 ACCAGCCAC	TCTGGCCGTC	GACATGGGTG	GTATGCAGGA	GCGTATTACC	450
ACCACCACCA	AGGGTTCCAT	TACCTCCGTC			480

35 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1174 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

50

CTCGAACAAG	AYAAGTTGCC	YGCCATTTTG	AACGCCCTTG	AAGTCAAGGA	50
YCACTCTGGT	GGACGTCTCG	TYCTCGAAGT	CTCTCAACAT	TTGGGTGAGA	100
AACTGTCCG	TACTATTGCT	ATGGATGGTA	CTGAAGGTAA	GTTATGTYCA	150
TCCCANNGGA	TACAGTCARA	CAGMAATGTC	TAGTGGTTAT	AGCAGYAGCA	200
55 GATGATTGAC	CAATATGTTA	GGTCTTGTC	GGTGGTCAA	AGGTGTTGA	250
CACTGGTGCT	CCCATTACCA	TCCCCGTTGG	TAAGGAAGTC	CTTGGTCGTA	300
TCATCAACGT	TATTGGTGAA	CCCATTGATG	AACGTGGTCC	CATTGACGCC	350
AAGACTCACC	GTCCTATTCA	CGCTGAAGCT	CCCGAATTCC	TTGATCAATC	400
CCCCACTCCC	GAAATCCTCG	AGACTGGTAT	CAAGGTYGTC	GATTGTTGG	450
60 CTCCTTATGC	TCGTGGTGGT	AAGATTGGTC	TCTTCGGTGG	TGCTGGTGTG	500

GGTAAGACTG TCTTGATTCA AGAATTGATT AACAAACATYG CCAAGGCTCA 550
 CCGTGGTTAC TCTATCTTCT GTGGTGTCGG TGAACGTACT CGTGAGGGTA 600
 ACGATTTGTA CCATGAAATG ATTGAAACCG GTGTCATTCA ATTGGAAGGC 650
 GAGTCCAAGT GTGCTCTCGT CTTTGGTCAA ATGAACGAAC CCCCAGGTGC 700
 5 TCGTGCCCGT GTCGCTTTGA CTGGTTTGAC TATTGCTGAA TACTTCCGTG 750
 ATGATGAGGG TCAAGATGTC TTGCTTTTCA TTGATAACAT TTCAGATTC 800
 ACTCAAGCTG GTTCTGAGGT ATCTGCCCTT TTGGGTCGTA TTCCTTCCGC 850
 TGTCGGTTAC CAACCCACTC TTTCCACYGA TATGGGTGGT ATGCAAGAGC 900
 GTATTACTAC CACCAAGAAC GGTTCATTA CCTCCGTCCA AGCTGTCTAC 950
 10 GTCCCTGCTG ATGATTGAC CGATCCTGCT CCTGCCACCA CTTTGCTCA 1000
 CTTGGATGCC ACCACTGTCT TGTCTCGTTC CATCGCTGAA TTGGGTATCT 1050
 AYCCCGCTGT CGATCCTCTT GATTCCAAGT CTCGTATCCT CGATCCCCGT 1100
 ATTGTCCGGT ATGAGCACTA CAAGGTTGCC ACTGAAGTTC AACAAATCCT 1150
 CCAAACTAC AAGTCTCTCC AAGA 1174
 15

2) INFORMATION FOR SEQ ID NO: 772

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Piedraia hortai*
 30 (B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

AGGAGCTTAT CAACAACATC GCCAAGGCTC ACGGTGGTTA CTCCGTCTTC 50
 35 ACTGGTGTCG GTGAGCGTAC TCGTGAGGGT AACGATTGTG ACCACGAGAT 100
 GCAAGAGACT TCCGTCAATC AGCTTGACSG CGAGTCCAAG GTCGCTCTCG 150
 TGTTCCGGTCA GATGAACGAG CCCCCGGGTG CCGTGCCCCG TGTTGCCCTG 200
 ACTGGTCTTA CCATCGCTGA GACTTCCGT GATGCCGAGG GTCAGGATGG 250
 TAAGTTCTAT AACTCTTGTC GCAAAGGTTT CATTCTGGTC GCTAACTTGC 300
 40 TCAGTGCTCC TGTTCAATCGA CAACATTTTC CGTTTCACCC AGGCTGGTAT 350
 GGAGGTGTCT GCCCTCCTCG GTCGTATTCC TTCTGCCGTC GGTTACCAAC 400
 CTACTCTCGC CGTCGACATG GGTGGTATGC AAGAGCGTAT TACCACTACC 450
 AAGAAGGGAT CCATTAC 467
 45

2) INFORMATION FOR SEQ ID NO: 773

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 578 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 55 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudallescheria boydii*
 60 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

```

5   TTGCCAAGGC CCACGGTGGT TACTCTGTCT TCACTGGTGT CGGTGAGCGT      50
    ACCCGTGAGG GTAACGATCT GTACCACGAA ATGCAGGAAA CCTCCGTCAT      100
    TCAGCTTGAT GGCAGATCCA AGGTCGCGCT TGTCTTCGGT CAGATGAACG      150
    AGCCCCCTGG TGCCCGTGCT CGTGTGCTC TTA CTGGTCT TACCGTTGCC      200
    GAGTACTTCC GTGATGAGGA GGGTCAGGAT GGTAAGTTAT ATCGTTTTTA      250
    TTATCTTCTT TGCCACCACC CCTCTACGAA TCCATGCCTC CGTTGGTGAA      300
    GGCATCGTTT GTAGGGCGGG TCGGAGTTTG CGGCAATTTC TGCCGTCGGC      350
10  TTGAAGCCGC GGATGCCCCG TGTGTTGACGC GTATCGATGC TAACAACAAT      400
    GACAACAGTG CTTCTCTTCA TTGACAACAT TTTCCGATTC ACCCAGGCCG      450
    GTTCCGAGGT GTCTGCCCTT CTCGGTCGTA TTCCCTCTGC CGTCGGTTAC      500
    CAGCCCACTC TTGCCGTAGA CATGGGTGCC ATGCAGGAAC GTATTACCAC      550
    CACCAAGAAG GGTTCGATTA CCTCCGTC      578
15

```

2) INFORMATION FOR SEQ ID NO: 774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhizopus oryzae*
- (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

```

35  AACTTACCYG CTATCTTGAA CGCTCTCGAA GTCCAAGATC ACTCTGGTGG      50
    ACGTCTTGTC CTTGAAGTTC GCTCAACACT TGGGTGAAAA TACTGTCCGT      100
    ACTATTGCTA TGGATGGTAC TGAAGGTAAG CTATACTATA ACCGTKTTAT      150
    CCGAGTATGA TATTAAGTTG AAAAAAGGTC TCGTYCGTGG TCAAAAGGTT      200
    ATTGACACTG GTGCTCCCAT TACCATTCTT GYTGGTAAGG AAGTTCTCGG      250
    TCGTATCATT AACGTCATTG GTGAACCCAT CGATGAACGT GGTCTTATCA      300
40  ACGCCAAGAG CCAACGTCCC ATTCACGCCG AAGCTCCCGA ATTCGTTGAC      350
    CAATCTCCTA CTCCCGAAAT TCTTGAAACT GGTATCAAGG TTGTCGACTT      400
    GTTGGCTCCT TATGCTCGTG GTGGTAAGAT TGGTCTTTTC GGTGGTGCTG      450
    GTGTCGGTAA GACTGTGTTG ATTCAAGAAT TGATTAACAA CATCGCCAAG      500
    GCTCACGGTG GTTACTCTAT TTTCTGTGCT GTCGGTGAAC GTACTCGTGA      550
45  AGGTAACGAT CTTTACCACG AAATGATTGA AACTGGTGTC ATCAAGCTCG      600
    ATGGTGACTC CAAGTGTGCT CTTGTCTTTG GTCAAATGAA CGAACCCCCA      650
    GGAGCTCGTG CCCGTGTTGC CTTGACTGGT TTGACCATTG CTGAATACTT      700
    CCGTGATGAT GAAGGTCAAG ATGTGTTGCT TTTCATTGAT AACATTTTCC      750
    GTTTCACCCA AGCTGGTTCW GAAGTATCTG CCCTTTTGGG TCGTATTTCC      800
50  TCCGCTGTGCG GTTACCAACC CACTCTTTCT ACTGATATGG GTGGTATGCA      850
    AGAACGTATT ACAACCACCA AGAACGGTTC CATTACATCC GTCCAAGCTG      900
    TCTACGTCCC TGCTGATGAT TTGACCGATC CTGCTCCCGC CACCACTTTT      950
    GCTCACTTGG ATGCCACCAC TGTCTTGTCT CGTTCCATTG CCGAATTGGG      1000
    TATTTACCCT GCCGTCGATC CTCTTGAYTC CAAGTCTCGT ATCTTGGATC      1050
55  CTCGTATCGT TGGTGACGAA CACTACAAGG TCGCTACCGA AGTTCAACAA      1100
    ATCCTTCAAA ACTACAAGTC TCT      1123

```

60 2) INFORMATION FOR SEQ ID NO: 775

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Scopulariopsis koningii*
 (B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

```

15  ATTCAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT      50
    GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG      100
    AAATGCAGGA GACTTCGGTC ATTACGCTCG AGGGCGAGTC CAAGGTGCGG      150
    CTTGTGTTTC GTCAGATGAA CGAGCCCCC GGTGCCCGTG CCCGTGTTCG      200
20  CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG      250
    ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG      300
    ACAACTAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG      350
    GTTCCGAGGT GTCCGCGCTT CTCGGCCGTA TCCCCTCTGC CGTCGGTTAC      400
    CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC      450
25  GACTCAGAAG GGCTCGATTA CCTCGGT                                477
  
```

2) INFORMATION FOR SEQ ID NO: 776

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

```

45  TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AAACAGAAGC      50
    TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT      100
    TCGAGTATTA ATTGTTTTTA TAGAACAAAC TTGCCAAGGC TCACGGTGGT      150
    TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT      200
    CTACCATGAA ATGCAGGAGA CCCGTGTCAT TCAGCTTGAT GGCGAGTCCA      250
50  AGGTCGCCCT GGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCGTGCC      300
    CGTGTGCTC TTACTGGTTT GACCATTGCT GAGTACTTCC GTGATGAGGA      350
    AGGTCAAGAC GGTGAGTTY TTATGGATAA AARATTTTTT TTTTTTTTTT      400
    TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT      450
    CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCGAA GTGTCTGCCC      500
55  TGCTTGGTCG TATCCCATCT GCCGTCGGTT ACCAACCAC TCTTGCCGTC      550
    GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT      600
    TACCTCCGTC                                610
  
```

2) INFORMATION FOR SEQ ID NO: 777

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

```

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAGAGAA CAGAAGCTAG      50
GTGAAAATTG GACAATTGAA CAATTTAGCC CTTGGAGAAA AGAAATTTTCG     100
AGTATTAATT ATTTTATAG AACAACTTG CCAAGGCTCA CGGTGGTTAC      150
20 TCTGTCTTCA CTGGTGTCTG AGAGCGTACC CGTGAAGGAA ACGATCTCTA     200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG     250
TCGCCCTGGT CTTCCGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT     300
GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG     350
TCAAGACGGT GAGTTTCTTA TGGATGAAAG ATTTTTTTTT TTCAAGAAAT     400
25 TCATGTTCTA ACAAAGTGTA TTCTAGTGCT TCTCTTCATC GACAACATTT     450
TCCGTTTCAC TCAGGCTGGT TCCGAAGTGT CTGCCCTGCT TGGTCGTATC     500
CCATCTGCCG TCGGTTACCA ACCCACTCTT GCCGTCGACA TGGGTGGTAT     550
GCAGGAACGT ATTACCACCA CCAAGAAGGG ATCCATTACC TCC              593

```

30

2) INFORMATION FOR SEQ ID NO: 778

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

```

CCGTGGTCAA GAAGTTATTG AACTGGTGC CCAATTACC ATTCCTGTTG      50
GTCGTGGTAC TCTTGGTAGA ATTATCAACG TCATTGGTGA ACCAATTGAC     100
50 GAACGTGGCC CTATCAAGGC TTCTAAGTAT GCTCCTATCC ATACTGAACC     150
ACCAACCTTT GCTGAACAAT CTACTTCTGC TGAAGTTCTT GAAACCGGTA     200
TCAAGGTTGT CGATCTTCTT GCTCCTTACG CCCGTGGTGG TAAGATTGGT     250
CTTTTCGGTG GTGCTGGTGT CGGTAAGACT GTCTTCATTC AAGAACTTAT     300
TAACAACATT GCCAAGGCTC ACGGTGGTTT CTCTGTCTTC ACTGGTGTCTG     350
55 GTGAAAGAAC CCGTGAAGGT AACGATCTTT ACCGTGAAAT GAAGGAAACT     400
GGTGTCAATCA ACCTCGAAGG TGAATCCAAG GTCGCTCTCG TTTTCGGTCA     450
AATGAACGAA CCTCCAGGTG CCCGTGCCCG TGTCGCTTTG ACTGGTCTTA     500
CCATTGCCGA ATACTTCCGT GATGAAGAAG GACAAGATGT CTTGCTTTTC     550
GTTGACAACA TTTTCAGATT CACCAAGGCC GGTCTCTGAAG TCTCTGCTCT     600
60 TTTGGGTCGT ATTCCATCTG CCGTCGGTTA CCAACCTACC CTTGCTACCG     650

```

	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCCGTC	700✓
	ACATCTGTCC	AAGCCGTCTA	TGTCCCAGCA	GACGATTTGA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
5	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTC	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
10	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 22864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

30	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTTCGAGAC	TCCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTAATGGTGA	GTTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
35	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACTTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTCT	TGCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
40	CTATCGACTC	CATCGACCCT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCCG	600
	CGGTCTGTGT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
45	CGTCTCCGTG	AAGGAGGTTC	GTCGTGGAAA	CGTTGCTGGT	GAATCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCCAGGT	CATCGTCCTC	850
	AACCACCTTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCCA	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
50	GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTCACCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

55 2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

10 TACTTGTAAG TGGTCTCAAG ATCGTTACAA CGAAATTGTT AAGGAAGTTT 50
 CTTCTTCAT CAAGAAGATT GGTACAATC CTAAATCCGT TCCTTTCGT 100
 CCTATCTCTG GTTGGCACGG TGATAACATG TTGGAAGCTT CTACCAACAT 150
 GCCTTGGTAC AAGGGATGGA CCAAGGAAAC TAAAGCTGGT TCTTCCACTG 200
 15 GTAAGACTCT CTTAGAAGCC ATTGACAGCA TTGAACCTCC TACCCGTCCT 250
 TCTGACAAGC CTTTACGTCT TCCTTTACAA GATGTTTACA AGATTGGTGG 300
 TATTGGTACT GTCCCTGTTG GTCGTGTTGA AACTGGTGTC ATCAAGGCTG 350
 GTATGGTTGT TACYTTCGCT CCCGCTAACG TCACCACTGA AGTTAAGTCC 400
 GTTGAAATGC ATCACAACA ATTAGAACA GGTGTTCTCT GTGACAACGT 450
 20 TGGTTTCAAC GTCAAGAACG TTTCCGTTAA GGATATCCGT CGTGGTAACG 500
 TCTGTTCCGA CTCCAAGAAC GACCCCGCTA AGGAATCTGC TTCCTTCAAC 550
 GCTCAAGTTA TCGTCTTGAA CCACCTGGT CAAATTGGTG CTGGTTATGC 600
 CCCAGTTCTT GACTGTCACA CTGCTCACAT TGCTTGTAAG TTCGCTGAAT 650
 TATTAGAAA GATCGATCGT CGTTCCGGTA AGAAACTCGA AGATGCTCCT 700
 25 AAATTCGTTA AATCTGGTGA CTCTGCTATC GTTAAGATGG TTCCTTCCAA 750
 GC 752

30 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

45 CAAGTGGTCT GAGGACCGTT ACCAGGAAAT CATCAAGGAG ACCTCCAAC 50
 TCATCAAGAA GGTCGGCTAC AACCCCAAGC ACGTTCCCTT CGTCCCCATC 100
 TCCGGTTTCA ACGGAGACAA CATGATTGAG GCCTCCACCA ACTGCCCTG 150
 GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC 200
 50 TCCTTGAGGC CATCGACGCC ATCGACCCTC CTGTCCGTCC TACCGACAAG 250
 CCCCTCCGCC TTCCCTCCA GGATGTTTAC AAGATTGGTG GTATTGGCAC 300
 GGTCCCGTC GGTGCTGTCG AGACCGGTAT CATCAAGCCC GGTATGGTCC 350
 TCACCTTCGC CCGCTGGT GTCACCACCG AAGTCAAGTC CGTCGAGATG 400
 CACCACGAGC AGCTTACTGA GGGTGTCCCC GGTGACAACG TCGGCTTCAA 450
 55 CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGGTAAC GTTGCCGGTG 500
 ACTCCAAGAA CGACCCCCC AAGGGTTGCG AGTCCTTCAA CGCCAGGTC 550
 ATCGTCCTCA ACCACCCTGG TCAGGTCGGT GCCGGTTACG CCCAGTCCT 600
 TGAAGCCAC ACTGCCACA TTGCCTGCAA GTTCTCCGAG CTCCTCGAGA 650
 AGATCGACCG CCGTACCGGA AAGTCTGTTG AGAACTCCCC CAAGTTCATC 700
 60 AAGTCCGGTG ACGCCGCCAT CGTCAAGA 728

2) INFORMATION FOR SEQ ID NO: 782

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

20	TGAAGTCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACTC	CCAAGTAAGG	CTCAACAGAC	ACAACAAGCA	AATGCATACT	100
	CGCTAACCTA	TTCACCCACC	ACAGGTACAA	CGTCACCGTC	ATTGACGCCC	150
	CCGGTCACCG	TGATTTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGCGCCA	TTCTCATCAT	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCCGG	250
25	TATCTCCAAG	GACGGTCAGA	CCCGTGAGCA	CGCTCTTCTC	GCCTACACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	350
	TGGTCTGAGG	CCCGTTACCA	GGAGATCATC	AAGGAGACCT	CCGGTTTCAT	400
	CAAGAAGGTC	GGCTTCAACC	CCAAGCACGT	TCCCTTCGTG	CCCATCTCCG	450
	GTTTCAACGG	TGACAACATG	ATCGACGTCT	CCACCAACTG	CCCCTGGTAC	500
30	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGCCATCG	ACCCCCCAC	TCGTCCCACC	GACAAGCCCC	600
	TCCGTCTTCC	CCTYCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGCACGGTT	650
	CCCGTCGGTC	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTCAC	700
	CTTCGCCCCC	GCTGGTGTCA	CCACTGAGGT	CAAGTCCGTC	GAGATGCACC	750
35	ACGAGCAGCT	TCCCCGAGGGT	CTCCCCGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGCAACGTCG	CCGGTGACTC	850
	CAAGAACGAC	CCCCCAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTCGGCGCCG	GCTACGCGCC	CGTCCTCGAC	950
	TGCCACACTG	CTCACATTGC	TTGCAAGTTC	TCTGAGCTCC	TCGAGAAGAT	1000
40	CGACCGCCGT	ACCGGCAAGT	CCATTGAGGC	CAGCCCCAAG	TTCATCAAGT	1050
	CTGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	TATGTGCGTT	1100
	GAGGCCTTCA	CCGACTACCC	CCCTCTTGA	CGTTTCGCCG	TCCGT	1145

45

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

60

	GCTCAAGGCT	GAGCGTGAGC	GTGGTATCAC	CATTGACATC	GCCCTCTGGA	50
	AGTTTCGAGAC	CCCCAAGTAC	ATGGTCACCG	TCATCGGTAT	GCTTTATCTG	100
	TTTCCCATT	ATAGTTGCGA	CAAGTAACATA	ATAAAAAGTA	GATGCCCCCG	150
5	GACACCGTGA	CTTCATCAAG	AACATGATTA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATTC	TCATCATTGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCT	TTCACCCTCG	300
	GTGTCAAGCA	GCTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAACTGG	350
	TCTGAGTCCC	GTTTCGGTGA	AATCATCAAG	GAAGTCACCA	ACTTCATCAA	400
10	GAAGGTCGGC	TACGACCCCA	AGGGTGTCCC	ATTCTGTCCT	ATCTCTGGCT	450
	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAAGTCCCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CACTCGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCACTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
15	GTACCAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	750
	ACCACCAGCA	GCTCGTTTCA	GGTGTTCCTG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAAGC	TCTCTGTCAA	GGAAGTCCGC	CGTGGTAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAAG	GCCCAGGTCA	900
20	TCGTCTCTCA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCGA	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
25	C					1151

2) INFORMATION FOR SEQ ID NO: 784

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Mucor circinelloides*
- (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

45	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GAAGGTAAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCCTTCTGA	250
50	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
	GTTGTCAACT	TCGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTTGA	400
	AATGCATCAC	GAAACCCCTC	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
55	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAATCATT	650
	GAGAAGATTG	ATCGTCGTTC	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
60	CTATAATGAT	GATTGCTCCT	TCAATTTTTG	ACATAATTTG	ATGATCTGAA	800

TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTA ^Δ GT	850
AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTCGTCAAG	TCTGGTGACT	950
CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

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2) INFORMATION FOR SEQ ID NO: 785

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1099 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Phialophora verrucosa*
 - 20 (B) STRAIN: ATCC 38561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
25 TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCCT	100
GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
30 GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
TTC AACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
TCGAGGCCAT	CGACGCGATT	GACCCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
35 CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
GCCCGTTGGT	CGTGTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCT	GCTTCAACGT	750
CAAGAACGTC	TCCGTCAAGG	AGGTTTCGTC	TGGAAACGTT	GCCGGTGACT	800
40 CCAAGAATGA	CCCCCCC AAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
GTCCTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
TCGATCGTCT	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
45 TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 55 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 60 (A) ORGANISM: *Saksenaea vasiformis*

448

(B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

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5  ACCACCAAGT GGTCTGAGGC CCGTTACCAG GAGATCATCA AGGAGACCTC      50
   CGGYTTCATC AAGAAGGTCG GCTTCAACCC CAAGCACGTT CCCTTCGTGC      100
   CCATCTCCGG TTTCAACGGT GACAACATGA TCGACGTCTC CACCAACTGC      150
   CCCTGGTACA AGGGTTGGGA GAAGGAGACC AAGGCCAAGG CCACCGGCAA      200
   GACCMTCCTC GAGGCCATTG ACGCCATCGA CCCCCCYAGY CGTCCCACCG      250
10  ACAAGCCCCCT YCGTCTTCCC CTMCAGGATG TYTACAAGAT TGGCGGTATT      300
   GGCACGGTTC CCGTCGGTCG TGTYGAGACC GGTRCCATCA AGGGTGGCAT      350
   GGTCGTCACC TTCCCCCCC CGTGGTGTCAC CACTGAGGTC AAGTCCGTCG      400
   AGATGCACCA CGAGCAGCTC GCCGAGGGTS TCCCCGGTGA CAACGTCGGC      450
   TTCAACGTCA AGAACGTCTC CGTCAAGGAG ATCCGTCGTG GCAACGTTGC      500
15  CGGTGACTCC AAGAACGACC CCCCCAAGGG CTGCGACAGC TTCAACGCCC      550
   AGGTCATCGT CCTCAACCAC CCCGGTCAGG TCGGCGCCGG CTACGCGCCS      600
   GTCCTSGACT GCCACACTGC TCACATTGCC TGCAAGTTCT CTGAGCTCCT      650
   CGAGAAGATC GACCGCCGTT CCGGCAAGTC CATCGAGTCC GGCCCCAAGT      700
   TCATCAAGTC TGGTGACGCC GCCATCGTCA AGATGGTTCC CTCCAAGCCC      750
20

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2) INFORMATION FOR SEQ ID NO: 787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
 (B) STRAIN: ATCC 32330

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

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GCTCAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA      50
40  AGTTCGAGAC CCCCAGGTAC CACGTCACCG TCATTGATGC CCCCAGGCCAT      100
   CGTGATTTC TCAAGAACAT GATCACTGGT ACCTCGCAGG CTGACTGCGG      150
   TATCCTCATC ATTGCCGCCG GTACTGGTGA GTTCGAGGCT GGTATCTCCA      200
   AGGATGGCCA GACCCGTGAG CACGCTCTGT TTGCCTTCAC CCTCGGTGTC      250
   CGTCAGCTGA TCGTCGCCAT CAACAAGATG GACTCGACCA AGTACTCTGA      300
45  GGCCCGTTAC AACGAAATCG TCAAGGAGGT CTCCACCTTC ATCAAGAAGA      350
   TCGGTTTCAA CCCCAGGTCC GTTCCCTTCG TCCCCATCTC TGGCTGGAAC      400
   GGTGACAACA TGTTGGAGGA GTCCTCCAAC ATGCCCTGGT TCAAGGGCTG      450
   GAAGAAGGAG ACCAAGGCTG GCGAGAAGTC CGGCAAGACC CTCCTTGAGG      500
   CCATTGACAA CATTGACCCC CCGGTCCGTC CCTCGGACAA GCCCCTCCGT      550
50  CTTCCCCTCC AGGATGTCTA CAAGATCGGT GGTATCGGCA CAGTCCCCGT      600
   CGGTCGTGTC GAGACTGGTG TCATCAAGGC TGGTATGGTC GTGACCTTCG      650
   CCCCCGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAGAT GCACCACGAG      700
   CAGCTCGTCG AGGGTGTCCC CCGTGACAAC GTCGGTTTCA ACGTCAAGAA      750
   CGTTTCCGTC AAGGATATCC GCCGTGGTAA CGTCTGCTCT GACTCCAAGA      800
55  ACGACCCCGC CAAGGAGTCT GCCTCGTTCA CCGCCCAGGT CATCGTCCTG      850
   AACCACCCCG GTCAGATCGG TGCCGGTTAC GCCCCGGTTC TTGACTGCCA      900
   CACCGCTCAC ATTGCCTGCA AGTTCGCTGA GTCCTCGAG AAGATCGACC      950
   GTCGTTCCGG YAAGAAGCTC GAAGAGTCCC CCAAGTTCGT CAAGTCGGGT      1000
   GACTCCGCCA TCGTCAAGAT GGTTCCTTCC AAGCCCATGT GCGTTGAGGC      1050
60  CTACACTGAG TACCCCCCTC TTGGCCGTTT CGCC      1084

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2) INFORMATION FOR SEQ ID NO: 788

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

20	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTTCGAGAC	CCCCAAGTAC	AATGTCACCG	TCATTGGTAT	GTTTTTCTTT	100
	ACCTTTCCCC	TCCATCGTCT	TGCTGTGCCA	TAACATAACGA	GAGTAGACGC	150
	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	200
	CTGACTGTGC	TATTCTCATC	ATTGCTGCCG	GTACTGGTGA	GTTCGAGGCT	250
25	GGTATCTCCA	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TCGCCTTCAC	300
	CCTTGGTGTC	AAGCAGCTCA	TCGTTGCCAT	CAACAAGATG	GACACCACCA	350
	ACTGGTCCGA	GGACCGTTTC	AAGGAAATCA	TCAAGGAAGT	CACCAACTTC	400
	ATCAAGAAGG	TTGGCTACGA	CCCCAAGGGT	GTTCCATTCT	TTCCAATCTC	450
	TGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCAGCAAC	TGCCCATGGT	500
30	ACAAGGGATG	GAACAAGGAG	ACCAAGGCCG	GTGGTGCCAA	GACTGGCAAG	550
	ACCCTYCTCG	AGGCCATCGA	TGCCATCGAC	ATGCCAACCC	GTCTTACCGA	600
	CAAGCCCCTY	CGTCTCCAC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	650
	GAAGTGTACC	AGTCGGTCGT	GTTGAGACCG	GTATCATCAA	GCCTGGTATG	700
	GTCGTACACT	TCGCCCCCTG	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	750
35	AATGCACCAC	CAGCAGCTTC	AGCAGGGTGT	CCCCGGTGAC	AACGTCGGCT	800
	TCAACGTCAA	GAACGTTTCC	GTCAAGGAAG	TCCGCCGTGG	TAACGTTGCC	850
	GGTGACTCCA	AGAACGACCC	ACCATCCGGC	TGTGCCTCCT	TCAACGCCCA	900
	GGTCATCGTC	CTCAACCACC	CCGGCCAGAT	CGGTGCTGGT	TACGCCCCAG	950
	TCCTCGACTG	CCACACTGCT	CACATTGCTT	GCAAGTTCGC	TGAGCTCCTC	1000
40	GAGAAGATTG	ACCGCCGTAC	CGGTAAATCC	GTCAAGCCA	ACCCCAAGTT	1050
	CGTCAAGTCT	GGTGATGCCG	CTATCGCCAA	GATGGTTCCC	TCCAAGCCCA	1100
	TGTGCGTTGA	GGCTTTCAC	GACTACCCCC	CACCTGGTTC	TTTCGCCGTC	1150
	CGTGA					1155

45

2) INFORMATION FOR SEQ ID NO: 789

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

	TCAAGGCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACCC	CCAAGTACAA	TGTCACCGTC	ATTGGTATGT	TTCTCTTTAC	100
5	CTTTCCCTC	CATCGTCTTG	CTGTGCCATA	ACTAACGAGA	GTAGACGCCC	150
	CCGGTCACCG	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGTGCTA	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	250
	TATCTCCAAG	GATGGCCAGA	CCCGTGAGCA	CGCTCTGCTC	GCCTTCACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	350
10	TGGTCCGAGG	ACCGTTTCAA	GGAAATCATC	AAGGAAGTCA	CCAACTTCAT	400
	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTCGTT	CCAATCTCTG	450
	GTTTCAACGG	TGACAACATG	ATTGAGGCCCT	CCACCAACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
15	AGCCCCCTCCG	TCTCCCCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCCTGCCA	ACGTCAACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCAAGA	GCAGCTTCAG	CAGGGTGTC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	850
20	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCTCCTTC	AACGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAC	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGGTTCCATC	CAAGCCTATG	1100
25	TGCGTTGAGG	CTTTCACTGA	CTACCCCCCA	CTTGGTTCG		1138

2) INFORMATION FOR SEQ ID NO: 790

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Bipolaris hawaiiensis*
- (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

45	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCCTACC	250
50	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCCGTA	350
	TGGTCGTCAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
55	CCGGTGACTC	CAAGAACGAC	CCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748
60						

2) INFORMATION FOR SEQ ID NO: 791

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Aspergillus fumigatus*
 15 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

	CGCTATTGTC	GTTGTTGCTG	CCTCCGACGG	TCAGATGTAG	GTGGAACATC	50
20	TTGGGAAATA	CGTCGTAAAA	CACGGCGCTT	ACGTTTTTCGC	GAATAGGCCC	100
	CAGACTCGTG	AGCATTGCT	GCTCGCCCGC	CAGGTTGGTG	TCCAGAAGAT	150
	CGTTGTCTTC	GTCAACAAAA	TCGATGCTAT	TGATGATCCG	GAGATGCTGG	200
	AACTGGTCGA	ACTCGAGATG	CGTGAGCTGC	TGAACAGCTA	CGGTTTCGAG	250
	GGTGAAGAGA	CTCCGATCAT	TTTCGGTTCC	GCTCTCTGTG	CTCTCGAAGG	300
25	ACGCCGTGAC	GACATCGGTA	AAGACAGAAT	TGAGCAGCTT	ATGAACGCTG	350
	TCGACACCTG	GATCCCCACT	CCTCAGCGTG	ACCTCGACAA	ACCTTTCTTG	400
	ATGTCTGTCTG	AGGAAGTGT	CTCTATCGCC	GGCCGTGGTA	CCGTGGCTTC	450
	TGGTCGTGTC	GAGCGTGGTA	TCTTGAAGAA	GGACTCTGAG	GTTGAGATTG	500
	TTGGAGGCTC	CTTCCAACCC	AAGAAGACCA	AAGTCACCGA	CATTGAAACC	550
30	TTCAAGAAGA	GCTGTGATGA	ATCGCGTGCT	GGTGACAACT	CTGGTCTCCT	600
	CCTGCGTGGT	ATCCGACGTG	AAGACGTCAA	GCGTGGTATG	GTCATTGCTG	650
	TTCCCGGCAG	CACCAAAGCT	CACGACAAGT	TCCTCGTCTC	CATGTACGTC	700
	CTGACCGAGG	CGGAGGGTGG	TCGTCGTACT	GGCTTCGGTG	CCAACACCG	750
	TCCCCAAGTC	TTCATCCGTA	CTGCAGGTAA	GTTCCCGCAC	ACCGTGTCCA	800
35	GATCTTCCGA	GAGATTAGCG	ATATATGCTA	ATGATTCATC	AGACGAGGCT	850
	GCTGACCTCA	GCTTCCCTGA	CGGCGACCAA	TCTCGCAGAG	TTATGCCTGG	900
	TGACAACGTC	GAGATGATCC	TGAAGACCCA	CCACCCTGTT	GCTGCTGAGG	950
	CTGGTCAA					958

40

2) INFORMATION FOR SEQ ID NO: 792

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

	CGTTGTGCGA	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACG	50
	GATGAAAGGA	TTTGACGTTT	CTAACATCAT	TCTAGGCCTC	AGACCAGAGA	100
60	ACATTTGCTC	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	150

	TTAACAAGGT	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	200
	CTTGAAATGC	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	250
	CCCCATCATT	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	300
	AGCTTGGTGT	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	350
5	ATCCCCACCC	CCGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	400
	GGAAGTGTTC	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	450
	AGCGTGGTAT	CCTCAAGAAG	GATTCCGACG	TCGAAATTGT	TGGTGGCTCT	500
	ACCACCCCTA	TCAAGACCAA	GGTCACAGAT	ATCGAAACCT	TCAAGAAGTC	550
	CTGCGATGAA	TCTCGAGCTG	GTGACAACTC	TGGTCTCCTT	CTCCGAGGTA	600
10	TCAAGCGTGA	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	650
	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTGCTA	ACTTGATTTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	850
15	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTCG	TGCCGA		936

20 2) INFORMATION FOR SEQ ID NO: 793

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

35

2) INFORMATION FOR SEQ ID NO: 794

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

50

GACGACAAGT CGGTGAACTT

20

55 2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

453

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

10 ACTTGCACGC GATGTGGCAG

20

2) INFORMATION FOR SEQ ID NO: 796

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

25

GGTCCAATGC CWCAAACWAG A

21

30 2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT

27

45

2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

60

TGTTGTCCC AGCCGATCGT TT

22

5 2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

20 ACCTGTGAAT ACAAGCAATC T

21

2) INFORMATION FOR SEQ ID NO: 800

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

40 GATGAAATCT TCAACGAAGT TGAT

24

2) INFORMATION FOR SEQ ID NO: 801

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

60 ACAACACCGA GAAGATCCCA

20

2) INFORMATION FOR SEQ ID NO: 802

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

TTGCCATTTC TGGTTTCGTT 20

20 2) INFORMATION FOR SEQ ID NO: 803

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

35 ACTTCAGTGG TAACACCAGC 20

40 2) INFORMATION FOR SEQ ID NO: 804

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

55 CCTGGGACGG CCTCTGGCAT 20

2) INFORMATION FOR SEQ ID NO: 805

- 60 (i) SEQUENCE CHARACTERISTICS:

456

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTCCTA TCTTAGCAGT

20

15

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

35

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

AAAGTGGCTT CAAAGGTGCT

20

55

2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

457

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

10

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

25

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

40

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

55

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

458

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

10 GTIACIGGIT CYTYRARRTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 813

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

25 AATCYGTYGA AATGCAYCAC GA 22

2) INFORMATION FOR SEQ ID NO: 814

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814
GCIGGCACGT ACACIGCCTG 20

45 2) INFORMATION FOR SEQ ID NO: 815

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815
TGGTGCATYT CKACRGACTT 20

60

2) INFORMATION FOR SEQ ID NO: 816

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

20

15

2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

20

30

2) INFORMATION FOR SEQ ID NO: 818

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

45 AGCCGGGCTG GATCTTCTTC

20

50

2) INFORMATION FOR SEQ ID NO: 819

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

60

TCGAGCTTCT GGAGGAAGAG

20

5 2) INFORMATION FOR SEQ ID NO: 820

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

20 GAAGGAGGTG TCTGCTTACA C

21

25 2) INFORMATION FOR SEQ ID NO: 821

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

40 GGCGCAAACG TCACCACATC A

21

45 2) INFORMATION FOR SEQ ID NO: 822

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

60 CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

15 GAGCGGTATG AYGAGATTGT 20

2) INFORMATION FOR SEQ ID NO: 824

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

30 GGCTTCTGCG GCACCATGCG 20

2) INFORMATION FOR SEQ ID NO: 825

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

45 ATGAGCARCG SAACCATCGT TCAGTG 26

50 2) INFORMATION FOR SEQ ID NO: 826

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

TCGATCGTGC CGACCATGTA GAACGC

26

5

2) INFORMATION FOR SEQ ID NO: 827

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 446 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium novyi*
- (B) STRAIN: ATCC 19402

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

	CACCAACTTG	CTAAATGGGG	AGATGCCCAG	ATTGTTGTAT	ATATAGGCTG	50
	TGGAGAACGT	GGAAATGAAA	TGACAGATGT	TCTTAATGAG	TTTCCAGAAC	100
	TTAAAGATCC	TAAGACTGGC	AAATCAATAA	TGGAAAGAAC	AGTTTTAATA	150
25	GCAAATACTT	CTAATATGCC	AGTTGCAGCC	CGTGAAGCTT	GTATATATAC	200
	AGGAATCACA	ATAGCAGAAT	ATTTTAGAGA	TATGGGATAT	TCAGTAGCAC	250
	TTATGGCGGA	TTCCACTTCA	CGTTGGGCAG	AGGCATTAAG	AGAAATGTCT	300
	GGAAGACTTG	AAGAAATGCC	TGGTGTATGAA	GGTTACCCAG	CTTATTTAGG	350
	ATCAAGACTT	GCTGATTTCT	ATGAAAGAGC	TGGAAAAGTT	GTGTGTTTAG	400
30	GAGACGATGA	AAGAGAAGGT	GCCATTACTG	CAATAGGTGC	TGTATC	446

35 2) INFORMATION FOR SEQ ID NO: 828

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: 9689

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

50	CAGCATCAGC	TTGCTAAATG	GGCAGATGCA	GATATAGTTG	TATATATAGG	50
	CTGTGGCGAG	CGTGGAAATG	AAATGACAGA	TGTTCTTCTT	GAATTTCCCTG	100
	AATTAAAGA	CCCAAGAACA	GGCGAGTCAC	TTATGCAAAG	AACTGTGCTT	150
	ATAGCAAATA	CATCAGATAT	GCCGGTTGCT	GCACGTGAAG	CTTCTATATA	200
	CACTGGTATT	ACAATAGCTG	AATATTTTAG	AGATATGGGA	TATAGTGTTG	250
55	CACTTATGGC	AGACTCTACA	TCAAGATGGG	CTGAGGCTCT	TAGAGAGATG	300
	AGTGGTCGTT	TAGAGGAGAT	GCCTGGTGAA	GAAGGTTATC	CTGCATACTT	350
	AGGTTACAGT	CTTGCTCAAT	TCTATGAGAG	AGCAGGAAAG	GTAAATTGTC	400
	TAGGTATGGA	TGAAAGAGAA	GGAACACTTA	CAGCAATTGG	TGCAG	445

60

2) INFORMATION FOR SEQ ID NO: 829

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

	ATGCTATAGC	TAAATGGGGA	GACAGCGAAA	TAGTTGTTTA	CGTTGGATGT	50
	GGAGAACGTG	GTAACGAAAT	GACAGACGTT	CTTAACGAAT	TCCCAGAACT	100
20	TATTGACCCA	AAAAC TG GGG	AAAGTTTAAT	GAAGAGAACA	GTACTTATAG	150
	CCTAATACTTC	AAACATGCCA	GTTGCTGCTA	GAGAAGCTTG	CATATACACA	200
	GGTATTACAA	TAGCTGAATA	CTTCAGAGAT	ATGGGATACT	CAGTATCTAT	250
	AATGGCTGAT	TCAACTTCAA	GATGGGCAGA	AGCATTAAGA	GAAATGTCAG	300
	GTAGACTTGA	AGAAATGCCA	GGTGATGAAG	GATATCCAGC	GTACTTAGGA	350
25	TCAAGACTTG	CTGATTATTA	CGAAAGAGCA	GGTAAGGTTG	TTTGTCTAGG	400
	TAAAGATGGT	AGAGAAGGTG	CTGTAACAGC	AATTGGAGCT	GTATC	445

30 2) INFORMATION FOR SEQ ID NO: 830

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 444 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

45	TCAAATTGCT	AAATGGGGAG	ATGCAGAAAT	CGTTGTTTAC	GTTGGATGCG	50
	GAGAACGTGG	TAACGAAATG	ACAGACGTTG	TTAATGAGTT	CCCAGAACTT	100
	ATTGACCCTA	AGACTGGCGA	AAGCTTAATG	AAGAGAACAG	TTCTTATAGC	150
	TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
50	GTATCACAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
	ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
	TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
55	AATGATGGAA	GAATTGGTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

2) INFORMATION FOR SEQ ID NO: 831

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 456 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: ATCC 13124

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTC	TTAACGAATT	100
15	CCCAGAACTT	AAAGACCCCTA	AAACTGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
20	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
	TATCCC					456

25 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

40	CCAAGTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAACTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
45	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350
	CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
	CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

50

2) INFORMATION FOR SEQ ID NO: 833

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 5 (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

```

10 TGAACCAAGG AAAAATAATA ACCGTTTCGG GACCTCTTGT TGTGGCTTCT 50
   GGGATGCAAG AAGCTAATAT TCAAGATATT TGTCGTGTGG GACATCTTGG 100
   CTTAGTCGGA GAAATTATTG AAATGCGTCG CGATCAAGCG TCTATTCAGG 150
   TTTATGAGGA AACATCAGGG ATCGGTCCAG GAGAACCAGT AGTGACTACT 200
   GGTGTGCTCT TGTCGGTCGA GTTAGGCCCG GGCCTGATTT CAGAAATGTT 250
   TGACGGTATT CAGCGACCGC TTGATCGTTT TCAAAAAGCA ACGGACAGCG 300
15 ACTTTTTAAT CCGTGGTGTG GCTATCCCAA GTCTTGATCG AAAGGCTAAG 350
   TGGGCATTTA TTCCCAAGCT AAGTGTTGGT CAAGAAGTAG TTGCAGGTGA 400
   TATTTTAGGA ACTGTGCAAG AACAGCTGT CATTGAGCAC CGTATCATGG 450
   TTCCTTATAA AGTTTCAGGG ACCTTGTTGG CTATTCATGC AGGGGACTTC 500
   ACAGTAACAG ATACAGTTTA TGAAATTAAG CAGGAAGACG GTTCCATTTA 550
20 CCAAGGTAGC CTCATGCAGA CTTGGCCAGT TCGTCAAAGT CGCCCTGTTG 600
   CTCAAAGCT TATCCCAGTC GAACCTTTGG TTACAGGTCA ACGGGTTATT 650
   GACACCTTTT TCCCTGTTAC AAAAGGTGGT GCCGCTGCCG TTCCTGGACC 700
   ATTTGGGGCA GGAAAAACAG TTGTGCAGCA TCAAATAGCT AAATTTGCCA 750
   ACGTTGATAT TGTTATTTAT GTCGGTTGTG GGGAACGCGG CAACGAGATG 800
25 ACCGACGTTT TGAATGAGTT TCCAGAGTTA ATTGACCCAA ATACAGGCCA 850
   GTCCATTATG GAGCGCACGG TGTTAATTGC AAACACCTCT AATATGCCAG 900
   TAGCAGCGCG TGAAGCGTCG ATTTACACAG GTATTACCAT TGCCGAATAT 950
   TTCCGTGATA TGGGCTATTC TGTGGCTATC ATGGCAGACT CGACATCACG 1000
   TTGGGCAGAA GCTCTGCGCG AGATGTCAGG ACGCCTACAA GAAATGCCTG 1050
30 GTGATGAAGG CTACCCGGCT TACTTAGGGA GTCGTATTGC CGAATATTAT 1100
   GAACGGGCTG GTCGTGTTCT GACCTTGGGA AGTCAAGAAC GTGAGGGAAC 1150
   CATTACAGCC ATCGGCGCGG TTTCTCCTCC TGGAGGGGAT ATTTCAGAGC 1200
   CTGTCACTCA AAACACCTT CGGATTGTCA AAGTTTCTG GGGGCTCGAC 1250
   GCGCCTCTTG CGCAACGGCG TCACTTCCCA GCGATTAAC TGGCTGACGTC 1300
35 TTATTCATTG TATCAAGATG ATGTAGGAAG CTATATTGAC CGTAAACAGC 1350
   AATCTAATTG GTCCAACAAG GTAACCTGTG CCATGGCTAT TTTGCAGCGT 1400
   GAAGCCAGTC TAGAAGAAAT TGTACGCTTG GTGGGGCTTG ATTCACTGTC 1450
   TGAACAAGAT CGTTTGACCA TGGCTGTTGC CCGGCAAATT CGGGAGGATT 1500
   ATCTCCAGCA AAATGCCTTT GATTGCGGTG ATACCTTTAC TTCCTTTCCG 1550
40 AAACAAGAGG CCATGCTAAC CAATATTTTG ACCTTTAATG AGGAAGCCAG 1600
   CAAAGCCCTT TCTTTGGGAG CTTATTTTAA TGAGATTATG GAAGGCACTG 1650
   CTCAGGTACG CGATCGCATC GCACGCAGCA AATTTATCCC AGAAGAAAAC 1700
   TTAGAGCAGA TTAAAGGGCT TACTCAGAAG GTTACCAAAG AGATTCACCA 1750
   CGTTTTAGCA AAGGGAGGAA TTTAGATGAG CGTTCT 1786
45

```

2) INFORMATION FOR SEQ ID NO: 834

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 60 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

```

5  TATCTCACGT AAGTTTTTGC GCGGCGGTTA TATATCACTC CAGGCCCTGG      50
   CTAAGTACGC TAATACTGAC GTTACTGTCT ATGTGGGATG TGGAGAGCGT      100
   GGAAACGAGA TTGCGGAGGT GCTTAAGGAG TTCCCTGAGC TGAAGACCAA      150
   GGTGTGATGGC AAGGAAGTGA GCATTATGAA ACGCACTTGC TTGGTGGCCA      200
   ATACTTCAAA CATGCCAGTG GCCGCCAGGG AGGCTAGTAT CTACACTGGC      250
   ATTACCCTAT GTGAATACTT CAGGGATATG GGATACAACG CCTGTGTGAT      300
10  GCGCGATTCC ACCAGTCGTT GGGCTGAGGC TTTGCGTGAG ATATCAGGTC      350
   GTTTAGCTGA GATGCCTGCT GATTCAGGTT ATCCCGCCTA CCTTGCTTCT      400
   AGGCTTTTCG CGTTCTATGA GCGTGCTGGT ACAGCTGAGT GTATTGGAAC      450
   ACCACTTCGT GAAGGTTTCA TTACCATTGT TGGTGCTGTA TCTCCACCA      499

```

15

2) INFORMATION FOR SEQ ID NO: 835

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 464 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

```

   TTTCTCAAGC TTTGAGTAAA TATAGTAACT CTGATGTTAT TATTTACATT      50
   GGTGTGAGAG AAAGAGGAAA TGAAATGGCA GAAGTTCTTA CAGAATTCCC      100
   TGAGCTTTAT ACTATGGTTG ATGGAAAGAA GGAGTCAATT ATGCAAAGAA      150
35  CTTGTTTAGT AGCTAATACA TCAAATATGC CTGTCGCTGC TAGAGAAGCT      200
   TCCATCTACA CTGGTATTAC ACTTTCTGAA TACTTTAGAG ATATGGGATG      250
   TAATGTTTCT ATGATGGCAG ATTCAACTTC TCGTTGGGCT GAAGCTCTTA      300
   GAGAAATTTT TGGTAGATTA GCTGAAATGC CTGCAGATTC GGGTTACCCA      350
   GCATATTTAG GCGCCAGACT TGCTTCATTC TATGAAAGAT CAGGAAGAGT      400
40  TAAATGTATG GGTTCCTCCAG ATAGAGAAGG TACAGTAACA ATTGTTGGTG      450
   CAGTTTCTCC ACCT                                     464

```

45 2) INFORMATION FOR SEQ ID NO: 836

3)

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

60

GCCCTCTCCA AGTACTCCAA CTCCGATTGC GTCATCTATG TCGGCTGCGG 50
 CGAGCGCGGT AATGAGATGG CCGAGGTGCT CATGGAGTTC CCGACCCTGA 100
 CGACCGTGAT CGATGGCCGC GAGGAGTCGA TCATGAAGCG CACCTGCCTC 150
 GTGGCGAACA CCTCGAACAT GCCAGTCGCA GCCCCGTGAGG CCTCTATTTA 200
 5 CACCGGCATC ACCCTGGCCG AGTACTACCG TGATATGGGC AAGCATATCG 250
 CCATGATGGC TGA CTGACG TCTCGCTGGG CCGAGGCGCT TCGTGAGATT 300
 TCGGGTCGTC TGGCGGAGAT GCCGGCGGAT GGTGGCTACC CCGCCTACCT 350
 CAGCGCTCGT CTCGCCTCCT TCTACGAGCG CGCCGGCCTC GTCACCTGCA 400
 TCGGCGGGCC GAAGCGCCAG GGCTCCGTCA CGATCGTCGG TGCCGT 446
 10

2) INFORMATION FOR SEQ ID NO: 837

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 25 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

TTAGTCAGGC CCTCTCCAAG TACTCCAAC TCCGACTGCGT CATCTATGTC 50
 30 GGCTGCGGCG AGCGCGGTAA TGAGATGGCT GAGGTGCTCA TGGATTTCCT 100
 AACTCTGACG ACCGTGATCG ATGGTCGCGA GGAGTCCATC ATGAAGCGCA 150
 CCTGCCTCGT GGCAAACACT TCGAACATGC CAGTCGCAGC CCGCGAGGCC 200
 TCTATTTACA CCGGCATCAC CCTGGCCGAG TACTACCGTG ATATGGGCAA 250
 GCATATTGCC ATGATGGCCG ACTCGACATC TCGCTGGGCC GAGGCGCTTC 300
 35 GTGAGATTTT CGGTCGTCTG GCGGAGATGC CAGCCGATGG TGGCTACCCT 350
 GCCTACCTCA GCGCTCGTCT CGCCTCCTTC TACGAGCGCG CCGGCCTCGT 400
 CACCTGCATC GGCGGGCCGA AGCGCCAGGG CTCCGTCACG ATCGTCGGTG 450
 CTGTGT 456

40

2) INFORMATION FOR SEQ ID NO: 838

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 55 (B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

AGGCCCTCTC CAAGTACTCC AACTCCGACT GCGTCATCTA CGTCGGCTGC 50
 GGCGAGCGCG GTAATGAGAT GGCCGAGGTG CTCATGGAGT TCCCGACCCT 100
 60 GACGACTGTG ATTGATGGCC GTGAGGAGTC GATCATGAAG CGGACCTGCC 150

	TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
	TACACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
	CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
	TTTCGGGTCG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
5	CTTAGTGCTC	GTCTTGCTC	CTTCTACGAG	CGTGCCGGCC	TCGTCACCTG	400
	CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

10 2) INFORMATION FOR SEQ ID NO: 839

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 bases
 - (B) TYPE: Nucleic acid
 - 15 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trypanosoma brucei*
 - (B) STRAIN: EATRO 795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

25	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGGC	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
30	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
35	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

2) INFORMATION FOR SEQ ID NO: 840

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trypanosoma cruzi*
 - 50 (B) STRAIN: MM3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
55	TTCGAGTCGC	CCAAGTCTGT	GTTACGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
60	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350

	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
5	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
10	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTC	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
15	CC					1052

2) INFORMATION FOR SEQ ID NO: 841

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

35	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTCGAGTCGC	CCAAGTCTGT	GTTACAGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCGCCC	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
40	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
	AAGTTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
45	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
50	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
55	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

60 2) INFORMATION FOR SEQ ID NO: 842

470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

```

15 GCTGAAGGCT GAGCGCGAGC GCGGCATCAC GATCGACATC GCGCTCTGGA      50
   AGTTCGAGTC GCCCAAGTCT GTGTTACAGA TCATCGACGC CCCCGGCCAC      100
   CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCTCAGG CGGACGCCGC      150
   CGTCCTTGTC ATTGCGTCAT CGCAGGTGA GTTTGAGGCG GGCATCTCGA      200
20 AGGACGGCCA GACACGCGAG CACGCGCTGC TCGCCTTCAC GCTCGGCGTG      250
   AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGT CGGTGAAGTT      300
   CGCCCAGGAG CGCTACGATG AGATTGTGAA GGAGGTGTCT GCGTACCTGA      350
   AGAAGGTTGG GTACAACGTG GAGAAGGTGC GCTTCATCCC CATCTCCGGC      400
   TGGCAGGGCG ACAACATGAT TGACAAGTCG GAAAATATGC CGTGGTACAA      450
25 GGGCCCCACG CTGCTGGAGG CACTCGACAT GCTGGAGCCC CCGGTGCGCC      500
   CCAGCGACAA GCCGCTGCGC CTGCCGCTGC AGGACGTGTA CAAGATCGGC      550
   GGTATCGGCA CCGTGCCGGT CGGTCGCGTG GAGACGGGCA CGATGAAGCC      600
   CGGCGACGTG GTGACGTTTG CGCCCGCCAA CGTGACGACG GAGGTGAAGT      650
   CGATTGAGAT GCACCACGAG CAGCTGGCCG AGGCCACGCC CGGCGACAAC      700
30 GTCGGCTTCA ACGTGAAGAA CGTGTCCTG AAGGACATCC GCCGTGGCAA      750
   CGTGTGCGGC AACTCGAAGA ACGACCCCCC AAAGGAGGCG GCCGACTTCA      800
   CGGCGCAGGT GATCATCCTG AACCACCCCG GCCAGATCGG CAACGGCTAT      850
   GCGCCGGTGC TCGACTGCCA CACCTGCCAC ATCGCGTGCA AGTTCGCCGA      900
   GATCGAGTCC AAGATCGACC GCCGCTCCGG CAAGGAGCTT GAGAAGAACC      950
35 CCAAGTCGAT CAAGTCCGGT GACGCCGCCA TGGTGCGCAT GGTGCCGCAG     1000
   AAGCCCATGT GCGTGGAGGT GTTCAACGAC TACGCTCCTC TTGGCCGCTT     1050
   TGCCGTGCGT GA                                     1062

```

2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

```

TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCATGGCG      50
AGTACACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT      100
GGTATTACTA TAAATTCGAC ACATGTTGAA TATGAGACTA AGAACCGTCA      150
60 TTACGGTCAC GTGGACTGTC CAGGTCACTC TGATTATGTG AAGAACATGA      200

```

	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTGTT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTTCGTG	GTTATTGAGT	400
5	GAGTTTGGTT	ACGACGGTGA	CAACACGCCT	ATCGTTCGTG	GCAGTGCTAT	450
	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTC	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTTCGT	TGTGGTGACC	650
10	CTATTGAGGT	TTGCGCCGGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750
	GATTGGTGTT	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGCGCGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTTGATGCT	850
	GACTTGTAAC	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
15	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

20

2) INFORMATION FOR SEQ ID NO: 844

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 943 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
40	TTCATCAACA	AAGTGGATAT	GACGAGCAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGCTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
45	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTGCGC	550
	ACCGGCGACA	CAACCAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
50	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACC GGGA	GGAGCTGAAC	AAGAAATTCTG	800
	GCCGCGGCCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
55	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTCGCGTAC	CCGATGCCCA	TTGAAAAGGG	CCTGAAGTTC	ACC	943

60 2) INFORMATION FOR SEQ ID NO: 845

472

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

15	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCATCT	CTTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
20	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAAG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AATGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
25	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGC	550
	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
30	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACC CGGA	GGAGCTCAAC	AAGAAATTTCG	800
	GCCGCGGCCC	CGAGGAGGAC	AAGCAGAAAG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGACAAGGG	TCTGAAGTT		939

2) INFORMATION FOR SEQ ID NO: 846

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

55	CATTGTGGTG	GCGGCCACCG	ACGGCGTCAT	GCCGCAGACA	CGCGAGCACC	50
	TCCTGATCTG	CTCGCAGATC	GGGCTTCCGG	CGCTCGTAGG	GTTCATCAAC	100
	AAGGTGGACA	TGACGGACGA	GGACACGTGC	GACCTGGTGG	ACATGGAGCT	150
	GCGCGAGCAG	CTGGAGAAAT	ACAAGTTTCC	GGCGGAGGAG	ACGCCAATCG	200
	TGCGCGGCTC	AGCCCTCAAA	GCCGTCGAGG	GCGATGCGAA	GTACGAGGAG	250
	AACATTCTCG	AACTGGTGCG	GAAGTGTGAC	GAGTGGATCC	CTGACCCGCC	300
60	GCGCAACACA	GACAAGCCTT	TCCTTATGGC	CATCGAGCAC	GTTTACGAGA	350

	TCGGCAAGGA	CAAGAAGAGC	GTTGTCGTGA	CCGGCCGCGT	CGATCAAGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTCGACGGTG	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCATGCC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCGG	GACCGGCGAC	550
5	ACGACCAGTC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
	GACGGGTAGC	ACGAACCTGT	ACAACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCACTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACCGCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
10	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900
	CCCGATGCCC	ATTGAAAAGG	GTCTGAAGTT	CACCATCCGT	GAGGG	945

15

2) INFORMATION FOR SEQ ID NO: 847

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
- (B) STRAIN: MOU

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	GCACCTCCTG	ATCTGCTCGC	AGATCGGGCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAGGT	GGACATGACG	GACGAGGACA	CGTGCGACCT	GGTGGACATG	150
35	GAGCTGCGCG	AGCAGCTGGA	GAAATACAAG	TTCCGGCGCG	AGGAGACGCC	200
	AATCGTGCGC	GGCTCAGCCC	TCAAAGCCGT	CGAGGGCGAT	GCGAAGTACG	250
	AGGAGAACAT	TCTCGAACTG	GTGCGGAAGT	GTGACGAGTG	GATCCCTGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTTGT	CGTGACCGGC	CGCGTCGATC	400
40	AGGGCGTTCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCTCC	450
	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATC	GAGATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCTGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTATCC	AAGGGCAACG	TGGAACGCGG	CATGGTGATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
45	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTT	AGTCCTCACT	700
	ACCGCCCGCA	GCTCTTCTTC	CATTGTGCTG	ACGTGACGGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAAGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	AGCGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
50	GCGTACCCGA	TGCCCATTTGA	AAAGGGTCTG	AAGTTCACC		939

2) INFORMATION FOR SEQ ID NO: 848

55

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 933 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

```

10 CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC      50
   AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG      100
   GACGAGGATA CGTGCGACCT CGTGGACATG GAGGTGCGGG AACAGCTGGA      150
   GAAGTACAAG TTTCCGGCCG AGGAGACGCC CATCGTACGT GGCTCGGCCC      200
   TCAAGGCCCT CGAGGGGGAT GCGCAATACG AGGGGAGTAT TCTCGAGCTG      250
15 GTGCGAAAGT GCGACGAGTG GATCCCCGAC CCGCCGCGCA ACACCGAAAA      300
   GCCTTTCCTC ATGGCTATCG AGCACGTTTA CGAGCTCGGC AAAGACAAGA      350
   AGAGCGTCAT CGTTACCGGC CGCGTCGATC AAGGTGTGCT GAAGCTCAAC      400
   ACAGACGCCG AGCTGGCCGG CTTCAGCGCC AAGAAGGCGA CAGTCAAAGT      450
   GACGGGCATC GAGATGTATC ACAAGACACT CAATGAGTGC ATGCCCGGCG      500
20 ACTCTGTCGG TGTACGATC GTCGGTACCG GTGACACGAC CAGCTTATCC      550
   AAGGATAATG TTGAGCGCGG TATGGTAATG GCGGCAACGG GTAGCACGAA      600
   CCTGTACAAC AAGCTGAAGG CGCAGGTTTA CGTGCTGACA AAGGAGGAGG      650
   GTGGCCGCCA CACCGGGTTC AGCCCCACT ACCGCCCGCA GCTCTTCTTC      700
   CACTGCGCTG ACGTGACCGC AGACATGAGC TTCCCGGAGG CGGAGAAGTA      750
25 CCGCGAGGAG CTCAACAAGA AGTTCGGCCG TGGCCCTGAG GAGGACAAGA      800
   AGAAAGAGGC GGAGATGAAG GAGTTCGAAA GCAAACCTGT CTGCATGCCA      850
   GGCATAACC GCGAGCTGAT CCTAACTCTG GCGTACCCGA TGCCCATCGA      900
   CAAGGGCCTG AAGTTCACCA TCCGTGAGGG CGG                      933

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30

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 943 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

```

CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
50 TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
   CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA      200
   CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
   TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCAGCG AGTGGATCCC      300
   CGACCCGCCG CGCAACACAG ACAAGCCTTT CTTATGGCC ATCGAGCACG      350
55 TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
   GATCAGGGCG TGCTGAAGCT CAACACGGAC GCCGAGCTGG CCGGCTTCAG      450
   CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATTGAGATG TACCACAAGA      500
   CGCTGAGCGA GTGCATGCCG GGTGACTCCG TCGGCGTCAG CATTGTGCGC      550
   ACCGGCGACA CGACCACTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT      600
60 AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650

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	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGSCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCTG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
5	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

10 2) INFORMATION FOR SEQ ID NO: 850

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

25	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	ACACCTCCTG	ATCTGCTCGC	AAATTGGCCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAAGT	GGACATGACG	GACGAGGACA	CGTGTGACCT	GGTGGACATG	150
	GAGGTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACACC	200
30	AATCGTGCGC	GGCTCGGCCC	TCAAGGCCGT	CGAGGGCGAC	GCGAAGTACG	250
	AGGAGAACAT	CCTCGAACTG	GTGCGGAAGT	GCGACGAGTG	GATCCCCGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTCAT	CGTGACCGGC	CGCGTCGATC	400
	AGGGCGTGCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCGCC	450
35	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATT	GAAATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCCCGGT	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTGTCC	AAGGACAACG	TGGAGCGCGG	CATGGTAATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTC	AGCCCCCACT	700
40	ACCGCCCCGA	GCTCTTCTTC	CATTGCGCTG	ACGTGACAGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAGGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
45	GCGTACCCGA	TGCCCCATT				918

2) INFORMATION FOR SEQ ID NO: 851

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 60 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

```

5   CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
   GCGAGCATCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
   TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGG      150
   CATGGAGGTG CGTGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAAGAGA      200
   CGCCCATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
   TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AATGGATCCC      300
10  CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATTGAGCACG      350
   TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
   GATCAGGGCG TGCTGAAGCT CAACACAGAC GCCGAGCTGG CCGGCTTCAG      450
   CGTCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA      500
   CGCTGAGTGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCGGC      550
15  ACCGGCGACA CGATCAGTCT CTCCAAGGAC AACGTTGAAC GCGGCATGGT      600
   AATGGCGGCA ACGGCTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650
   TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACTGG CTTCAGCCCC      700
   CACTACCGCC CGCAGCTCTT CTTCCATTGT GCTGACGTGA CGGCGGACAT      750
   GAGCTTCCCG GAGGCGGAGA AGCACC GCGA GGAGCTCAAC AAGAAATTTC      800
20  GCCGCGGCCC CGAGGAGGAC AAGCAGAAGG AGGCGGAGAT GAAAGAGTTC      850
   GAGAGCAAGC TCGTCTGCAT GCCGGGCGAC AACCGCGAGC TGATCCTGAC      900
   GCTGGCGTAC CCGATGCCCA TTGAGAAGGG TCTGAAGTT      939

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25

2) INFORMATION FOR SEQ ID NO: 852

(i) SEQUENCE CHARACTERISTICS:

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30  (A) LENGTH: 912 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Leishmania tarentolae
   (B) STRAIN: MOU-2

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40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

```

   TCATTGTGGT GGCCGCCACC GACGGCGTCA TGCCGCAAAC ACGGGAGCAC      50
   CTTTTGATCT GCTCGCAGAT CGGGCTGCCG GCGCTCGTAG GGTTCATCAA      100
   CAAAGTGGAC ATGACAGACG AAGACACGTG CGACCTGGTA GACCTGGAGG      150
45  TGC GTGAGCA GCTGGAGAAG TACAAGTTTC CGGCAGAGGA AACACCAATC      200
   GTGCGTGGCT CGGCCCTCAA GGCCGTTGAG GGCATGCAA AGTACGAGGA      250
   GAACATCCTC GAACTGGTGC GGAAGTGCGA CGAGTGGATC CCAGACCCGC      300
   CACGCAATAC GGACAAGCCT TTCCTTATGG CCATTGAACA CGTGTACGAG      350
   ATCGGCAAGG ATAGGAAAAG CGTCATCGTA ACCGGCCGCG TCGATCAAGG      400
50  TGTGCTGAAG CTGAACACAG ACGCCGAGCT GGCCGGCTTC AGCGCCAAGA      450
   AGTCGACGGT GAAAGTGACG GGCATTGAGA TGTACCACAA GACACTGACA      500
   GAGTGCATGC CCGGCGACTC TGTCGGCGTC AGCATTGTGG GCACTGGYGA      550
   CACGACCAGC CTCTCTAAGG ACAATGTTGA GCGTGGCATG GTACTGGCCG      600
   CTACGGGTAG CACGAACCTG TACAACAAAG TAAAGGCGCA GGTGTATGTA      650
55  CTCACGAAGG ATGAGGGCGG CCGCCACACC GGCTTCAGCC CCCACTACCG      700
   TCCGCGAGTC TTCTTCCACT GCGCTGACGT AACGGCGGAC ATGAGCTTCC      750
   CGGAGGCGGA GAAGCACCGC GAGGAACTCA ATAAGAAATT CGGCCGCGGC      800
   CCCGAGGAGG ACAAGAAAAA GGAGGCGGAG ATGAAGGAGT TCGAGAGCAA      850
   GCTGGTCTGC ATGCCAGGCG ATAACCGCGA GCTGATCCTG ACATTGGCGT      900
60  ACCCGATGCC TA      912

```

2) INFORMATION FOR SEQ ID NO: 853

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

```

20  ATTCTTGTGG TGGCAGCTAA CGACGGATGC ATGCCGCAGA CGCGTGAGCA      50
    CCTGCTTATT TGTCGCAGA TTGGCCTTCC TGCTCTTGTA TGCTTTATCA      100
    ATAAGTGTGA CATGATGCAA GGGCAGGAGG AAATGATTGA ACTTGTTGAA      150
    ATGGAGGTAC GTGAACTTTT GGAGAAGTAC AAGTTCCTTG CGGAGGAGAC      200
    GCCATTGTG CGGGGGTCTG CGGTGAAGGC ATTGGAGGGT GATGCTGAAA      250
25  ATGAAGGAAA GATTTTGGAG CTTGTAAAAA AATGTGATGA ATGGATTCCC      300
    GACCCACCGC GTGCCATTGA AAAACCGTTC CTTATGGCCA TTGAGCACGT      350
    TTTTGAGGTT GGAAAGGATA AGAAGGCCGT TGTGTGAGC GGGCGTGTGG      400
    ACCAGGGGCA GTTGAAGGTC GGCGCAGATG CAGAACTTTC CGGGTTTAGC      450
    GCAAAGAAGC TGACGGTGAA GGTTGCTAGC ATCGAAATGT ACCATAAAAT      500
30  TCTGGAGGAT TGCATGCCTG GTGACTCTGT TGGCGCGAAG ATCGTTGGCA      550
    GCGGTGAAAC AGTGAACCTG TCGAAGGAAA ATGTGGAACG CGGCATGGTA      600
    CTCTCCGCAC CAGGTGCAAC GACACTGTTC AACAAGGTCC GCGCGCAGGT      650
    GTACGTGTTG ACAAAGGAAG AAGGCGGTCTG TCACACAGCC TTTAGTCCTC      700
    ACTATCGTCC GCAGCTTTTC TTCCACTGTG CTGATGTCAC GGCAGATATT      750
35  AACTTCCC GG AAAGCGAGAA GCTTGCAGGG GAGCTGAACA AAAAGTATGG      800
    CCGTGATGCG GCGGAACAGA AGAAGAAGGA GGCAGAACTG AAAGAGTTTG      850
    AAAAGACGCT TGTCTGCATG CCTGGTGATA ACCGCGAACT CCTGCTCACC      900
    CTTGCCTATC CAATGCCAAT GGAAAAGGGA CTCAAG      936
  
```

40

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

```

CGGCATTCTT GTGGTGGCAG CTAACGACGG ATGCATGCCG CAGACGCGTG      50
AGCACCTGCT TATTTGTTCT CAGATTGGCC TTCCTGCTCT TGTATGCTTT      100
60  ATCAATAAGT GTGACATGAT GCAAGGGCAG GAGGAAATGA TTGAGCTTGT      150
  
```

	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCGACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCTTATG	GCCATTGAGC	350
5	ACGTTTTTGA	GGTTGGAAG	GATAAGAAGG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTTGC	TAGCATCGAA	ATGTACCATA	500
	AAATTCTGGA	GGATTGCATG	CCTGGTGAAT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTCGAAG	GAAAAATGTG	AACGCGGCAT	600
10	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAACCTC	CCGGAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
15	TTTGAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

20 2) INFORMATION FOR SEQ ID NO: 855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

35	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGG	GAAGTACAAG	TTCCCTGCGG	200
40	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAT	GTGATGAATG	300
	GATTCCTGAT	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
	AGCAGTTTTC	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACTTTCCGG	450
45	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTGC	AAGGAAAATG	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTCGTCA	CACAGCCTTT	700
50	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
55	GCTCACCTT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

2) INFORMATION FOR SEQ ID NO: 856

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

15	CTTATTATGG AGCTGATCAA CAACGTCGCG AAGAAGCACG GTGGTTTCTC	50
	CGTGTTCGCC GCGGTCGGCG AGCGCACCAG GGAGGGCAAC GAGCTGTACC	100
	ACGAGATGAT GGAGACCGGC GTCATCAAGC GCCGCCAGCT GGATGACGGC	150
	ACGTTGACT TCTCCGGCTC CAAGGCCGCG CTGGTGTACG GCCAGATGAA	200
	CGAGCCGCCA GGTGCCAGGG CCGGTGTTGC CCTCACTGGC CTGACGGTGG	250
	CCGAGTACTT CCGTGATGAG GACGGCCAGG ACGTGCTGCT CTTCATCGAC	300
20	AACATCTACC GTTTCACCCA GGTTGGTTCT GAGGTGAGTG CCCTTTTGGG	350
	GCGCATCCCG TCCGCCGTCG GTTACCAGCC GACCCTCGCC ACCGACCTTG	400
	GCGCGCTGCA GGAGCGTATC ACGACGACCA ACAAGGGCTC CATCACCTCC	450
	GTGCAGGCCG TCTACGTGCC GGCCGACGAT ATCACCAGCC CGGCGCCTGC	500
	GACCACCTTC ACCCATCTGG ACGCGACCAC TGTGCTCTCC CGTTCCATCG	550
25	CCGAGCTGGG TATCTACCCC GCCGTCGACC CGCTCGACTC CACCTCGCGT	600
	ATGCTGTCCG CGAACATCGT CGGCGAGGAG CAGTACAACG TGGCGCGTGG	650
	CGTGCAGAAA ATACTGCAGG ACTACAAATC GCTGCAGGAT ATCATCGCCA	700
	TCCTGGGTAT GGACGAGCTG TCTGAGCAGG ACAAGTTCGT CGTCGCGCGT	750
	GCGCGCAAGG TTCAGCGTTT CCTATCCAG CCCTTCCAGG TGGCTGAGGT	800
30	ATTACCGGC AAGCCCGGAC GTTTCGTCGA GCTGCAGGAC ACCATCAGCG	850
	GCGTCAAGGA GATTTTGGAC GGCGAGTGCG ACGACATG	888

35 2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

50

55	TGATTATGGA ATTGATCAAC AATGTCGCCA AGAAACACGG TGGGTTCTCC	50
	GTGTTGCTG GTGTTGGTGA ACGTACGAGG GAAGGTAACG AACTGTACCA	100
	TGAAATGATG GAAACGGGTG TCATCAAGCG CCGTCAACTG GAAGACGGAA	150
	CATTTGACTT CTCGGGCTCT AAAGCTGCTT TGGTGTACGG ACAAATGAAC	200
	GAACCACCAG GTGCTAGAGC CCGTGTGCA CTCACGGGAT TGACCGTTGC	250
	CGAGTATTTT CGTGATGAAG AGGGGCAGGA TGTGCTACTC TTCATCGATA	300
	ACATCTACCG TTTCACCCAG GCCGGTTCG AAGTGAGTGC GCTGTTAGGA	350
	AGAATTCCAT CCGCCGTGGG TTATCAACCT ACATTGGCCA CTGATCTCGG	400
	AGCACTCCAG GAACGCATTA CTACAACCA CAAGGGTTTC ATTACATCAG	450
60	TCCAGGCAGT ATACGTCCCA GCCGATGATA TCACTGATCC CGCTCCAGCT	500

ACCACTTTCT CGCACTTGGG TGCCACTACA GTGCTTTCTC GTTCAATTGC 550
 GGAGTTGGGT ATTTACCCTG CGGTCGACCC GCTTGACTCA ACGTCACGTA 600
 TGCTGTCGGC CAACATTGTA GGACAGGAAC AGTACGATGC CGCACGTGGT 650
 GTACAGAAAA TTTTACAGGA CTACAAATCA CTGCAGGATA TCATTGCCAT 700
 5 TCTGGGTATG GACGAGCTGT CTGAGCAGGA CAAGTTCGTT GTAGCACGCG 750
 CCCGTAAGGT ACAGCGTTTC CTGTCTCAGC CGTTCCAAGT GGCTGAGGTG 800
 TTCACCGGCA AGCCTGGGAG GTTCGTTGAA CTACAGGATA CCATCAGCGG 850
 TGTCAAGGAA ATCTGGAAGG TGAGTGTGAC GATA 884

10

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

TGGAAGTAT TAATAATGTG GCCAAAAAGC ATGGCGGTTA CTCTGTTTTT 50
 GCAGGTGTAG GTGAAAGGAC GAGGGAGGGT AATGAATTGT ACCATGAAAT 100
 30 GATGGAGACA GGTGTTATAA AGAAAAAGGC ACTAGGTGGT GGAAGTTTG 150
 ATTTCACTGG ATCTAAAGCA GCGCTGGTCT ATGGACAAAT GAACGAGCCA 200
 CCTGGGGCCC GTGCTAGAGT GGCCTAAGT GGATTAACAG TCGCAGAATA 250
 TTTCCGTGAC GAACAAGGAC AAGACGTGTT GTTGTATTATT GATAATATTT 300
 ACCGATTTAC TCAGGCAGGG TCTGAGGTTT CAGCCTTGCT AGGCCGTATA 350
 35 CCTTCAGCTG TGGGATACCA GCCTACATTG GCAACAGATC TTGGCTGTTT 400
 ACAAGAACGA ATTACTACGA CCAAATCTGG TTCAATCACC AGTGTACAAG 450
 CTGTGTATGT GCCAGCAGAT GATATTACTG ATCCAGCGCC TGCCACAAC 500
 TTTACTCACT TGGACGCTAC TACTGTACTT AGCAGGCCAA TTGCTGAACT 550
 CGGTATTTAT CCAGCGGTAG ACCCGTTGGA TTCAACAAGC CGTATGCTAA 600
 40 GCGCGAACAT TGTGGGAAAT GAACACTATA GTGTAGCCCG TTCCGTGCAG 650
 AAGATACTGC AAGATTACAA ATCGCTTCAG GACATTATTG CCATTTTGGG 700
 TATGGATGAA CTGTGCGAAC AAGACAAAAA TATAGTAGCC CGAGCAAGGA 750
 AGATGCAAAG GTTCTTATCA CAGCCATTCC AAGTGGCGGA AGTTTTTACT 800
 GGTAAACCGG GAAGATTTGT GGAATTGGAA GATACAATTG CCGGGGCACG 850
 45 AGATATAATT GCGGGTAATT G 871

2) INFORMATION FOR SEQ ID NO: 859

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Leishmania guyanensis*

481

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

```

5  TGACGGCGCT GGACGTGACG GAGGACCTCG GCCGCGATGA GCCGCTGACG      50
   CTGGAGATCG TGCAGCACTT GGATGCGAAC ACCGGCCGCT GCATTGCGAT      100
   GCAGACGACG GACCTGCTGA AGCTGAAGTC GAAGGTTGTG TCGACCGGCG      150
   GCAACATCTC CGTGCCGGTG GGCCGCGAGA CACTGGGCCG CATCTTCAAC      200
   GTGCTGGGCG ACGCGATTGA CCACCGCGGC CCCGTGTGCG AGAAGATGCG      250
10  CATGGCGATC CACGCCGAGG CGCCGAAGCT GGCGGACCAG GCTGCGGAGG      300
   ACACGATCCT GACGACCGGC ATCAAGGTGA TCGACCTGAT TCTGCCCTAC      350
   TGCAAGGGCG GCAAGATCGG CCTGTTCGGC GGTGCCGGTG TGGGCAAGAC      400
   TGTGATCATC ATGGAGCTGA TCAACAACGT CGCGAAGGGG CACGGCGGCT      450
   TCTCCGTGTT CGCCGGCGTT GGCGAGCGCA CGCGCGAGGG CACGGACCTG      500
15  TACCTGGAGA TGATGCAGTC AAAGGTGATT GACCTGAAGG GCGAGTCGAA      550
   GTGCGTGCTT GTGTACGGGC AGATGAACGA GCCCCCGGGT GCGCGCGCGC      600
   GCGTTGCGCA GTCTGCGCTG ACGATGGCCG AGTACTTCCG CGACGTGGAG      650
   GGCCAGAAGC TGCTGCTGTT CATCGACAAC ATCTTCCGCT TCACGCAGGC      700
   GAACTCCGAG GTGTCTGCGC TGCTGGGCCG CATCCCGGCC GCCGTGGGTT      750
20  ACCAGCCGAC GCTTGCGGAG GATCTTGCCA TGCTGCAGGA GCGCATTACG      800
   TCGACGACGA AGGGATCGAT TACGTCTGTG CAGGCTGTGT ACGTGCCTGC      850
   GGATGATATC ACGGACCCCG CGCCCGCGAC GACGTTCTCG CACCTGGACG      900
   CGACGACTGT GCTGGACCGC GCGGTGGCGG AGTCGGGCAT CTACCCTGCC      950
   GTGAACCCGC TGGAGTGCGC GTCGCGCATC ATGGACCCCG ATGTGATCGA     1000
25  CGTGGACCAT TACAACGTTG CACAGGATAT CGTCCAGATG CTGACCAAGT     1050
   ACAAGGAGCT GCAGGACATC ATTGCGGTGC TTGGCATCGA CGAGCTGAGC     1100
   GAGGAGGACA AGGTCTGTTG GGACCGCGCG CGCAAGGTGA CGCGGTTCTT     1150
   GTCGCAGCCG TTCCAGGTTG CGGAGGTGTT CACCGGCATG ACGGGCCACT     1200
   ACGTGCAGCT GAGCGACACG GTGGAGTCGT TCTCTGGCCT GCTGATGGGG     1250
30  TCGTA

```

2) INFORMATION FOR SEQ ID NO: 860

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1222 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
40  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

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      (vi) ORIGINAL SOURCE:
45  (A) ORGANISM: Leishmania mexicana
      (B) STRAIN: ATCC 50156

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

```

50  CTCGGAGGGC GTCCCGCCCG TGCTGACGGC GCTGGATGTG ACGGAGGACC      50
   TTGGCCGCGA TGAGCCGCTG ACGCTGGAGA TCGTGCAGCA CCTGGACGCG      100
   AACACCGGCC GCTGCATTGC GATGCAGACG ACGGACCTGC TGAAGCTGAA      150
   GTCGAAGGTT GTGTGACCGG GCGGCAACAT CTCTGTGCCG GTGGGCCGTG      200
   AGACGCTGGG CCGCATCTTC AACGTGCTGG GCGACGCGAT CGACCAGCGC      250
55  GGCCCCGTGG GTGAGAAGAT GCGCATGGCG ATCCACGCCG AGGCCCCGAA      300
   GCTGGCGGAT CAGGCCGCGG AGGACACGAT CCTGACGACC GGCATCAAGG      350
   TGATCGACCT GATTCTGCCC TACTGCAAGG GTGGCAAGAT CGGCCTGTTT      400
   GGCGGCGCCG GTGTGGGCAA GACCGTGATC ATCATGGAGC TGATTAACAA      450
   CGTCGCGAAG GGCCACGGTG GTTTCTCGGT GTTTGCCGGC GTTGGCGAGC      500
60  GCACGCGCGA GGGCACGGAC CTGTACCTGG AGATGATGCA GTCGAAGGTG      550

```

ATTGACCTGA AGGGCGAGTC GAAGTGCGTG CTTGTGTACG GGCAGATGAA 600
 CGAGCCCCCG GGTGCGCGCG CGCGCGTTGC GCAGTCTGCG CTGACGATGG 650
 CGGAGTACTT CCGAGACGTG GAGGGCCAGA ATGTGCTGCT GTTCATCGAC 700
 AACATCTTCC GCTTCACGCA GGCGAACTCC GAGGTCTCTG CGCTGCTGGG 750
 5 CCGCATTCCG GCCGCCGTGG GCTACCAGCC GACGCTTGCG GAGGATCTTG 800
 GTATGCTGCA GGAGCGCATC ACGTCGACGA CGAAGGGGTC GATCACGTCC 850
 GTGCAGGCCG TGTACGTGCC TGC GGATGAT ATCACGGATC CGGCGCCCCG 900
 GACGACGTTT TCGCACCTGG ACGCGACGAC TGTGCTGGAC CGCGCGGTGG 950
 CGGAGTCGGG GATCTACCCT GCCGTGAACC CGCTGGAGTG CGCGTCGCGT 1000
 10 ATCATGGACC CCGATGTGAT CGACGTGGAC CACTACAACG TTGCGCAGGA 1050
 TATCGTGCAG ATGCTGACCA AGTACAAGGA GCTGCAGGAT ATCATTGCGG 1100
 TGCTTGGTAT CGACGAGCTG AGCGAGGAGG ACAAGGTCGT GGTGGACCGC 1150
 GCGCGCAAGG TGACCCGGTT CCTGTGCGAG CCGTTCCAGG TTGCGGAGGT 1200
 GTTCACGGGC ATGACGGGCC AC 1222
 15

2) INFORMATION FOR SEQ ID NO: 861

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1246 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tropica*
 30 (B) STRAIN: ATCC 50129
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

CCGTGCTGAC GCGCTGGAT GTGACGGAGG ACCTTGGCCG CGATGAGCCG 50
 35 CTGACGCTGG AGATCGTGCA GCACTTGGAC GCGAACACCG GCCGCTGCAT 100
 TGC GATGCAG ACGACGGACC TGCTGAAGCT GAAGTCGAAG GTTGTGTCTGA 150
 CCGGCGGCAA CATCTCTGTG CCGGTGGGCC GTGAGACGCT GGGCCGCATC 200
 TTCAACGTTT TGGGCGACGC GATCGACCAG CGCGGCCCCG TGGGCGAGAA 250
 GATGCGCATG GCGATCCACG CCGAGGCCCC GAAGCTGGCG GATCAGGCCG 300
 40 CGGAGGACAC GATCCTGACG ACCGGCATCA AGGTGATCGA CCTGATTCTG 350
 CCCTACTGCA AGGGTGGCAA GATCGGCCTG TTCGGCGGTG CCGGTGTGGG 400
 CAAGACTGTG ATCATCATGG AGCTGATCAA CAACGTCGCG AAGGGCCACG 450
 GTGGTTTCTC CGTGTGTGCC GCGCTTGGCG AGCGCACGCG CGAGGGCACG 500
 GACCTGTACC TGGAGATGAT GCAGTCGAAG GTGATTGACC TGAAGGGCGA 550
 45 GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT GAACGAGCCC CCGGTGCGC 600
 GCGCGCGCGT TGC GCACTT GCGCTGACGA TGGCGGAGTA CTTCCGCGAC 650
 GTGGAGGGCC AGAACGTGCT GCTGTTTCATC GACAACATCT TCCGCTTCAC 700
 GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT GGGCCGCATT CCGGCCGCCG 750
 TGGGCTACCA GCCGACGCTT GCGGAGGATC TTGGTATGCT GCAGGAGCGC 800
 50 ATCACGTCGA CAACGAAGGG GTCGATCACG TCCGTGCAGG CCGTGTACGT 850
 GCCAGCGGAT GATATCACGG ATCCCGCGCC CGCGACGACG TTCTCGCACC 900
 TGGACGCGAC GACTGTGCTG GACCGCGCGG TGGCGGAGTC GGCATCTAC 950
 CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG CGTATCATGG ACCCGCATGT 1000
 GATCGATGTG GACCACTACA ACGTTGCGCA GGATATCGTG CAGATGCTGA 1050
 55 CCAAGTACAA GGAGCTGCAG GATATCATTG CCGTGCTTGG CATCGACGAG 1100
 CTGAGCGAGG AAGACAAGGT TGTGTGGAC CGCGCGCGCA AGGTGACCCG 1150
 GTTCCTGTCT CAGCCGTTCC AGGTGCGGGA GGTGTTACG GGCATGACGG 1200
 GCCACTACGT GCAGCTGGTC GACACGGTGG AGTCGTTCTC TGGCCT 1246

60

2) INFORMATION FOR SEQ ID NO: 862

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

```

GGCGTGCCGC CCGTGCTGAC GGCCTGGAT GTGACGGAGG ACCTTGGCCG      50
CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC GCGAACACGG      100
GCCGCTGCAT TGCATGCAG ACGACGGACC TGCTGAAGCT GAAGTCGAAG      150
GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC GTGAGACGCT      200
GGGCCGCATC TTCAAYGTTT TGGGCGACGC GATCGACCAG CGCGGCCCCG      250
TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC GAAGCTGGCG      300
GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA AGGTGATCGA      350
25 CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG TTCGGCGGTG      400
CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA CAACGTCGCG      450
AAGGGCCACG GCGGTTTCTC CGTGTTTGCC GGCCTTGGCG AGCGCACGCG      500
CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG GTGATTGACC      550
TGAAGGGCGA GTCGAAGTGY GTGCTTGTGT ATGGGCAGAT GAACGAGCCC      600
30 CCGGGTGCAG GCGCGCGCGT TGCAGAGTCT GCGCTGACGA TGGCGGAGTA      650
CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCAT GACAACATCT      700
TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT GGGCCGCATT      750
CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC TTGGTATGCT      800
GCAGGAGCGC ATCAGTCGA CAACGAAGGG GTCGATCACG TCCGTGCAGG      850
35 CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC CGCGACGACG      900
TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG TGGCGGAGTC      950
GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG CGTATCATGG      1000
ACCCTGATGT GATCGATGTG GACCACTACA ACGTTGCGCA GGATATCGTG      1050
CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG CCGTGCTTGG      1100
40 CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGTGGAC CGCGCGCGCA      1150
AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA GGTGTTACG      1200
GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG AGTCGTTCTC      1250
TGGCCTGCTG ATGGG

```

45

2) INFORMATION FOR SEQ ID NO: 863

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bordetella pertussis*
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

	ATGGCAAAAG	GCAAGTTTGA	ACGTACCAAG	CCGCACGTGA	ACGTGGGTAC	50
	GATTGGTCAC	GTTGACCACG	GCAAAACGAC	GTTGACGGCG	GCGATCACGA	100
	CGGTGCTGTC	GAACAAGTTC	GGCGGCGAGG	CTCGCGGCTA	CGACCAGATT	150
5	GACGCGGCGC	CGGAAGAGAA	GGCGCGTGGG	ATCACGATCA	ACACCTCGCA	200
	CGTTGAGTAC	GAGACGGAGA	CGCGTCACTA	CGCGCACGTT	GATTGCCCCG	250
	GTCACGCTGA	CTACGTGAAG	AACATGATCA	CGGGTGCTGC	GCAGATGGAC	300
	GGCGCGATCC	TGGTGGTGTC	GGCCGCAGAC	GGCCCGATGC	CGCAGACGCG	350
	CGAGCACATT	TTGCTGTGCG	GCCAGGTGCG	CGTGCCGTAC	ATCATCGTGT	400
10	TCCTGAACAA	GGCGGACATG	GTTGATGACG	CGGAGCTGCT	CGAGCTGGTG	450
	GAGATGGAAG	TCCGCGAACT	GCTGAGCAAG	TACGATTTC	CGGGCGATGA	500
	CACGCCGATC	GTGAATGGTG	CGGCCAAGCT	GGCGCTGGAA	AGCGACAACG	550
	GCGACCTGGG	CGAGCAGGCG	ATTCTGTGCG	TGGCGCAAGC	GCTGGACACG	600
	TACATTCCGA	CGCCGGAGCG	CGCGGTGCGC	GGTGCGTTCC	TGATGCCGGT	650
15	GGAAGACGTG	TTCTCGATCT	CGGGCCGTGG	CACGGTGGTG	ACTGGCCGTA	700
	TCGAGCGCGG	CGTGGTGAAG	GTTGGCGAGG	AAATCGAAAT	CGTGGGCATC	750
	AAGCCGACCG	TGAAGACGAC	CTGCACGGGC	GTGGAGATGT	TCCGCAAGCT	800
	GCTGGACCA	GGCCAGGCGG	GCGACAACGT	GGGTATCTTG	CTGCGCGGCA	850
	CCAAGCGTGA	AGACGTCGAG	CGTGGCCAGG	TGCTGGCCAA	GCCGGGTTCG	900
20	ATCAACCCCG	ACACGGACTT	CACGGCCGAG	GTGTACATTC	TGTCCAAGGA	950
	AGAGGGTGGC	CGTCACACGC	CGTTCTTCAA	CGGCTATCGT	CCGCAGTTCT	1000
	ACTTCCGCAC	GACGGACGTG	ACCGGCACGA	TCGACCTGCC	GGCGGACAAG	1050
	GAAATGGTGC	TGCCGGGCGA	CAACGTGTCG	ATGACCGTCA	AGCTGCTGGC	1100
	CCCGATCGCC	ATGGAAGAAG	GTCTGCGTTT	CGCCATCCGT	GAAGGCGGTC	1150
25	GTACCGTCCG	TGCCGGCGTC	GTCGCCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 864

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: LVH/75/USAMRU-K/18
 (C) ACCESSION NUMBER: extracted from U10562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

45

	ATGGGAAAGG	AAAAGGTGCA	CATGAATCTT	GTGGTGGTGG	GCCACGTGCA	50
	TGCCGGTAAA	TCCACTGCAA	CGGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
	TTGACAAACG	TACGATCGAG	AAGTTCGAGA	AAGAAGCTGC	CGACATTGGT	150
	AAGGCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
50	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CACTATTATT	GATGCTCCTG	GGCACCGTGA	CTTCATCAAG	300
	AACATGATCA	CCGGCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTGC	350
	CTCTGCGCAG	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCACTTTGG	GTGTGAAGCA	GATGGTTGTG	450
55	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCACT	GCGTCCGAGC	GACAAGCCCC	700
60	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TGGGTGGTAT	TGGCACCGTG	750

	CCCGTTGGTC	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGTGAC	800,
	GTTTGGCCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
	ACGAGCAGCT	CGCTGAGGCG	ACCCCGGGTG	ACAACGTCGG	CTTTAACGTG	900
	AAGAACGTTT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
5	CAAGAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
	TCCTGAACCA	CCCCGGACAG	ATTGGAACG	GTTATGCGCC	CGTGCTGGAC	1050
	TGCCACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
	CGACCGTCGC	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
	CTGGCGACGC	CGCGATCGTG	CGCATGGTGC	CGCAGAAGCC	TATGTGCGTG	1200
10	GAGGTCTTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCCG	TGCGTGACAT	1250
	GCGCCAGACC	GTCGCTGTCT	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
	GTTCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

15

2) INFORMATION FOR SEQ ID NO: 865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

30

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
	GCAATTCGAA	ACCCCAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCTTTATTGG	TTGTCCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
35	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTCAGAC	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
	TTACAACACC	GAGAAGATCC	CATTCGTTGC	CATTTCTGGT	TTCGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
40	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCATTAC	AAGATGTTTA	CAAGATAGGT	GGTGTAGGTA	550
	CTGTCCCAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
	GTTACCTTCG	TCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATGAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
45	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
	TATCGTCCTC	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
	TTGACTGTCA	CACCGCTCAC	ATTTCCTGCA	AATCCAGAC	TATCACTGCT	900
	AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
50	CAAGTCTGGT	GATGCTGCTT	TGGTTGTTAT	GCAACCTTTG	AAGCCACTTT	1000
	GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
	GA					1052

55

2) INFORMATION FOR SEQ ID NO: 866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 35552

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
15	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
20	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
25	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

30

2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zoogloea ramigera*

(B) STRAIN: ATCC 25935

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

	AAGGTATTTCG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
	ACAACAGCAG	CTGGGCGACG	GCATTGTCCG	TACCATTGCA	CTGGGTACCT	100
50	CCGACGGCCT	GCGTCGCGGC	ATGATGATCC	AGAACACCGG	CAAACCTATC	150
	ATGGTGCCAG	TCGGTAAAGC	AACCCTGGGT	CGCATCATGG	ACGTGCTGGG	200
	TAACCCGATC	GACGAATGCG	GCGCGGTCGC	TCACGACCAG	ATCGCTTCGA	250
	TCCACCGCGC	TCCTCCTGCG	TACGACGAAC	TGTCGCCATC	GCAAGATCTG	300
	CTGGAACCG	GCATTAAAGT	TATTGACCTG	GTGTGCCCCG	TCGCCAAGGG	350
55	CGGTAAAGTC	GGTCTGTTCG	GCGGTGCAGG	TGTGGGCAAG	ACCGTGAACA	400
	TGATGGAAC	GATCAACAAC	ATCGCCAAAG	CACACTCGGG	TCTGTCCGTG	450
	TTTGCCGGTG	TGGGTGAGCG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	GATGGCTGAC	GCCAAAGTGG	TCGATCTGGA	AAATCCAGAG	AACTCCAAGG	550
	TTGCGATGGT	CTACGGTCAG	ATGAATGAAC	CACCAGGCAA	CCGTCTGCGC	600
60	GTGGCGCTGA	CCGGTCTGAC	CATGGCTGAA	GCATTCCGTG	ACGAAGGCAA	650

487

AGACGTTCTG	TTCTTCGTGG	ACAACATCTA	C C G C T T C A C C	CTGG C C C G G T A	700
CCGAAGTATC	GGCACTGCTG	GGCCGTATGC	CATCGGCTGT	GGGTTACCAG	750
CCTACGCTGG	CCGAAGAAAT	GGGTCGCCTG	CAAGAGCGCA	TCACTTCGAC	800
CAAGACCGGT	TCGATCAC				818

5

2) INFORMATION FOR SEQ ID NO: 868

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 20 (B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

CTATCTTAGT	AGTATCTGCT	GCTGATGGCC	CAATGCCACA	AACTCGTGAA	50
25 CACATTCTTT	TATCACGTAA	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	100
AAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	150
TGGAAGTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	200
CCTGTAATCT	CTGGTTCTGC	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	250
TGAGCAAAAA	ATCTTAGACT	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	300
30 CACCAGAACG	TGATTCTGAC	AAACCATTC	TGATGCCAGT	TGAGGACGTA	350
TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	400
TCAAATCAAA	GTCGGTGAAG	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	450
CAAGCAAAAC	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	500
TACGCTGAAG	CTGGTGACAA	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	550
35 TGATGACGTA	CAACGTGGTC	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	600
CACATACAAA	ATTCAAAGCG	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	650
GGTCGTCATA	CACCATTCTT	CACTAACTAC	CGCCCAACAAT	TCTATTTCCG	700
TACTACTGAC	GTAACGTGGT	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
40 TTATGCCTGG	CGATAACGTT	GAAATGGA			778

2) INFORMATION FOR SEQ ID NO: 869

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 55 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

TGGTCCTATG	CCTCAAACAC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
60 GTGTACCATA	CATCGTTGTT	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	100

488

	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCTGACT	TATTGTGAGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGCGATGCT	TCATACGAAG	AAAAAATCAT	GGAATTAATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGACA	CTGACAAACC	300
5	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAATCGTTG	GTATTGCTGA	AGAAACTGCT	AAAACAACCTG	TAAGTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGTGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
10	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	600
	TTACGTTTTA	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

15 2) INFORMATION FOR SEQ ID NO: 870.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

30	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
	GTACCATAACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	TCGTGACTTA	TTGTCAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCTGGTTC	TGCTTTGAAA	200
35	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AAACTGCTAA	AACAACTGTA	ACTGGTGTGG	450
40	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTTTAA	AAAAGAAGAA	GGTGGACGTC	ACACACCATT	CTTC	644

45

2) INFORMATION FOR SEQ ID NO: 871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R758

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTC	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
5	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCTGTAAAT	CGCTGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
10	CTACAGGCCG	TGTTGAACGT	GGACAAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACTGTAA	CTGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTA	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTTAAAG	CTGAAGTTTA	600
15	CGTTTTAACA	AAAGAAGAAG	GTGGACGTCA	CACTCCA		637

2) INFORMATION FOR SEQ ID NO: 872

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

35	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
40	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAAGT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AAACTGCTAA	AACAACTGTA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
45	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	AACTCCATT	CTT	643

50

2) INFORMATION FOR SEQ ID NO: 873

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

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GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC      50
GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA      100
AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT      150
10 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA      200
GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC      250
TGCAGTTGAC GAATACGTTC CAACTCCAGA ACGTGATACT GACAAACCAT      300
TCATGATGCC AGTCAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA      400
15 AATCGTTGGT ATTGCTGACG AAACCTGCTAA AACCACTGTA ACAGGTGTTG      450
AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAA GCTGAAGTTT      600
ATGTTTTGAC AAAAGAAGAA GGTGGACGTC ACACTCCATT C              641
20

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2) INFORMATION FOR SEQ ID NO: 874

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: LSPQ 2514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

```

ACCAGCATTG GTAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
40 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC      100
GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC      150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG      200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC      250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC      300
45 TACAGGCCGT GTTGAACGTG GGCAAATCAA AGTTGGTGAA GAAGTTGAAA      350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGAGAAATG      400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT      450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG      500
CTCCAGGTTT AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT      550
50 TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAACTATCG      600
TCCACAATTC TATTTCCGTA CTAATGACGT AACTGGTGTT GTTAACCTAC      650
CAGAAGGTAC TGAAATGGTT ATGCCTGGCG A              681

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55 2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 bases
 (B) TYPE: Nucleic acid

491

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: R591

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

	ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTG	TTAAACAAAG	50
	TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
	CGTGACTTAT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
15	CGCTGGTTCT	GCATTAAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
	AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
	CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
	CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
	AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
20	ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
	TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
	AACGTGGTCA	AGTATTAGCT	GCTCCTGGTT	CTATTACACC	ACACACAAAA	550
	TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
	TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCCTG	ACTACTGACG	650
25	TAACTGGTGT	TGTAAACTTA	CCAGA			675

2) INFORMATION FOR SEQ ID NO: 876

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

45	TCTTATTATC	ACGTAACGTT	GGTGTAACAG	CATTAGTTGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
	TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200
	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACCTC	250
50	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTTGC	ACGTGAAGAC	500
55	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCAC	AATTCTATTT	CCGTACTACT	650
	GACGTAACCTG	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
	TGGC					704

60

2) INFORMATION FOR SEQ ID NO: 877

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 15 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

	TCTTAGTTGT	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	50
20	ATCTTATTAT	CACGTAACGT	TGGTGACCA	GCATTAGTTG	TATTCTTAAA	100
	CAAAGTTGAC	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTTCGTGA	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	200
	GTAATCGCTG	GTTCTGCATT	AAAAGCATTA	GAAGGCGATG	CTGAATACGA	250
	ACAAAAATC	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	300
25	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	400
	AATCAAAGTT	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	450
	AAACAACGTG	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	500
	GAAGCTGGTG	ACAACATCGG	TGCTTTATTA	CGTGGTGTG	CACGTGAAGA	550
30	CGTACAACGT	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	600
	CAAAATTCAA	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	700
	TGACGTAAC	GGTGTTGTAA	ACTTACCAGA	AGGTACAGAA	ATGGTTATGC	750
35	CTGGCGACAA	CGTTGAAATG				770

2) INFORMATION FOR SEQ ID NO: 878

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 50 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

	TTGTATTCTT	AAACAAAGTT	GACATGGTAG	ACGACGAAGA	ATTATTAGAA	50
55	TTAGTTGAAA	TGGAAGTTTC	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	100
	TGACGATGTA	CCTGTAATCG	CTGGTTCTGC	ATTAAAAGCA	TTAGAAGGCG	150
	ATGCTGAATA	CGAACAAAAA	ATCTTAGACT	TAATGCAAGC	AGTTGATGAT	200
	TACATTCCAA	CTCCAGAACG	TGATTCTGAC	AAACCATTC	TGATGCCAGT	250
	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	300
60	TTGAACGTGG	TCAAATCAAA	GTTGGTGAAG	AAGTTGAAAT	CATCGGTATG	350

CACGAAACTT CTAAAAACAAC TGTTACTGGT GTAGAAATGT TCCGTAAATT 400
 ATTAGACTAC GCTGAAGCTG GTGACAACAT CCGTGCTTTA TTACGTGGTG 450
 TTGCACGTGA AGACGTACAA CGTGCTCAAG TATTAGCTGC TCCTGGTTCT 500
 ATTACACCAC ACACAAAATT CAAAGCTGAA GTATACGTAT TATCTAAAGA 550
 5 TGAAGGTGGA CGTCACACTC CATTCTTCAC TAACTATCGC CCACAATTCT 600
 ATTTCCGTAC TACTGACGTA ACTGGTGTG TAAACTTACC AGAAGGTACA 650
 GAAATGGTTA TGCCTGGCGA CAACGTTGAA ATGACAGTTG AATTAATCGC 700
 TCCAATCGCT ATCGAA 716

10

2) INFORMATION FOR SEQ ID NO: 879

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R764

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

CGGTCCTATG CCTCAAACCTC GTGAACACAT CTTGTTATCA CGTAACGTTG 50
 GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT GGTGATGAC 100
 30 GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA 150
 ATATGACTTC CCAGGCGACG ATGTTCCCTGT AATCGCCGGT TCTGCTTTGA 200
 AAGCTCTTGA AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG 250
 GCTGCAGTTG ACGAATACGT TCCAACCTCCA GAACGTGATA CTGACAAACC 300
 ATTCATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG 350
 35 TTGCTACAGG CCGTGTTGAA CGTGGAACAAG TTCGCGTTGG TGATGAAGTA 400
 GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACTG TAACAGGTGT 450
 TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG 500
 GTGCATTGCT ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA 550
 TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTCA AAGCTGAAGT 600
 40 TTATGTTTTG ACAAAGAAG AAGGTGGACG TCACACTCCA 640

2) INFORMATION FOR SEQ ID NO: 880

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

60 CGGCGCGATC CTGGTTTGCT CGGCTGCCGA CGGCCCCATG CCGCAGACCC 50

	GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCTTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAAGTGGT	150
	CGAGATGGAA	GTTGCGGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
	AACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
5	GACAACGGCA	TCGGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
	CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCCTGATGC	350
	CGATCGAAGA	CGTGTTCTCG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
	CGTGTAGAGC	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCGG	450
	CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
10	AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
	GGCACCAAGC	GTGAAGACGT	AGAGCGTGGC	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTAC	GTGCTGTCCA	650
	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
15	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
	TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

20 2) INFORMATION FOR SEQ ID NO: 881

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 642 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
 - (B) STRAIN: R421

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

35	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
40	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
	TACAGGCCGT	GTTGAACGTG	GACAAGTTTC	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAAA	450
45	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
	GTTTAAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

50

2) INFORMATION FOR SEQ ID NO: 882

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 636 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
10	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCCTG	CTTTGAAAGC	200
	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
15	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
20	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAT	ACACCA		636

2) INFORMATION FOR SEQ ID NO: 883

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

40	GGTCCTATGC	CTCAAACACG	TGAACATATC	TTATTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTAT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTATT	AGAATTAGTA	GAAATGGAAG	TTCGTGACTT	ATTATCAGAA	150
	TACGATTTCC	CAGGCGATGA	TGTTCCAGTT	ATCGCAGGTT	CTGCTTTGAA	200
	AGCTTTAGAA	GGCGACGAGT	CTTATGAAGA	AAAAATCTTA	GAATTAATGG	250
45	CTGCAGTTGA	CGAATATATC	CCAACTCCAG	AACGTGATAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGTGAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTAAAGAC	GAAACATCTA	AAACAACGTG	TACAGGTGTT	450
	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
50	TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
	TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAAATTCAA	AGCTGAAGTA	600
	TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

55

2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R575

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

TATGCCTCAA ACACGTGAAC ATATCTTATT ATCACGTAAC GTTGGTGTAC 50
 CATACATCGT TGTATTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA 100
 TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAT CAGAATACGA 150
 15 TTTCCCAGGC GATGATGTTC CAGTTATCGC AGGTTCTGCT TTGAAAGCTT 200
 TAGAAGGCGA CGAGTCTTAT GAAGAAAAAA TCTTAGAATT AATGGCTGCA 250
 GTTGACGAAT ATATCCCAAC TCCAGAACGT GATACTGACA AACCATTCAT 300
 GATGCCAGTC GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA 350
 CAGGCCGTGT TGAACGTGGT GAAGTTCGCG TTGGTGACGA AGTTGAAATC 400
 20 GTTGGTATTA AAGACGAAAC ATCTAAAAACA ACTGTTACAG GTGTTGAAAT 450
 GTTCCGTAAA TTATTAGACT ACGCTGAAGC AGGCGACAAC ATCGGTGCTT 500
 TATTACGTGG TGTTGCACGT GAAGATATCG AACGTGGACA AGTATTAGCT 550
 AAACCAGCTA CAATCACTCC ACACACAAAA TTCAAAGCTG AAGTATACGT 600
 ATTATCAAAA GAAGAAGGCG GACGTCACAC TCCATTCTTC 640
 25

2) INFORMATION FOR SEQ ID NO: 885

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

40 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

TGCCTCAAAC TCGTGAACAC ATCCTATTGT CTCGTCAAGT TGGTGTTCCT 50
 45 TACATCGTTG TATTCTTGAA CAAAGTAGAC ATGGTTGATG ACGAAGAATT 100
 ACTAGAATTA GTTGAAATGG AAGTTCGTGA CCTATTAACA GAATACGAAT 150
 TCCCTGGTGA CGATGTTTCT GTAGTTGCTG GATCAGCTTT GAAAGCTCTA 200
 GAAGGCGACG CTTCATACGA AGAAAAAATT CTTGAATTAA TGGCTGCAGT 250
 TGACGAATAC ATCCCAACTC CAGAACGTGA CAACGACAAA CCATTTCATGA 300
 50 TGCCAGTTGA AGACGTGTTT TCAATTACTG GACGTGGTAC TGTGCTTACA 350
 GGTTCGTGTTG AACGTGGACA AGTTCGCGTT GGTGACGAAG TTGAAGTTGT 400
 TGGTATTGCT GAAGAACTT CAAAAACAAC AGTTACTGGT GTTGAAATGT 450
 TCCGTAAATT GTTAGACTAC GCTGAAGCTG GAGACAACAT TGGTGCTTTA 500
 CTACGTGGTG TTGCACGTGA AGACATCCAA CGTGGACAAG TTTTAGCTAA 550
 55 ACCAGGTACA ATCACACCTC ATACAAAATT CTCTGCAGAA GTATACGTGT 600
 TGACAAAAGA AGAAGGTGGA CGTCATACTC CA 632

60 2) INFORMATION FOR SEQ ID NO: 886

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

15 CGGCCCAATG CCTCAAATC GTGAACACAT CCTATTGTCT CGTCAAGTTG 50
 GTGTTCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT GGTTGATGAC 100
 GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA 150
 ATACGAATTC CCTGGTGACG ATGTTCTGT AGTTGCTGGA TCAGCTTTGA 200
 20 AAGCTCTAGA AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG 250
 GCTGCAGTTG ACGAATACAT CCAACTCCA GAACGTGACA ACGACAAACC 300
 ATTCATGATG CCAGTTGAAG ACGTGTCTC AATTACTGGA CGTGGTACTG 350
 TTGCTACAGG TCGTGTGAA CGTGACAAG TTCGCGTTGG TGACGAAGTT 400
 GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTAGTGGTGT 450
 25 TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCTGGA GACAACATTG 500
 GTGCTTTACT ACGTGGTGT GCACGTGAAG ACATCCAACG TGGACAAGTT 550
 TTAGCTAAAC CAGGTACAAT CACACCTCAT ACAAATTCT CTGCAGAAGT 600
 ATACGTGTTG ACAAAGAAG AAGGTGGACG TCATACTCCA 640

30

2) INFORMATION FOR SEQ ID NO: 887

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

ATCCTGGTTT GCTCCGACG TGACGGCCCA ATGCCACAGA CCCGCGAGCA 50
 CATCCTGCTG GCCCGCCAAG TTGGCGTTCC ATACATCATC GTGTTCTTGA 100
 50 ACAAGTGCGA CCTGGTTGAC GACGCAGAAC TGCTGGAAC TGTGAAATG 150
 GAAGTGCGTG AATTGCTGTC GAAATACGAG TTCCCAGGCG ACGACGTACC 200
 AATCATCAAG GGTTCGGCAC GTATGGCGCT GGAAGGCAA GAAGGCGAGA 250
 TGGGCGTTGA CGCCATCATG CGTCTGGCCG ATGCACTGGA CAGCTACATC 300
 CCTACGCCAG AGCGCGCAGT CGATGGCGCC TTCCTGATGC CAGTGGAAGA 350
 55 CGTGTCTCTG ATCTCGGGTC GCGGTACCGT TGTGACCGGT CGTATCGAGC 400
 GCGGCGTGAT CAAGGTCGGC GAAGAGATCG AAATCGTCGG CATTATCGAC 450
 ACCGTCAAAA CCACTTGACG CGGCGTGGAA ATGTTCCGCA AGCTGCTGGA 500
 CCAGGGTCAA GCCGGCGACA ACGTTGGTCT GCTGCTGCGC GGCACCAAGC 550
 GTGAAGACGT ACAGCGTGGT CAGGTTCTGG CCAAGCCAGC GTCGATCAAG 600
 60 CCGCACAACC ACTTCACCGG CGAGATCTAC GTTCTGTCTGA AAGATGAAGG 650

CGGCCGTCAC	ACCCCGTTCT	TCAACAACATA	TCGTCCACAG	TTCTACTTCC	- 700
GTACGACTGA	CGTGACCGGT	TCGATCGAAC	TGCCAGCAGA	CAAAGAAATG	750
GTCATGCCAG	GCGACAACGT	GTCGATCACC	GTCAAGCTGA	TCAACCCGAT	800
CGCGAT					806

5

2) INFORMATION FOR SEQ ID NO: 888

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R503

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
25 CATAATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
TTTCCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
30 GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
CAGGCCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
35 AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCA		634

40 2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

55 TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
TTCGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTACTCGTGA	150
GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTGAGCTCG	200
60 AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTC	GACAGATGAA	CGAGCCCCCC	250

	GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
5	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

2) INFORMATION FOR SEQ ID NO: 890

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Penicillium marneffe*
- (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

25	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	TGTCTTCACT	100
	GGTGTGCGTG	AACGTACTCG	TGAGGGTAAC	GATTGTGACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTACGC	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCGGTGCCC	GTGCCCCTGT	CGCTCTTACT	250
30	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATTT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCGTATC	CCCTCTGCCG	TCGGTTACCA	GCCCACCCTT	400
	GCCGTCGACA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
	TTCCATCACC	TCCGTC				466

35

2) INFORMATION FOR SEQ ID NO: 891

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Paecilomyces lilacinus*
- (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

	AGGAGCTGAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
55	ACTGGTGTCTG	GTGAGCGTAC	CCGTGAGGGT	AACGATCTGT	ACCACGAAAT	100
	GCAGGAGACC	TCGGTCATTC	AGCTCGAGGG	CGAGTCTAAG	GTGGCCCTGG	150
	TCTTTGGTCA	GATGAACGAG	CCCCCGGGTG	CTCGTGCCCG	TGTCGCTCTT	200
	ACTGGTCTTA	CCGTCGCCGA	GTA CTTCCTG	GACCAGGAGG	GTCAGGATGG	250
	TTAGTTCTCG	TCCACTCATG	CCGAAACATG	TGCGTGTTCC	GAGGCTAATC	300
60	AACGTGCCAG	TGCTGCTTTT	CATCGACAAC	ATTTTCCGAT	TCACACAGGC	350

500